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GENCORE version 3.1.1.3

OM nucleic - nucleic search, using sw model

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Run on:      February 28, 2003, 19:58:51 ; Search time 45.0389 Seconds
            (without alignments)
            15700.357 Million cell updates
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Title: US-09-750-240-1

Perfect score:

Sequence: 1 atgtcatgggttagtggcct.....acaccggcggaaccgctgaa 314

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_101002:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	313	99.7	314	22	AA0808561		Human partial card
2	313	99.7	2127	19	AAV23246		Human adenylyl cycl
3	295.2	94.0	3549	22	AA0808563		Human cardiac aden
4	295.2	94.0	3552	22	AA0808567		Human cardiac aden
5	295.2	94.0	3562	22	AA0808568		Human modified car
6	295.2	94.0	4942	20	AA0X00461		Human type VI aden
7	227.4	72.4	4046	14	AAQ042525		Cardiac adenylyl c
8	199.2	63.4	5841	24	AB1399680		Mouse ischaemic c
9	198.2	63.1	4131	21	AAAS53923		Type VI adenylyl c

c	10	39.8	12.7	236303	22	ASL11614	Human genomic DNA
c	11	38.2	12.2	3050	22	AAO6036	Angiotensin conver
c	12	38.2	12.2	3174	21	AAO7370	Human ORF2925
c	13	38.2	12.2	3243	15	AAQ79401	Human NMDAR2 recep
c	14	38.2	12.2	3698	15	AAQ79400	Human NMDAR2 recep
c	15	38.2	12.2	4274	15	AAQ79407	Human NMDAR2 recep
c	16	38.2	12.2	4289	15	AAQ79405	Human NMDAR2 recep
c	17	38.2	12.2	4325	15	AAQ79404	Human NMDAR2 recep
c	18	38.2	12.2	4340	15	AAQ79372	Human N-methyl-D-a
c	19	38.2	12.2	4349	15	AAQ79406	Human NMDAR2 recep
c	20	38.2	12.2	4364	15	AAQ79403	Human NMDAR2 recep
c	21	38.2	12.2	160771	24	ABQ88179	Human osteoblast d
c	22	37.6	12.0	4046	14	AAQ42325	Cardiac adenylyl c
c	23	37.2	11.8	668	9	AAN60926	Longisporus trypsi
c	24	37.2	11.8	1438	18	AAAT91179	Human apoptosis pr
c	25	37	11.8	1700	21	AAAC69681	Novel human protei
c	26	36.8	11.7	5317	23	ABL17087	Drosophila melanog
c	27	36.8	11.7	5538	23	ABL19835	Drosophila melanog
c	28	36.8	11.7	9579	23	ABL17086	Drosophila melanog
c	29	36.8	11.7	9579	23	ABL19834	Drosophila melanog
c	30	36.6	11.7	1734	22	AAAD01196	Pseudorabies virus
c	31	36.6	11.7	3243	20	AAV82910	Human N-methyl-D-a
c	32	36.6	11.7	3243	21	AAAG95033	Human N-methyl-D-a
c	33	36.6	11.7	3243	21	AAAC38724	Human clone NMDA22
c	34	36.6	11.7	3243	24	ALA47377	Human NMDAR2C codi
c	35	36.6	11.7	3243	24	ABR05910	Human NMDA recepto
c	36	36.6	11.7	3698	20	AAV82909	Human N-methyl-D-a
c	37	36.6	11.7	3698	21	AAAG95032	Human N-methyl-D-a
c	38	36.6	11.7	3698	21	AAZ38723	Human clone NMDA22
c	39	36.6	11.7	3698	24	ALA47376	Human NMDAR2C codi
c	40	36.6	11.7	3698	24	ABT199189	Human NMDA recepto
c	41	36.6	11.7	4002	20	AAV82915	Human N-methyl-D-a
c	42	36.6	11.7	4002	21	AAAG95038	Human N-methyl-D-a
c	43	36.6	11.7	4002	21	AAZ38729	Human NMDAR2 subun
c	44	36.6	11.7	4002	24	AAAT47382	Human NMDAR2C codi
c	45	36.6	11.7	4002	24	ABT199194	Human NMDA2C enco

## ALIGNMENTS

## RESULT 1

AAD08561

UID AAD08561 standard; cDNA; 314 BP.

AAC AAD08561;

04-SEP-2001 (first entry)

Human partial cardiac adenylyl cyclase VI (ACVI) isoform #1 cDNA.

Human; cardiant; beta-adrenergic signalling protein; beta-ASP;

myocardium; gene therapy; beta-adrenergic receptor; beta-AR; adenylylcyclase; adenylylate cyclase; CAMP synthetase;

cardiac adenylylcyclase VI: ACVI isoform: beta-ASP transgene: ss

Homo sapiens

**XX**

**Key**

**Location/Qualifiers**

ETH	Key	Location/Qualifiers
ETH	CDS	1 312

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/ord= a

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/translate= (pos
#type=
/secto=

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include stop codon"
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XX 27-DEC-1999; 99US-0472667.
XX (RECC ) UNIV CALIFORNIA.
XX PI Hammond HK, Gao M;
XX DR WPI; 2001-418260/44.
XX P-PSDB; AAE04308.
XX Novel polynucleotide encoding a modified adenylcyclase polypeptide
XX useful for enhancing cardiac function in mammalian hearts, and for
XX treating heart disease, especially congestive heart failure -
XX Example 5; Page 114; 153pp; English.
XX The present invention relates to methods and compositions for enhancing
XX cardiac function in mammalian hearts by inserting transgenes encoding
XX beta-adrenergic signalling proteins (beta-ASP) which increase
XX beta-adrenergic responsiveness within the myocardium using in vivo
XX gene therapy. The beta-ASPs of the invention include beta-adrenergic
XX receptors (beta-AR), adenylcyclases (also referred as adenylcyclase,
XX adenylate cyclase and camp synthetase) and G-protein receptor kinase
XX (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function
XX in mammalian hearts and for treating heart disease, especially
XX congestive heart failure. The present cDNA sequence encodes human
XX partial cardiac adenylcyclase VI (ACVI) isoform which is used for
XX generating a third beta-ASP transgene, used in the exemplification
XX of the invention.
XX Sequence 314 BP; 60 A; 98 C; 108 G; 47 T; 1 other;
XX
XX Query Match 99.7%; Score 313; DB 22; Length 314;
XX Best Local Similarity 100.0%; Pred. No. 1.7e-69;
XX Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 ATGTGCTATATGAGTGGCTCTCTGCTCCCTAAAGTGGATGAACGGAAACACGCTGGGGT 60
DB 1 ATGTGCTATATGAGTGGCTCTCTGCTCCCTAAAGTGGATGAACGGAAACACGCTGGGGT 60
QY 61 GAACGCAATGGCGAGAAGGTTTCGGGGGCGCCGTGGCACTCGGGCAGGTGGCTTCGACG 120
DB 61 GAACGCAATGGCGAGAAGGTTTCGGGGGCGCCGTGGCACTCGGGCAGGTGGCTTCGACG 120
QY 121 CCCGCTATATGAGTGGCTCTCTGCTCCCTAAAGTGGATGAACGGAAACACGCTGGGGT 180
DB 121 CCCGCTATATGAGTGGCTCTCTGCTCCCTAAAGTGGATGAACGGAAACACGCTGGGGT 180
QY 181 CCTCGTATATGAGTGGCTCTCTGCTCCCTAAAGTGGATGAACGGAAACACGCTGGGGT 240
DB 181 CCTCGTATATGAGTGGCTCTCTGCTCCCTAAAGTGGATGAACGGAAACACGCTGGGGT 240
QY 241 GAACCTGGGGCTCGGGCAGTGGCCCTGGCTTCGAGATACCGAAGTGCACACGACCG 300
DB 241 GAACCTGGGGCTCGGGCAGTGGCCCTGGCTTCGAGATACCGAAGTGCACACGACCG 300
QY 301 GCGGGACCGCTGAA 314
DB 301 GCGGGACCGCTGAA 314
XX
RESULT 2
AAV23246
ID AAV23246 standard; cDNA; 2127 BP.
XX AC AAV23246;
XX 17-JUL-1998 (first entry)
XX Human adenylcyclase isoform VI encoding cDNA.
XX Human; adenylcyclase VI; AC-VI; beta-adrenergic signalling protein;
XX transgene; gene therapy; congestive heart failure; cardiac function;
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KW adenovirus; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 1..2127
XX FT /*tag= a
XX FT /product= "adenylcyclase isoform VI"
XX FT /transl_except= (pos:229..231,aa:Xaa)
XX FT /transl_except= (pos:315..317,aa:Xaa)
XX FT /note= "no stop codon given; Xaa = unknown"
XX FT misc_difference 315
XX FT /*tag= b
XX FT /note= "n indicates a gap of about 0.5 kb"
XX PN WQ9810085-A2.
XX PD 12-MAR-1998
XX PF 05-SEP-1997; 97WO-US15610.
XX PR 16-JUN-1997; 97US-0048933.
XX PR 05-SEP-1996; 96US-0708661.
XX PA (COLL-) COLLATERAL THERAPEUTICS.
XX PA (RECC ) UNIV CALIFORNIA.
XX PI Gao M, Hammond HK, Insel PA, Ping P, Post SR;
XX DR WPI; 1998-193633/17.
XX DR P-PSDB; AAW53345.
XX Vectors containing transgene(s) encoding beta-adrenergic signalling
XX proteins - useful for gene therapy of congestive heart failure
XX Claim 60; Fig 12A; 114pp; English.
XX The present sequence encodes human adenylcyclase isoform VI (AC-VI)
XX from the present invention. The present invention describes a
XX recombinant replication-defective viral particle (I) comprising a gene
XX encoding a beta-adrenergic signalling protein (beta-ASP) operably
XX linked to a promoter. Also described are: (1) a recombinant pro-viral
XX plasmid (Ia) comprising a gene encoding a beta-ASP, as above, operably
XX linked to a promoter and further comprising a replication-defective
XX viral genome; (2) a (mammalian) cell transfected with (I) or (Ia); (3)
XX an isolated polynucleotide comprising a sequence encoding a human
XX adenylcyclase isoform VI (AC-VI), or a variant having AC activity;
XX (4) a human AC-VI encoded by (3); (5) an isolated polynucleotide
XX sequence which hybridises at high stringency to (3); and (6) a vector
XX comprising the polynucleotide of (3). (I) can be used to form a
XX filtered adenovirus particle preparation. (I) is used to enhance
XX cardiac function in mammals.
XX Sequence 2127 BP; 421 A; 637 C; 615 G; 452 T; 2 other;
XX
XX Query Match 99.7%; Score 313; DB 19; Length 2127;
XX Best Local Similarity 100.0%; Pred. No. 2.2e-69;
XX Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 ATGTGCTATGTTAGTGGCTCTCTGCTCCCTAAAGTGGATGAACGGAAACACGCTGGGGT 60
DB 1 ATGTGCTATGTTAGTGGCTCTCTGCTCCCTAAAGTGGATGAACGGAAACACGCTGGGGT 60
QY 61 GAACGCAATGGCGAGAAGGTTTCGGGGGCGCCGTGGCACTCGGGCAGGTGGCTTCGACG 120
DB 61 GAACGCAATGGCGAGAAGGTTTCGGGGGCGCCGTGGCACTCGGGCAGGTGGCTTCGACG 120
QY 121 CCCGCTATATGAGTGGCTCTCTGCTCCCTAAAGTGGATGAACGGAAACACGCTGGGGT 180
DB 121 CCCGCTATATGAGTGGCTCTCTGCTCCCTAAAGTGGATGAACGGAAACACGCTGGGGT 180
QY 181 CCTCGGTCCTCGGCTGGCAGTACGCTTCATCCGAGGGGGCGGCCCAAGGCGCAAG 240
DB 181 CCTCGGTCCTCGGCTGGCAGTACGCTTCATCCGAGGGGGCGGCCCAAGGCGCAAG 240
XX
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Db 181 CCTGGTCCCTGGCAGGATGACGCTTCATCCGGAGGGGGCCCGCCANGCAAG 240  
QY 241 GAACTGGGGCTGGGGCAGTGGCCCTGGGCTTCGAAGATACCAAGTGAACAAGCACCG 300  
Db 241 GAACTGGGGCTGGGGCAGTGGCCCTGGGCTTCGAAGATACCAAGTGAACAAGCACCG 300  
QY 301 GCGGGACCGCTGAA 314  
Db 301 GCGGGACCGCTGAA 314

RESULT 3  
AAD08563  
ID AAD08563 standard; DNA; 3549 BP.  
XX  
AC AAD08563;  
XX  
DT 04-SEP-2001 (first entry)  
XX  
DE Human cardiac adenylylase VI (ACVI) isoform #1 DNA.  
XX  
KW Human; cardiac; beta-adrenergic signalling protein; beta-ASP;  
KW myocardium; gene therapy; beta-adrenergic receptor; beta-AR;  
KW adenylylase; adenylylase; adenylylase; adenylylase;  
KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;  
KW cardiac adenylylase VI; ACVI isoform; beta-ASP transgene; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
CDS 1..3504  
FT /\*tag= a  
FT /product= "Human cardiac adenylylase VI isoform #1"  
FT /EC\_number= "4.6.1.1"  
XX  
PN WO200148164-A2.  
XX  
PD 05-JUL-2001.  
XX  
PF 26-DEC-2000; 2000WO-US35411.  
XX  
PR 27-DEC-1999; 99US-0472667.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Hammond HK, Gao M;  
XX  
DR WPI; 2001-418260/44.  
DR P-PSDB; AAE04310.  
XX  
PT Novel polynucleotide encoding a modified adenylylase polypeptide  
PT useful for enhancing cardiac function in mammalian hearts, and for  
PT treating heart disease, especially congestive heart failure -  
XX  
XX Example 5; Page 122-129; 153pp; English.  
XX  
CC The present invention relates to methods and compositions for enhancing  
CC cardiac function in mammalian hearts by inserting transgenes encoding  
CC beta-adrenergic signalling proteins (beta-ASP) which increase  
CC beta-adrenergic responsiveness within the myocardium using in vivo  
CC gene therapy. The beta-ASPs of the invention include beta-adrenergic  
CC receptors (beta-AR), adenylylases (also referred as adenylylase,  
CC adenylylase and CAMP synthetase) and G-protein receptor kinase  
CC (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function  
CC in mammalian hearts and for treating heart disease, especially  
CC congestive heart failure. The present DNA sequence encodes human  
CC cardiac adenylylase VI (ACVI) isoform which is used for generating  
CC a third beta-ASP transgene, used in the exemplification  
XX  
SQ Sequence 3549 BP; 699 A; 1025 C; 1061 G; 764 T; 0 other;  
Query Match 94.0%; Score 295.2; DB 22; Length 3549;

Best Local Similarity 97.1%; Pred. No. 7.1e-65;  
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ATGTCATGTTTGTAGTGGCTCCCTGGTCCCTAAAGTGAAGCAAGCAAGCGCTGGGT 60  
Db 1 ATGTCATGTTTGTAGTGGCTCCCTGGTCCCTAAAGTGAAGCAAGCAAGCGCTGGGT 60  
QY 61 GAACGAATGGCAGAGCGTTCCGGCGCCGCTGGCACTCGGCAGGTGGCTTCTGCACG 120  
Db 61 GAACGAATGGCAGAGCGTTCCGGCGCCGCTGGCACTCGGCAGGTGGCTTCTGCACG 120  
QY 121 CCCGCTATATGAGCTCCCTCCGGGATGACAGCCAGCCACCCACCCCTGCGGGCCCC 180  
Db 121 CCCGCTATATGAGCTCCCTCCGGGATGACAGCCAGCCACCCACCCCTGCGGGCCCC 180  
QY 181 CCTCGGTGCCCCCTGGCAGGATGACGCTTCATCCGGAGGGGGCCCGCCANGCAAG 240  
Db 181 CCTCGGTGCCCCCTGGCAGGATGACGCTTCATCCGGAGGGGGCCCGCCANGCAAG 240  
QY 241 GAACTGGGGCTGGGGCAGTGGCCCTGGGCTTCGAAGATACCAAGTGAACAAGCACCG 300  
Db 241 GAACTGGGGCTGGGGCAGTGGCCCTGGGCTTCGAAGATACCAAGTGAACAAGCACCG 300  
QY 301 GCGGGACCG 309  
Db 301 GCGGGACCG 309

RESULT 4  
AAD08567  
ID AAD08567 standard; DNA; 3552 BP.  
XX  
AC AAD08567;  
XX  
DT 04-SEP-2001 (first entry)  
XX  
DE Human cardiac adenylylase VI (ACVI) isoform #2 DNA.  
XX  
KW Human; cardiac; beta-adrenergic signalling protein; beta-ASP;  
KW myocardium; gene therapy; beta-adrenergic receptor; beta-AR;  
KW adenylylase; adenylylase; adenylylase; adenylylase;  
KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;  
KW cardiac adenylylase VI; ACVI isoform; beta-ASP transgene; ds.  
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OS Homo sapiens.  
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FH Key Location/Qualifiers  
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FT /product= "Human cardiac adenylylase VI isoform #2"  
FT /EC\_number= "4.6.1.1"  
XX  
PN WO200148164-A2.  
XX  
PD 05-JUL-2001.  
XX  
PF 26-DEC-2000; 2000WO-US35411.  
XX  
PR 27-DEC-1999; 99US-0472667.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Hammond HK, Gao M;  
XX  
DR WPI; 2001-418260/44.  
DR P-PSDB; AAE04311.  
XX  
PT Novel polynucleotide encoding a modified adenylylase polypeptide  
PT useful for enhancing cardiac function in mammalian hearts, and for  
PT treating heart disease, especially congestive heart failure -  
XX  
XX Claim 6; Page 134-140; 153pp; English.  
XX

CC The present invention relates to methods and compositions for enhancing  
CC cardiac function in mammalian hearts by inserting transgenes encoding  
CC beta-adrenergic signalling proteins (beta-ASP) which increase  
CC beta-adrenergic responsiveness within the myocardium using in vivo  
CC gene therapy. The beta-ASPs of the invention include beta-adrenergic  
CC receptors (beta-AR), adenylyl cyclases (also referred as adenylylase,  
CC adenylyl cyclase and CAMP synthetase) and G-protein receptor kinase  
CC (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function  
CC in mammalian hearts and for treating heart disease, especially  
CC congestive heart failure. The present DNA sequence encodes human  
CC cardiac adenylyl cyclase VI (ACVI) isoform which is used for generating  
CC a fourth beta-ASP transgene, used in the exemplification  
CC of the invention.  
XX SQ Sequence 3552 BP; 686 A; 1037 C; 1068 G; 761 T; 0 other;

Query Match 94.0%; Score 295.2; DB 22; Length 3552;  
Best Local Similarity 97.1%; Pred. No. 7.1e-65;  
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ATGTCATGTTAGTGGCTCTCTGCTCCCTAAAGTGGATGAACGGAAACACGCTGGGGT 60  
|||||  
DB 1 ATGTCATGTTAGTGGCTCTCTGCTCCCTAAAGTGGATGAACGGAAACACGCTGGGGT 60  
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QY 61 GAACGCAATGGGCGAGAGGTTTCGGGGCCGCTGGCACTCGGGCAGGTGGCTTCTGCACG 120  
|||||  
DB 61 GAACGCAATGGGCGAGAGGTTTCGGGGCCGCTGGCACTCGGGCAGGTGGCTTCTGCACG 120  
|||||

QY 121 CCCCCTATATAGCTGCTCCGGGATGCAGAGCCACCCAGCCCGCCCTCGGGCCCC 180  
|||||  
DB 121 CCCCCTATATAGCTGCTCCGGGATGCAGAGCCACCCAGCCCGCCCTCGGGCCCC 180  
|||||

QY 181 CCTCGGTGCCCCCTGGCAGGATGACGCTTCATCCGGAGGGGGCCGCAAGGGCAAG 240  
|||||  
DB 181 CCTCGGTGCCCCCTGGCAGGATGACGCTTCATCCGGAGGGGGCCGCAAGGGCAAG 240  
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QY 241 GAACCTGGGGCTCGGGCGAGTGGCCCTGGGCTTCGAAGATACCGAAGTGACAACGACCG 300  
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DB 241 GAGCTGGGGCTCGGGCGAGTGGCCCTGGGCTTCGAGGATACCGAAGTGACAACGACCG 300  
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QY 301 GCGGGACCG 309  
| || ||  
DB 301 GCGGGACCG 309

RESULT 5  
AAD08568  
ID AAD08568 standard; cDNA; 3582 BP.  
XX  
AC AAD08568;  
XX  
DT 04-SEP-2001 (first entry)  
XX  
DE Human modified cardiac adenylyl cyclase VI (ACVI) isoform cDNA.  
XX  
KW Human; cardiant; beta-adrenergic signalling protein; beta-ASP;  
KW myocardium; gene therapy; beta-adrenergic receptor; beta-AR;  
KW adenylyl cyclase; adenylylase; CAMP synthetase;  
KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;  
KW cardiac adenylyl cyclase VI; ACVI isoform; beta-ASP transgene; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT CDS 22..3525  
FT /\*tag= a  
FT /product= "Human modified cardiac ACVI isoform"  
XX  
PN WO200148164-A2.  
XX  
PD 05-JUL-2003

PF 26-DEC-2000; 2000WO-US35411.  
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PR 27-DEC-1999; 99US-0472667.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Hammond HK, Gao M;  
XX  
DR WPI; 2001-418260/44.  
XX  
DR P-FSDB; AAE04312.  
XX  
PT Novel polynucleotide encoding a modified adenylyl cyclase polypeptide  
PT useful for enhancing cardiac function in mammalian hearts, and for  
PT treating heart disease, especially congestive heart failure -  
XX  
XX Claim 4; Page 143-150; 153pp; English.

CC The present invention relates to methods and compositions for enhancing  
CC cardiac function in mammalian hearts by inserting transgenes encoding  
CC beta-adrenergic signalling proteins (beta-ASP) which increase  
CC beta-adrenergic responsiveness within the myocardium using in vivo  
CC gene therapy. The beta-ASPs of the invention include beta-adrenergic  
CC receptors (beta-AR), adenylyl cyclases (also referred as adenylylase,  
CC adenylyl cyclase and CAMP synthetase) and G-protein receptor kinase  
CC (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function  
CC in mammalian hearts and for treating heart disease, especially  
CC congestive heart failure. The present cDNA sequence encodes human  
CC modified cardiac adenylyl cyclase VI (ACVI) isoform which is used for  
CC generating a beta-ASP transgene, used in the exemplification of the  
CC invention.

XX SQ Sequence 3582 BP; 703 A; 1036 C; 1067 G; 776 T; 0 other;

Query Match 94.0%; Score 295.2; DB 22; Length 3582;  
Best Local Similarity 97.1%; Pred. No. 7.1e-65;  
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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|||||  
DB 22 ATGTCATGTTAGTGGCTCTCTGCTCCCTAAAGTGGATGAACGGAAACACGCTGGGGT 81  
|||||

QY 61 GAACGCAATGGGCGAGAGGTTTCGGGGCCGCTGGCACTCGGGCAGGTGGCTTCTGCACG 120  
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DB 82 GAACGCAATGGGCGAGAGGTTTCGGGGCCGCTGGCACTCGGGCAGGTGGCTTCTGCACG 141  
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QY 121 CCCCCTATATAGCTGCTCCGGGATGCAGAGCCACCCAGCCCGCCCTCGGGCCCC 180  
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DB 142 CCCCCTATATAGCTGCTCCGGGATGCAGAGCCACCCAGCCCGCCCTCGGGCCCC 201  
|||||

QY 181 CCTCGGTGCCCCCTGGCAGGATGACGCTTCATCCGGAGGGGGCCGCAAGGGCAAG 240  
|||||  
DB 202 CCTCGGTGCCCCCTGGCAGGATGACGCTTCATCCGGAGGGGGCCGCAAGGGCAAG 261  
|||||

QY 241 GAACCTGGGGCTCGGGCGAGTGGCCCTGGGCTTCGAAGATACCGAAGTGACAACGACCG 300  
|||||  
DB 262 GAGCTGGGGCTCGGGCGAGTGGCCCTGGGCTTCGAGGATACCGAAGTGACAACGACCG 321  
|||||

QY 301 GCGGGACCG 309  
| || ||  
DB 322 GCGGGACCG 330

RESULT 6  
AAX00461  
ID AAX00461 standard; cDNA; 4942 BP.  
XX  
AC AAX00461;  
XX  
DT 21-MAY-1999 (first entry)  
XX  
DE Human type VI adenylyl cyclase cDNA.  
XX  
KW Adenylyl cyclase type VI; human; hAC6; therapy; diagnosis; ds.

XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
XX FT 145...3651  
XX FT /\*tag= a  
XX PN WO9901547-A1.  
XX PD 14-JAN-1999.  
XX PF 01-JUL-1998; 98WO-US13694.  
XX PR 01-JUL-1997; 97US-0886550.  
XX PR 01-JUL-1997; 97US-0070904.  
XX PA (CORT-) COR THERAPEUTICS INC.  
XX PI Tomlinson JA;  
XX DR WPI: 1999-106049/09.  
XX DR P-PSDB; AAW30599.  
XX PT Newly isolated and purified human type VI adenylyl cyclase (hac6)  
XX PT polypeptide - useful for identifying potential therapeutic agents  
XX PT that modulate hac6 activity, and for the diagnosis of  
XX PT hac6-associated diseases and disorders  
XX PS Claim 3; Fig 1A-I; 42pp; English.  
XX CC This DNA sequence encodes human type VI adenylyl cyclase (hac6, see  
CC AAW30599) that is expressed mainly in the heart and brain. hac6 has  
CC a similar putative structure to other adenylyl cyclase isoforms  
CC but, like type V, is distinguishable in that it has a larger  
CC N-terminus and a relatively shorter C-terminus as it lacks the C2b  
CC region. hac6 cDNA was initially isolated from a human heart cDNA  
CC library using an adenylyl cyclase PCR fragment as probe. It was  
CC used to design primers that were used in a PCR-based RACE to obtain  
CC the full-length cDNA sequence. The invention relates to the hac6  
CC gene, methods for the recombinant production of purified hac6 and  
CC the proteins made by these methods, antibodies against hac6,  
CC vectors, probes and host cells (especially HEK-293) transformed by  
CC genes encoding polypeptides having hac6 activity, along with hac6  
CC diagnostic and therapeutic uses for these various reagents. hac6  
CC can be used as a tool to screen for agonists and antagonists that  
CC stimulate/inhibit hac6. Such compounds have therapeutic utility  
CC in treating diseases caused by aberrant activity of this enzyme,  
CC and diseases whose symptoms can be ameliorated by stimulating or  
CC inhibiting the activity of hac6.  
XX SQ Sequence 4942 BP; 953 A; 1404 C; 1512 G; 1073 T; 0 other;  
Query Match 94.0%; Score 295.2; DB 20; Length 4942;  
Best Local Similarity 97.1%; Pred. No. 7.5e-65;  
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 1 ATGTCATGTTAGTGGCTCTCTGTCCTAAAGTGGATGAACGGAACACGCTGGGT 60  
DB 145 ATGTCATGTTAGTGGCTCTCTGTCCTAAAGTGGATGAACGGAACACGCTGGGT 204  
QY 61 GAACGCAATGGGAGGAGGTTTCGGCGCCCTGTCGACCTCGGCGAGGTCTCTGCACG 120  
DB 205 GAACGCAATGGGAGGAGGTTTCGGCGCCCTGTCGACCTCGGCGAGGTCTCTGCACG 264  
QY 121 CCCCCTATATAGTGGCTCTCGGGATGAGAGCCACCCAGGCCCTCTGGGGCCCC 180  
DB 265 CCCCCTATATAGTGGCTCTCGGGATGAGAGCCACCCAGGCCCTCTGGGGCCCC 324  
QY 181 CCTCGGTGCCCTGGCAGGATGACGCTTCATCCGGAGGGGGCCCAAGGAGGCAAG 240  
DB 325 CCTCGGTGCCCTGGCAGGATGACGCTTCATCCGGAGGGGGCCCAAGGAGGCAAG 384  
QY 241 GAACTGGGGCTGCGGGAGTGGCCCTGTTGAGATACCGAAGTACGACGACACCG 300

DB 385 GAGCTGGGCTGGGGACGTGGCCCTGGGCTTCGAGGATACCGAGGTGACACGACGCG 444  
QY 301 GCGGGACCG 309  
DB 445 GCGGGACG 453  
RESULT 7  
AAQ42525  
ID AAQ42525 standard; DNA; 4046 BP.  
XX AC AAQ42525;  
XX 14-SEP-1993 (first entry)  
XX DE Cardiac adenylyl cyclase gene.  
XX KW Regulation; cardiac function; heart; heart failure; ss.  
XX OS Canis familiaris.  
XX FH Key Location/Qualifiers  
XX FT CDS 131..3627  
XX FT /\*tag= a  
XX PN EP543137-A  
XX PD 26-MAY-1993.  
XX PF 12-OCT-1992; 92EP-0117374.  
XX PR 18-NOV-1991; 91US-0793961.  
XX PA (AMCY ) AMERICAN CYANAMID CO.  
XX PI Ishikawa Y;  
XX DR WPI: 1993-168873/21.  
XX DR P-PSDB; AAR37309.  
XX PT Purified DNA encoding cardiac adenylyl cyclase - useful to screen  
XX for cpds. which stimulate activity of the cyclase  
XX PS Claim 1; Fig 2; 34pp; English.  
XX CC A canine heart cDNA library was constructed in lambda gt10 and was  
CC screened with a 970 bp AatI-HincII fragment from type I adenylyl  
CC cyclase cDNA probe (encodes the first cytoplasmic domain of adenylyl  
CC cyclase, which has significant homology to other previously known  
CC types of adenylyl cyclase). One positive clone, of 5.4 kb was obtd.  
CC Positive colonies were subcloned into pUC18 and further subcloned  
CC and sequenced bidirectionally. The 5.4 kb clone was used to  
CC rescreen the library and on overlapping clone contg. the 5' end of  
CC the gene was isolated. Together the two clones cover the complete  
CC canine cardiac adenylyl cyclase gene. The gene is suspected of  
CC being involved in the regulation of cardiac function and it is thought  
CC that decreased activity of adenylyl cyclase in the heart may be a  
CC major factor in the development of heart failure. Thus the adenylyl  
CC cyclase gene is useful to screen cpds. which stimulate the activity  
CC of the cyclase.  
XX SQ Sequence 4046 BP; 743 A; 1206 C; 1254 G; 843 T; 0 other;  
Query Match 72.4%; Score 227.4; DB 14; Length 4046;  
Best Local Similarity 89.5%; Pred. No. 7.7e-48;  
Matches 256; Conservative 0; Mismatches 27; Indels 3; Gaps 1;  
QY 1 ATGTCATGTTAGTGGCTCTCTGTCCTAAAGTGGATGAACGGAACACGCTGGGT 60  
DB 131 ATGTCGTTAGTGGCTCTCTGTCCTAAAGTGGATGAACGGAACACGCTGGGT 190  
QY 61 GAACGCAATGGGAGGAGGTTTCGGCGCCCTGTCGACCTCGGCGAGGTCTCTGCACG 120

Db 191 GAACCAATGGCAGACGCT---CCACGCCGCGGACTCGACCAAGTGTCTTCGACG 247  
 Qy 121 CCACGCTATATGAGTGTCTTCGGGATGAGAGCCACCCACCCACCCCTCGGGCCCC 180  
 Db 248 CCCGCTATATGAGTGTCTTCGGGATGAGAGCCACCCACCCACCCCTCGGGCCCC 307  
 Qy 181 COTCGGTCCTCGCAGATGACCCCTTCATCCGGAGGGCGGCCANGCAAGGCAAG 240  
 Db 308 COTCGGTCCTCGCAGATGAGCCCTTCATCCGGAGGGCGGCCANGCAAGGCAAG 367  
 Qy 241 GAACCTGGGGCTCGGGCAGTGGCCCTGGGCTTCGAGATACCGAAG 286  
 Db 368 GAGCTGGGGCTCGGGCAGTGGCCCTGGGCTTCGAGGACACTGAGG 413

## RESULT 8

AB199680  
 ID AB199680 standard; cDNA; 5841 BP.  
 AC AB199680;  
 XX  
 DT 07-MAR-2002 (first entry)  
 DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:716.  
 KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;  
 KW vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.  
 OS Mus musculus.

XX WO200108188-A2

XX PD 22-NOV-2001.

XX PF 18-MAY-2001; 2001WO-JP04192.

XX PR 18-MAY-2000; 2000JP-0145977.

XX PA (UYN1-) UNIV NIHON SCHOOL JURIDICAL PERSON.

XX PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;

XX DR WPI; 2002-034733/04.

XX PF P-PSDB; ABB57257.

XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring  
 PT expression levels of particular genes defined in the specification or  
 PT by determining the expression profile of a gene group comprising these  
 PT genes -

XX Claim 2; Page 1771-1780; 2690pp; English.

XX The present invention describes a method for examining ischaemic  
 CC conditions, comprising measuring the expression levels of particular  
 CC genes (I) in a test sample or determining the expression profile of a  
 CC gene group in the sample comprising genes selected from (I). The method  
 CC is useful for examining the ischaemic condition (e.g. compressive  
 CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring  
 CC expression levels of particular genes (ABI99202 to ABI99912, encoding  
 CC the protein sequences in ABB57020 to ABB57374) or by determining the  
 CC expression profile of a gene group comprising these genes. The  
 CC expression levels or expression profiles produced by these genes are  
 CC used as an indicator when screening for ischaemic condition-improving  
 CC drugs or therapeutics for ischaemic diseases. ABI99913 and ABI99914  
 CC represent PCR primers for a mouse ischaemic condition related sequence,  
 CC which are used in the exemplification of the present invention.

XX Sequence 5841 BP; 1214 A; 1558 C; 1673 G; 1396 T; 0 other;

XX Query Match 63.4%; Score 199.2; DB 24; Length 5841;

XX Best Local Similarity 82.3%; Pred. No. 9.8e-41;

XX Matches 241; Conservative 0; Mismatches 49; Indels 3; Gaps 1;

Qy 1 ATGTCATGTTTAGTGGCTCTCTGTCCTTAAAGTGGATGAACGGAAACACGCTTGGGT 60  
 Db 96 ATGTCATGTTTAGTGGCTCTCTGTCCTTAAAGTGGATGAACGGAAACACGCTTGGGT 155  
 Qy 61 GAACCAATGGCAGACGCTTCGGGATGAGAGCCACCCACCCACCCCTCGGGCCCC 120  
 Db 156 GAACCAATGGCAGACGCTTCGGGATGAGAGCCACCCACCCACCCCTCGGGCCCC 212  
 Qy 121 CCCGCTATATGAGTGTCTTCGGGATGAGAGCCACCCACCCACCCCTCGGGCCCC 180  
 Db 213 CCTCGCTACATGAGCTCGCTCAAGATCGGAGCCACCCACCCACCTCTGACGCTCAC 272  
 Qy 181 COTCGGTCCTCGCAGATGACCCCTTCATCCGGAGGGCGGCCANGCAAGGCAAG 240  
 Db 273 ACTCGGTCCTCGCAGATGAGCCCTTCATCAGGAGGGCGGCCANGGAGGTGTG 332  
 Qy 241 GAACCTGGGGCTCGGGCAGTGGCCCTGGGCTTCGAGATACCGAAGTGAACAC 293  
 Db 333 GAGCTGGGGCTCGGGCAGTGGCCCTGGGCTTCGAGGACACTGAGGTGACCAC 385

## RESULT 9

AAA53923  
 ID AAA53923 standard; cDNA; 4131 BP.

XX AAA53923;

XX DT 03-JAN-2001 (first entry)  
 XX

XX Type VI adenyllyl cyclase coding sequence.

XX Adenyllyl cyclase; type I; type II; recombinant; enzyme; cAMP;  
 KW cyclic AMP; adenosine monophosphate; screening; stimulation;  
 KW inhibition; treatment; cholera; pituitary tumour; heart failure;  
 KW ischaemia; endocrine disorder; cell necrosis;  
 KW pseudohypoparathyroidism; endocrine deficiency; human; ss.

XX Homo sapiens.

XX Key Location/Qualifiers  
 XX CDS 14..3556

XX FT /\*tag= a

XX FT /product= Type VI adenyllyl cyclase

XX US6107076-A.

XX PD 22-AUG-2000.

XX PF -04-OCT-1996; 96US-0726214.

XX PR 04-OCT-1995; 95US-0005498.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX Gilman AG, Tang W;

XX WPI; 2000-578539/54.

XX DR P-PSDB; AAB02010.

XX Novel soluble mammalian polypeptide composition comprising adenyllyl  
 PT cyclase activity for screening stimulators and inhibitors of adenyllyl  
 PT cyclase, is activated by Galpha

XX Disclosure; Columns 75-78; 73pp; English.

XX A recombinant Adenyllyl cyclase is described which lacks membrane  
 CC bound domains. Separation and purification of the recombinant  
 CC enzyme is much easier compared with wild type enzymes and the  
 CC recombinant enzyme is more stable than the wild type enzyme which  
 CC allows easier screening of compounds that stimulate and inhibit  
 CC Adenyllyl cyclase activity. The recombinant adenyllyl cyclase comprises  
 CC a chimera of adenyllyl cyclase C\_1 and C\_2 domains linked covalently.

FT	intron	79225..101022
FT		/*tag= f
FT		/number= 4
FT	exon	101023..101144
FT		/*tag= g
FT		/number= 5
FT	intron	101145..113377
FT		/*tag= h
FT		/number= 5
FT	exon	113378..113560
FT		/*tag= i
FT		/number= 6
FT	intron	113561..115985
FT		/*tag= j
FT		/number= 6
FT	exon	115986..116183
FT		/*tag= k
FT		/number= 7
FT	intron	116184..135707
FT		/*tag= l
FT		/number= 7
FT	exon	135708..135836
FT		/*tag= m
FT		/number= 8
FT	intron	135837..146471
FT		/*tag= n
FT		/number= 8
FT	exon	146472..146628
FT		/*tag= o
FT		/number= 9
FT	intron	146629..148761
FT		/*tag= p
FT		/number= 9
FT	exon	148762..148883
FT		/*tag= q
FT		/number= 10
FT	intron	148884..150044
FT		/*tag= r
FT		/number= 10
FT	exon	150045..150254
FT		/*tag= s
FT		/number= 11
FT	intron	150255..153815
FT		/*tag= t
FT		/number= 11
FT	exon	153816..154031
FT		/*tag= u
FT		/number= 12
FT	intron	154032..158580
FT		/*tag= v
FT		/number= 12
FT	exon	158581..158802
FT		/*tag= w
FT		/number= 13
FT	intron	158803..173982
FT		/*tag= x
FT		/number= 13
FT	exon	173983..174177
FT		/*tag= y
FT		/number= 14
FT	intron	174178..181006
FT		/*tag= z
FT		/number= 14
FT	exon	181007..181129
FT		/*tag= aa
FT		/number= 15
FT	intron	181130..183612
FT		/*tag= ab
FT		/number= 15
FT	exon	183613..183800
FT		/*tag= ac
FT		/number= 16
FT	intron	183801..185152

Query Match 63.1%; Score 198.2; DB 21; Length 4131;  
Best Local Similarity 79.9%; Pred. NO. 1.7e-40;  
Matches 246; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

RESULT 10  
AAS11614/c  
ID AAS11614 standard; DNA; 236303 BP.

DT 24-OCT-2001 (first entry)

KW CRIM-1; Human; human chromosome 2p21-16.3; ophthalmological;  
 KW neuroprotective; renal; osteopathic; dental; vulnery; immunogen;  
 KW antibody; gene therapy; neurodegenerative disease; eye disorder;  
 KW cataract; bone morphogenic protein; BMG; renal disease; bone abnormality;  
 KW tooth abnormality; wound; ds.

Key	Location/Qualifiers
AA	
FH	

FT	intron	33278..77746	/number= 2
FT			

```
FT exon 1147..17989
FT /*taq= c
```

```
FT /*tag= d
FT /number= 3
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**FF** /number= 4

```
FT      /*tag= ad
FT      /number= 16
FT      exon      185153..187765
FT      /*tag= ae
FT      /number= 17
XX      WO200138519-A1.
XX      31-MAY-2001.7
XX      24-NOV-2000.--2000WO-AU01435.
XX      26-NOV-1999; 99AU-0004348.
XX      (UYQU ) UNIV QUEENSLAND.
XX      Little M, Yamada T, Holmes G, Georgas K, Kolle G, Wilkinson L;
XX      WPI; 2001-343951/36.
XX      Nucleic acids from human chromosome 2p21-16.3 and the encoded peptide,
XX      especially cataract formation
XX      Claim 4; Fig 3; 16pp; English.
XX      The invention relates to nucleic acids from human chromosome 2p21-16.3
XX      and the encoded peptide (and mouse and chicken orthologues) that
XX      comprises a PEGCEPLP group, an insulin-like growth factor binding protein
XX      (IGFBP)-like domain, cysteine-rich domains, an RGD (undefined) group
XX      and a transmembrane domain. The protein, e.g. CRIM1, interacts with
XX      peptides of the transforming growth factor superfamily. A composition
XX      comprising an expression construct comprising the nucleic acids of the
XX      invention or a mimetic which antagonises or mimics an activity of a CRIM1
XX      polypeptide may be used in a method for modulating the biological
XX      activity of a polypeptide of the bone morphogenic protein (BMP) family.
XX      In this way they may be used to prevent or treat an eye disease,
XX      especially cataract formation. They may also be used to treat
XX      neurodegenerative diseases, renal and kidney disease, bone and tooth
XX      abnormalities, wounds and skin damage, e.g. by use of the nucleic acid in
XX      gene therapy by using antibodies directed against CRIM1 polypeptides.
XX      The present sequence is a Human genomic DNA containing exons 2-17 of
XX      the CRIM1 gene.
XX      Sequence 236303 BP; 70199 A; 46544 C; 47996 G; 71563 T; 1 other;
XX      Query Match 12.7%; Score 39.8; DB 22; Length 236303;
XX      Best Local Similarity 55.4%; Pred. No. 1.8;
XX      Matches 77; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
XX      QY 78 GCGTTCCGGCGCCGTCGACACCTCGGCAGGTGGCTTCTGCACGCCCGCGCTATATGAGCTG 137
XX      Db 234505 GAGTCGGGGGCGCGCGGAGTGGCGGAGACCTTCCCTACCTCCGCGCGGAGTCCCGGCC 234446
XX      QY 138 CCTCCGGGATGACAGACCCACCCAGCCACCCCTCGGGGCCCGCCCTCGGTGCCCTGGCA 197
XX      Db 234445 CCTACGGCGCGAGCTCCCTCCCTCGCGCCCTCTCCGCCGACGCGGAGTCCCGGCC 234386
XX      QY 198 GGATGACGCTTCATCCCG 216
XX      Db 234385 TCTCGCCCTCTTCTCCCG 234367
XX      RESULT 11
XX      AAS06036/c
XX      ID AAS06036 standard; DNA; 3050 BP.
XX      AC AAS06036;
XX      DT 12-SEP-2001 (first entry)
XX      DE Angiotensin converting enzyme (ACEV) splice variant DNA #36.
XX
```

```
KW      Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
KW      granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
KW      platelet-derived endothelial cell growth factor; cardiovascular disease;
KW      cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; ds;
KW      vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;
KW      myocardial infarction; coronary arterial thrombosis; renal disease;
KW      diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
KW      multiple sclerosis; immune complex nephritis; deep vein thrombosis;
KW      nonaroidotic pulmonary granulomatous disease; endothelial abnormality;
KW      vascular disorder; asbestosis.
XX      Homo sapiens.
OS      Homo sapiens.
XX      WO200136632-A2.
XX      25-MAY-2001.
XX      17-NOV-2000; 2000WO-IL00766.
XX      17-NOV-1999; 99IL-0132978.
XX      10-DEC-1999; 99IL-013455.
XX      (COMP-) COMPUGEN LTD.
XX      Levine Z, David A, Azar I, Khosravi R, Bernstein J;
XX      WPI; 2001-336004/35.
XX      P-PSDB; AAU02936.
XX      Novel alternative splicing variants e.g. variant of angiotensin
XX      converting enzyme (ACEV), useful in identifying candidate compounds
XX      capable of binding to the variant and to detect anti-variant antibodies
XX      Claim 1; Page 335-336; 519pp; English.
XX      The sequence represents a DNA encoding an angiotensin converting enzyme
XX      splice variant (ACEV) polypeptide. The polypeptides of the invention
XX      include variants of granulocyte colony stimulating factor receptor,
XX      glucagon, interleukin 6, platelet-derived endothelial cell growth factor,
XX      cyclin-dependent kinase inhibitor 1C, cellular tumour antigen P53, and
XX      vasoactive intestinal polypeptide receptor 2. The polypeptides and their
XX      associated nucleic acids are useful for identification of binding
XX      molecules and detection of candidate compounds capable of binding the
XX      molecules. The sequences of the invention can be used in the treatment
XX      and diagnosis of various disorders including cardiovascular diseases such
XX      as arteriosclerosis, myocardial infarction and coronary arterial
XX      thrombosis, renal diseases such as diabetic nephropathy, muscular
XX      diseases such as hypertrophy, immune disorders such as immune complex
XX      nephritis, multiple sclerosis, cancer, sarcoidosis, nonaroidotic
XX      pulmonary granulomatous diseases such as asbestosis and vascular
XX      pathologies involving an endothelial abnormality such as deep vein
XX      thrombosis.
XX      Sequence 3050 BP; 520 A; 1032 C; 942 G; 555 T; 1 other;
XX      Query Match 12.2%; Score 38.2; DB 22; Length 3050;
XX      Best Local Similarity 46.0%; Pred. No. 2.4;
XX      Matches 127; Conservative 0; Mismatches 149; Indels 0; Gaps 0;
XX      QY 13 AGTGGCCTCTCTGTCCTCTAAAGTGGATGAACGGAACACAGCCTGGGTGAACGCAATGGG 72
XX      Db 2623 AGAGGCCCCCGCGCGGAGAGCCAGGAGCCGTGGTGGACAGGTGGAAGGTGAGGA 2564
XX      QY 73 CAGAAGCGTTCCGGCGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACGCCCGCGCTATATG 132
XX      Db 2563 CAGACAGGCCCCCAGCAAAATGGCAGGTGGCGGTGGCAGGACGACGCTGCTCTG 2504
XX      QY 133 AGCTGCTCCGGGATGCAGAGCCACCGACCCACCCCTCGCGGCCCGCCCTCGGTGCCCC 192
XX      Db 2503 TGCTCCAGGCGGGGGCGCCCTCGCTGCGCCCTCTGTCAGGCGCTCCCGGTAGATCGGC 2444
XX      QY 193 TGGCAGGATGACGCTTTCATCCGGAGGGCGGCCCCANGCAGGCAAGCACTGGGGCTG 252
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DB 2443 AAGCACATCGACTGCGCTGGCCAGCGCTGCAGGCCGAGTGGCGTGGCGGGCG 2384  
QY 253 CGGCGAGTGGCCCTGGCTTCAGAGATACCGAGTG 288  
DB 2383 CAGCGGGGCGGTGTCACCGAGCGGCGAGCGTG 2348  
RESULT 12  
AAC77370  
ID AAC77370 standard; cDNA; 3174 BP.  
XX AAC77370;  
XX  
DT 08-FEB-2001 (first entry)  
XX  
DE Human ORFX ORF7925 polynucleotide sequence SEQ ID NO:5849.  
XX  
KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;  
KW vulnery; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;  
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;  
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;  
KW hypotensive; dermatological; immunosuppressive; antinflammatory;  
KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;  
KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;  
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;  
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;  
KW cholesterol ester storage; systemic lupus erythematosus; infection;  
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;  
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;  
KW bone damage; cartilage damage; antinflammatory disease; coagulation;  
KW thrombosis; contraceptive; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200058473-A2.  
XX  
PD 05-OCT-2000.  
XX  
PF 31-MAR-2000; 2000WO-US08621.  
XX  
PR 31-MAR-1999; 99US-0127607.  
PR 02-APR-1999; 99US-0127636.  
PR 05-APR-1999; 99US-0127728.  
PR 30-MAR-2000; 2000US-0540763.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Shinkets RA, Leach M;  
XX  
XX WPI; 2000-602362/57.  
DR P-PSDB; AAB43161.  
XX  
PT Novel nucleic acids and peptides derived from open reading frame X,  
PT useful for treating e.g. cancers, proliferative disorders,  
PT neurodegenerative disorders and cardiovascular disease -  
XX  
XX Claim 5; Page 5022-5024; 5507pp; English.  
XX  
XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,  
XX which represent the human ORFX open reading frames 1 to 3161. The ORFX  
XX sequences have activities such as: cytostatic; hepatotropic; vulnery;  
XX antipsoriatic; antiparkinsonian; nootropic; neuroprotective;  
XX osteopathic; anticonvulsant; antiarthritic; immunosuppressant;  
XX immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;  
XX antidiabetic; hypotensive; dermatological; antirheumatic; antithyroid;  
XX antinflammatory; antibacterial; antiviral; antifungal; antirheumatic;  
XX antithyroid; and antianemic. The sequences can be used for determining  
XX the presence of or predisposition to, or preventing or treating  
XX pathological conditions associated with an ORFX-associated disorder. The  
XX nucleic acids can be used to express ORFX proteins in gene therapy  
XX vectors. The proteins and nucleic acids may be used to treat cancers,  
XX proliferative disorders, neurodegenerative disorders, osteoarthritis,

CC graft vs host disease, cardiovascular disease, diabetes mellitus,  
CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus  
CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,  
CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,  
CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,  
CC nocturnal haemoglobinuria, antinflammatory disease; to enhance  
CC coagulation; to inhibit thrombosis; and as a contraceptive.  
XX  
SQ Sequence 3174 BP; 737 A; 897 C; 904 G; 620 T; 16 other;  
Query Match 12.2%; Score 38.2; DB 21; Length 3174;  
Best Local Similarity 53.4%; Pred. No. 2.4;  
Matches 79; Conservative 0; Mismatches 69; Indels 0; Gaps 0;  
QY 137 GCCTCGGGATGAGAGCCACCCACCCCTGGGGGCGGCGGCTGGCTGGCGGCG 196  
DB 2049 GCGGCTCCAGGCTGAGTTCACCCACACAGCTCCCGGCTGCCACATTTGCCCTCAGC 2108  
QY 197 AGGATGAGCGCTTTCATCCGGAGGGGGCCGANGCAGAGGCAAGAACTGGGCTGGCGG 256  
DB 2109 AGGGCTTAGTCCAGTTCCTGGGTGGGGGCGAGCAGTGCCTTGGGACAGTGGCCAGG 2168  
QY 257 CAGTGGCGCTGGCTTGGAGATACCGA 284  
DB 2169 CAGGCGCGCTGGCTAGCTGGACATCCA 2196  
RESULT 13  
AAQ79401/c  
ID AAQ79401 standard; cDNA; 3243 BP.  
XX AAQ79401;  
XX  
DT 06-JUL-1995 (first entry)  
XX  
DE Human NMDAR2 receptor subunit clone NMDA24 gene.  
XX  
KW N-methyl-D-aspartate; receptor; human; NMDA; cation-selective; channel;  
KW glutamate; hippocampus; rat; pcdnal; NMDA receptor; antagonist; ds.  
XX  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
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FT /note= "11 bp insertion found in clone NMDA24"  
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PN WO9424284-A.  
XX  
PD 27-OCT-1994.  
XX  
PF 20-APR-1994; 94WO-US04387.  
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PR 20-APR-1993; 93US-0052449.  
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XX  
PI Daggett LP, Ellis SB, Liaw CW, Lu C;  
XX  
XX WPI; 1994-341863/42.  
DR P-PSDB; AAR66059.  
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PT Isolated DNA encoding a human N-methyl-D-aspartate receptor  
PT subunit - used as probes in the identification and isolation of  
PT nucleic acids encoding related receptor subunits.  
XX  
PS Claim 11; Page 99-104; 156pp; English.





RESULT 15  
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XX 06-JUL-1995 (first entry)  
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XX Human NMDAR2 receptor subunit clone NMDAR2C-delta15-delta51 gene.  
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XX N-methyl-D-aspartate; receptor; human; NMDA; cation-selective; channel;  
KW glutamate; hippocampus; rat; pcDNA1; NMDA receptor; antagonist; ds.  
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XX  
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FT these bases"  
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XX 27-OCT-1994.  
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XX 20-APR-1994; 94WO-US04387.  
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XX 20-APR-1993; 93US-0052449.  
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XX (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.  
XX  
XX Daggett LP, Ellis SB, Liaw CW, Lu C;  
XX  
XX WPI; 1994-341863/42.  
XX P-PSDB; AAR66065.  
XX  
XX Isolated DNA encoding a human N-methyl-D-aspartate receptor  
PT subunit - used as probes in the identification and isolation of  
PT nucleic acids encoding related receptor subunits.  
XX  
XX Claim 11; Page 99-104; 156pp; English.  
XX  
XX The nucleotide sequence of the novel N-methyl-D-aspartate (NMDA)  
CC receptor 2C (NMDAR2C) gene clone NMDAR2C-delta15-delta51. This clone  
CC contains bases 1-1959, 1975-2350 and 2402-4068 of the complete NMDAR2C  
CC sequence (AAQ79372). The variant differs from the full length sequence by  
CC a 15 bp deletion of bases 1960-74 and a 51 bp deletion of bases  
CC 2351-2401. A series of variants (AAQ79403-7) of the NMDAR2C receptor  
CC were constructed, by recombination, based on the sequence of the 4 basic  
CC clones: NMDA21 (AAQ79399), NMDA22 (AAQ79400), NMDA24 (AAQ79401) and  
CC NMDA26 (AAQ79402). The NMDA receptor contains two subunits: subunit R1  
CC (AAQ79370) and subunit R2 selected from the subunits 2A (AAQ79375), 2B  
CC (AAQ79377), 2C and 2D (AAQ79378). The receptor forms part of a family of  
CC NMDA receptors which have cation-selective channels and bind glutamate  
CC and NMDA. The expression of the genes allows the reconstruction of the  
CC NMDA receptor. The complete receptor can be used to identify compounds  
CC which bind or are antagonistic to the human NMDA receptor.  
XX  
XX Sequence 4274 BP; 713 A; 1462 C; 1331 G; 768 T; 0 other;  
SQ

Search completed: February 28, 2003, 23:38:23  
Job time : 77.0389 secs

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QY 193 TGGCAGGATGACGCTTCATCCGAGGGCGGCGCCCAAGCAAGGGCAAGAACTGGGGCTG 252  
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QY 253 CGGGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTG 288  
Db 3445 CAGGCGGGCGGTGCACCCAGCGGCGAGAGCTG 3410



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model  
Run on: February 28, 2003, 21:13:01 ; Search time 539.139 Seconds  
(without alignments)  
16949.756 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 4109280

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Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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  - 4: gb.om.\*
  - 5: gb.ov.\*
  - 6: gb.pat.\*
  - 7: gb.ph.\*
  - 8: gb.pl.\*
  - 9: gb.pr.\*
  - 10: gb.ro.\*
  - 11: gb.sts.\*
  - 12: gb.sy.\*
  - 13: gb.un.\*
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  - 15: em.ba.\*
  - 16: em.fun.\*
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  - 19: em.mu.\*
  - 20: em.om.\*
  - 21: em.or.\*
  - 22: em.ov.\*
  - 23: em.pat.\*
  - 24: em.ph.\*
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  - 26: em.ro.\*
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  - 36: em.htg\_mam.\*
  - 37: em.htg\_vrt.\*
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  - 39: em.htgo\_hum.\*
  - 40: em.htgo\_mus.\*
  - 41: em.htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	313	99.7	314	6	ARI74471	Sequence ARI74471
2	313	99.7	314	6	AXI89757	Sequence AXI89757
3	295.2	94.0	3549	6	ARI74473	Sequence ARI74473
4	295.2	94.0	3549	6	AXI89761	Sequence AXI89761
5	295.2	94.0	3552	6	AXI89766	Sequence AXI89766
6	295.2	94.0	3582	6	AXI89768	Sequence AXI89768
7	295.2	94.0	5877	9	AB007882	Sequence AB007882
8	295.2	94.0	205248	2	ACI17498	Homo sapi ACI17498
9	293.6	93.5	193283	2	AC021647	Homo sapi AC021647
10	292	93.0	6463	9	AF250226	Homo sapi AF250226
11	283.2	90.2	171945	2	AC025557	Homo sapi AC025557
12	227.4	72.4	4046	4	DOGADENCYC	Canis faml M94568
13	227.4	72.4	4046	4	DOGADENCYC	Sequence I29958
14	199.2	63.4	5841	6	AX305965	Sequence AX305965
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16	199.2	63.4	139619	2	AC074028	Mus muscu AC074028
17	198.2	63.1	4131	6	ARI06659	Sequence ARI06659
18	198.2	63.1	4131	10	RATADCYB	Sequence M96160
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20	196.6	62.6	151706	2	ACI29405	Rattus norv ACI29405
21	186.2	59.3	108689	2	AC096835	Rattus no AC096835
22	178	56.7	3465	10	MUSADNLCYC	Mus musculu M96653
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26	43.2	13.8	139513	2	AP005659	Oryza sat AP005659
27	43	13.7	318696	2	ACI02955	Rattus no ACI02955
28	42	13.4	74721	2	AC096161	Rattus no AC096161
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31	41.6	13.2	126868	2	ACI28569	Rattus no ACI28569
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36	41	13.1	69282	2	AC040912	Homo sapi AC040912
37	41	13.1	186187	2	ACI10369	Rattus no ACI10369
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ALIGNMENTS

RESULT 1  
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LOCUS ARI74471  
DEFINITION Sequence 1 from patent US 6306830.  
ACCESSION ARI74471  
VERSION ARI74471.1  
KEYWORDS GI:17914791  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 314)  
AUTHORS Hammond,H.Kirk., Insel,P.A., Ping,P., Post,S.R. and Gao,M.  
TITLE Gene therapy for congestive heart failure  
JOURNAL Patent: US 6306830-A 1 23-OCT-2001;  
FEATURES Location/Qualifiers

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ACCESSION	AX189757											
VERSION	AX189757.1 GI:15143133											
KEYWORDS												
SOURCE	human.											
ORGANISM	Homo sapiens											
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;											
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.											
TITLE	1 (bases 1 to 314)											
JOURNAL	Hammond, H. K. and Gao, M.											
FEATURES	Gene therapy for congestive heart failure											
Location/Qualifiers												
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ACCESSION	ARI74473											
VERSION	ARI74473.1 GI:17914793											
KEYWORDS	Unknown.											
SOURCE	Unknown.											
ORGANISM	Unclassified.											
REFERENCE	1 (bases 1 to 3549)											
AUTHORS	Hammond, H. Kirk., Insel, P. A., Ping, P., Post, S. R. and Gao, M.											
TITLE	Gene therapy for congestive heart failure											
JOURNAL	Patent: US 6306830-A 5 23-Oct-2001;											
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VERSION	AX189761.1 GI:15143135											
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SOURCE	Homo sapiens											
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;											
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.											
TITLE	1 (bases 1 to 314)											
JOURNAL	Hammond, H. K. and Gao, M.											
FEATURES	Gene therapy for congestive heart failure											
Location/Qualifiers												
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Sodergren,E., Sonalke,T., Sparks,A., Stanley,H., Stone,H.,  
 Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,  
 Tansley,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,  
 Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R., Wang,Q.,  
 Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,  
 Williams,G., Williamson,A., Wleczek,R., Wooden,S., Worley,K.,  
 Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,  
 Weinstein,G. and Gibbs,R.  
 Direct Submission  
 Unpublished  
 2 (bases 1 to 205248)  
 Worley,K.C.  
 Direct Submission  
 Submitted (10-APR-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 3 (bases 1 to 205248)  
 Worley,K.C.  
 Direct Submission  
 Submitted (31-JUL-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 On Jul 29, 2002 this sequence version replaced gi:21956504.  
 ----- Genome Center  
 Center: Baylor College of Medicine  
 Web site: <http://www.hgsc.bcm.tmc.edu/>  
 Drafting Center Code: WUGSC  
 Contact: hgsc-help@bcm.tmc.edu  
 ----- Project Information  
 Center project name: HEAU  
 Center clone name: RP11-422021  
 ----- Summary Statistics  
 Sequencing vector: Plasmid;  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.990329  
 Consensus quality: 216840 bases at least Q40  
 Consensus quality: 220255 bases at least Q30  
 Consensus quality: 222408 bases at least Q20  
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 \* NOTE: Estimated insert size may differ from sequence length  
 (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 20 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
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 \* 2026 2125: gap of unknown length  
 \* 2126 4437: contig of 2312 bp in length  
 \* 4438 4537: gap of unknown length  
 \* 4538 6633: contig of 2096 bp in length  
 \* 6634 6733: gap of unknown length  
 \* 6734 9148: contig of 2415 bp in length  
 \* 9149 9248: gap of unknown length  
 \* 9249 11635: contig of 2387 bp in length  
 \* 11636 11735: gap of unknown length  
 \* 11736 13780: contig of 2045 bp in length  
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 \* 16898 16997: gap of unknown length  
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 \* 23015 23114: gap of unknown length  
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 \* 25346 25446: gap of unknown length  
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\* 35864 35963: gap of unknown length  
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 Db 168879 GAGCTGGGGCTGGCGGCGAGTGGCCCTGGGGCTTCGAGGATACCGAGGTGACAACGACACG 168820  
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 KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_FULLTOP.  
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 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 193283)  
 AUTHORS  
 Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,  
 Alsbrooks,S.L., Amaraturge,H.C., Are,J.R., Ayale,M., Banks,T.,  
 Barbaria,J., Benton,J., Binage,K., Blankenburg,K., Bonnin,D.,  
 Bouay,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,  
 Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,  
 Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,  
 Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,

Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulsegue, H., Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, G., Minal, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Ogih, M., Okuwonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rivers, M., Rojas, A., Rojubokan, I., Roife, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shoostari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Tang, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstein, G., and Gibbs, R.

Direct Submission  
Unpublished  
2 (bases 1 to 193283)  
Worley, K.C.  
Submitted (19-JAN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 193283)  
Worley, K.C.  
Direct Submission  
Submitted (09-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On Apr 28, 2002 this sequence version replaced gi:15809061.  
----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: HAAF  
Center clone name: RP11-455122  
----- Summary Statistics  
Sequencing vector: Plasmid;  
Sequencing vector: M13;  
Chemistry: Dye-terminator Big Dye; 2% of reads  
Chemistry: Dye-terminator Big Dye; 98% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 219180 bases at least Q40  
Consensus quality: 233400 bases at least Q30  
Consensus quality: 243367 bases at least Q20  
Estimated insert size: 209025; sum-of-ctgts estimation  
Quality coverage: 10x in Q20 bases; sum-of-ctgts estimation  
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\* NOTE: Estimated insert size may differ from sequence length  
(see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
consists of 8 contigs. The true order of the pieces  
is not known and their order in this sequence record is

\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
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KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE



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thyroid tissues
Biochim. Biophys. Acta 1493 (1-2), 279-283 (2000)
20435313
PUBMED
10978539
2 (bases 1 to 6463)
Wicker, R., Gascon Catalan, A., Caillex, A.-F., Starenki, D.,
Stengel, D., Sarasin, A. and Suarez, H.G.
Direct Submission
TITLE
JOURNAL
(28-MAR-2000) Lab Etude des Relations - Instabilite
genetique et Cancer
CNS IFR 1221, 7 rue Guy Moquet, Villejuif 94801, France
CNRS IFR 1221, 7 rue Guy Moquet, Villejuif 94801, France
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Matches 298; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
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DB 695 ATGTCATGTTTAGTGGCTCTCTGTCCTTAAGTGGATGAACGGAACACACCCCTGGGGC 754
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Db 79261 GCGGGACCG 79253
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## RESULT 12

## DOGADENCYC

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## FEATURES

## Source

## Location/Qualifiers

## 1..4046

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## /db\_xref="taxon:9615"

## /tissue\_type="cardiac muscle"

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## Best Local Similarity 89.5%; Pred. No. 6.2e-41;

## Matches 256; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

## Qy 1 ATGTCATGGTTTACTGGCTCCTAAAGTGGATGAACGAAACACAGCCTGGGGT 60

## Db 131 ATGTCGTTGGTTTACTGGCTCCTAAAGTGGATGAACGAAACACAGCCTGGGGT 190

## Qy 61 GAACGCAATGGCAGAACGTTCCGGCGCGCTGGCACTCGGGCAGGTGGCTTCTGCACG 120

## Db 191 GAACGCAATGGCAGAACGTTCCGGCGCGCTGGCACTCGGGCAGGTGGCTTCTGCACG 247

## Qy 121 CCCGCTATATAGCTGCCTCCGGGATGCAGAGCCACCAGCCGCCACCCCTCGGGGCCCC 180

## Db 248 CCCGCTATATAGCTGCCTCCGGGATGCAGAGCCACCAGCCGCCACCCCTCGGGGCCCC 307

## Qy 181 CCTCGGTCCCTCGGAGGATGACGCTTCATCCGGAGGGCGGCCCGCANGAGGCAAG 240

## Db 308 CCTCGGTCCCTCGGAGGATGACGCTTCATCCGGAGGGCGGCCCGCANGAGGCAAG 367

## Qy 241 GAACCTGGGCTGGCGGAGTGGCCCTGGGCTTCGAAGATACCGAAG 286



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Best Local Similarity 82.3%; Pred. No. 1.le-34;
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Db 96 ATGTCATGCTTTAGTGGCTCCTGCTTCCAAAGTGGATGACGGAACACAGCCTGGGGG 155
QY 61 GAACGCAATGGCGAGAAGCGTTTCGGGGGCCGCTGCGACTCGGGGAGGTGGCTTCTGCACG 120
Db 156 GAACGCAATGGCGACAGCG---CCACGCCACGCGAATCGAGCCAGTGGCTTCTGCACA 212
QY 121 CCCCCTATATGAGTGGCTCGGGGATGAGAGCCACCCACCCCTGCGGGCCCC 180
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Db 273 ACTCGGTGCCCTGGCAGGATGAAGCCTTATCAGGAGGGGGGGCCCGGGCAGGGGTGTG 332
QY 241 GAACCTGGGCTGCGGGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTGACAAAC 293
Db 333 GAGCTGGGGCTGCGGTCACTGGCCTTGGGTTTGACGACACTGAGGTGACCAC 385
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Job time : 710.139 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 28, 2003, 22:03:11 ; Search time 7.69093 Seconds  
(without alignments)  
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Perfect score: 314  
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Scoring table: IDENTITY\_NUC  
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Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: /cgn2.6/ptodata/1/ina/6B\_COMB.seq:\*  
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6: /cgn2.6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	295.2	94.0	3549	US-09-008-097-5	Sequence 5, Appl
3	295.2	94.0	4942	US-09-474-076-1	Sequence 1, Appl
4	227.4	72.4	4046	US-07-793-961A-1	Sequence 1, Appl
5	227.4	72.4	4046	US-08-240-357-1	Sequence 1, Appl
6	198.2	63.1	4131	US-08-726-214-11	Sequence 11, Appl
7	38.6	12.3	6503	US-09-404-650-12	Sequence 12, Appl
8	37.6	12.0	4046	US-07-793-961A-1	Sequence 1, Appl
9	37.6	12.0	4046	US-08-240-357-1	Sequence 1, Appl
10	37.2	11.8	668	5498529-5	Patent No. 5498529
11	37.2	11.8	1438	US-08-828-069-5	Sequence 5, Appl
12	37.2	11.8	1438	US-08-828-683A-5	Sequence 5, Appl
13	36.6	11.7	3243	US-08-231-193A-44	Sequence 44, Appl
14	36.6	11.7	3243	US-08-486-273A-44	Sequence 44, Appl
15	36.6	11.7	3243	US-08-480-474-44	Sequence 44, Appl
16	36.6	11.7	3243	US-08-480-474-44	Sequence 44, Appl
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18	36.6	11.7	3243	US-08-940-035A-44	Sequence 44, Appl
19	36.6	11.7	3243	US-08-935-105A-44	Sequence 44, Appl
20	36.6	11.7	3698	US-09-648-797-44	Sequence 44, Appl
21	36.6	11.7	3698	US-08-231-193A-43	Sequence 43, Appl
22	36.6	11.7	3698	US-08-486-273A-43	Sequence 43, Appl
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C 29	36.6	11.7	4002	3	US-08-480-474-53	Sequence 53, Appl
C 30	36.6	11.7	4002	3	US-08-940-086A-53	Sequence 53, Appl
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C 33	36.6	11.7	4002	4	US-09-648-797-53	Sequence 53, Appl
C 34	36.6	11.7	4017	2	US-08-231-193A-49	Sequence 49, Appl
C 35	36.6	11.7	4017	2	US-08-486-273A-49	Sequence 49, Appl
C 36	36.6	11.7	4017	3	US-08-480-474-49	Sequence 49, Appl
C 37	36.6	11.7	4017	3	US-08-940-086A-49	Sequence 49, Appl
C 38	36.6	11.7	4017	4	US-08-940-035A-49	Sequence 49, Appl
C 39	36.6	11.7	4017	4	US-08-935-105A-49	Sequence 49, Appl
C 40	36.6	11.7	4017	4	US-09-648-797-49	Sequence 49, Appl
C 41	36.6	11.7	4053	2	US-08-231-193A-47	Sequence 47, Appl
C 42	36.6	11.7	4053	2	US-08-486-273A-47	Sequence 47, Appl
C 43	36.6	11.7	4053	3	US-08-480-474-47	Sequence 47, Appl
C 44	36.6	11.7	4053	3	US-08-940-086A-47	Sequence 47, Appl
C 45	36.6	11.7	4053	4	US-08-940-035A-47	Sequence 47, Appl

ALIGNMENTS

RESULT 1  
US-09-008-097-1  
; Sequence 1, Application US/09008097  
; Patent No. 6306830  
; GENERAL INFORMATION:  
; APPLICANT: Hammond, H. Kirk  
; APPLICANT: Insel, Paul A.  
; APPLICANT: Ping, Peipei  
; APPLICANT: Post, Steven R.  
; APPLICANT: Gao, Meihua  
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE  
; TITLE OF INVENTION: HEART FAILURE  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FORSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/008,097  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dylan, Tyler M  
; REGISTRATION NUMBER: 37,612  
; REFERENCE/DOCKET NUMBER: 22000-20567.21  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-813-5600  
; TELEFAX: 650-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 314 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Coding Sequence  
; LOCATION: 1...312  
; OTHER INFORMATION:

US-09-008-097-1

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Query Match          99.7%; Score 313; DB 4; Length 314;
Best Local Similarity 100.0%; Pred. No. 7.1e-71;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTCATGTTTAGTGGCTCTCTGGTCCCTAAAGTGGATGAACGGAAACAGCCTGGGGT 60
   |||||||
Db 1 ATGTCATGTTTAGTGGCTCTCTGGTCCCTAAAGTGGATGAACGGAAACAGCCTGGGGT 60

QY 61 GAACGCAATGGGAGAGGCTTCGGCGGCGCTGGGACCTCGGCGAGGTGCTTCTGCACG 120
   |||||||
Db 61 GAACGCAATGGGAGAGGCTTCGGCGGCGCTGGGACCTCGGCGAGGTGCTTCTGCACG 120

QY 121 CCCCCTATATGAGCTGCTCCGGGATGAGAGCCACCCAGCCCTCGCGGCCCC 180
   |||||||
Db 121 CCCCCTATATGAGCTGCTCCGGGATGAGAGCCACCCAGCCCTCGCGGCCCC 180

QY 181 CTTGGTGGCCCTGGCAGGATGACGCTTCATCTCGGAGGGGGGCCCAAGGCGCAAG 240
   |||||||
Db 181 CTTGGTGGCCCTGGCAGGATGACGCTTCATCTCGGAGGGGGGCCCAAGGCGCAAG 240

QY 241 GAACGCAATGGGAGAGGCTTCGGCGGCGCTGGGACCTCGGCGAGGTGCTTCTGCACG 300
   |||||||
Db 241 GAACGCAATGGGAGAGGCTTCGGCGGCGCTGGGACCTCGGCGAGGTGCTTCTGCACG 300
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RESULT 2

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US-09-008-097-5
; Sequence 5, Application US/09008097
; Patent No. 6306830
; GENERAL INFORMATION:
; APPLICANT: Hammond, H. Kirk
; APPLICANT: Insel, Paul A.
; APPLICANT: Ping, Peipei
; APPLICANT: Post, Steven R.
; APPLICANT: Gao, Meihua
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE
; HEART FAILURE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/008,097
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dylan, Tyler M
; REGISTRATION NUMBER: 37,612
; REFERENCE/DOCKET NUMBER: 22000-20567.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 3549 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...3501
; OTHER INFORMATION:
US-09-008-097-5
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Query Match          94.0%; Score 295.2; DB 4; Length 3549;
Best Local Similarity 97.1%; Pred. No. 3.4e-66;
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ATGTCATGTTTAGTGGCTCTCTGGTCCCTAAAGTGGATGAACGGAAACAGCCTGGGGT 60
   |||||||
Db 1 ATGTCATGTTTAGTGGCTCTCTGGTCCCTAAAGTGGATGAACGGAAACAGCCTGGGGT 60

QY 61 GAACGCAATGGGAGAGGCTTCGGCGGCGCTGGGACCTCGGCGAGGTGCTTCTGCACG 120
   |||||||
Db 61 GAACGCAATGGGAGAGGCTTCGGCGGCGCTGGGACCTCGGCGAGGTGCTTCTGCACG 120

QY 121 CCCCCTATATGAGCTGCTCCGGGATGAGAGCCACCCAGCCCTCGCGGCCCC 180
   |||||||
Db 121 CCCCCTATATGAGCTGCTCCGGGATGAGAGCCACCCAGCCCTCGCGGCCCC 180

QY 181 CTTGGTGGCCCTGGCAGGATGACGCTTCATCTCGGAGGGGGGCCCAAGGCGCAAG 240
   |||||||
Db 181 CTTGGTGGCCCTGGCAGGATGACGCTTCATCTCGGAGGGGGGCCCAAGGCGCAAG 240

QY 241 GAACGCAATGGGAGAGGCTTCGGCGGCGCTGGGACCTCGGCGAGGTGCTTCTGCACG 300
   |||||||
Db 241 GAACGCAATGGGAGAGGCTTCGGCGGCGCTGGGACCTCGGCGAGGTGCTTCTGCACG 300

QY 301 GCGGGACCG 309
   || || ||
Db 301 GCGGGACCG 309
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RESULT 3

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US-09-474-076-1
; Sequence 1, Application US/09474076
; Patent No. 6465237
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, James E.
; APPLICANT: COR Therapeutics, Inc.
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
; CYCLASE
; FILE REFERENCE: 44481-5028-01-US
; CURRENT APPLICATION NUMBER: US/09/474,076
; CURRENT FILING DATE: 1999-12-12
; PRIOR APPLICATION NUMBER: PCT/US98/13694
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/070,904
; PRIOR FILING DATE: 1997-07-01
; PRIOR APPLICATION NUMBER: 08/886,550
; PRIOR FILING DATE: 1997-07-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4942
; TYPE: DNA
; ORGANISM: human type VI adenylyl cyclase
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (145)..(3648)
US-09-474-076-1
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Query Match          94.0%; Score 295.2; DB 4; Length 4942;
Best Local Similarity 97.1%; Pred. No. 3.5e-66;
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ATGTCATGTTTAGTGGCTCTCTGGTCCCTAAAGTGGATGAACGGAAACAGCCTGGGGT 60
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RESULT 4
US-07-793-961A-1
; Sequence 1, Application US/07793961A
; Patent No. 5334521
; GENERAL INFORMATION:
; APPLICANT: Yoshihiro Ishikawa
; TITLE OF INVENTION: Cloning and Character-
; TITLE OF INVENTION: ization of a Cardiac Adenylyl Cyclase
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Alan M. Gordon
; ADDRESSEE: American Cyanamid Company
; STREET: 1937 West Main Street,
; STREET: P.O. Box 60
; CITY: Stamford
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06904
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: ASCII from DW4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/793,961A
; FILING DATE: 19911118
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gordon, Alan M.
; REGISTRATION NUMBER: 30,637
; REFERENCE/DOCKET NUMBER: 31,705
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203 321 2719
; TELEFAX: 203 321 2971
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4046 base pairs listed
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-793-961A-1

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: ASCII from DW4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/793,961A
; FILING DATE: 19911118
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gordon, Alan M.
; REGISTRATION NUMBER: 30,637
; REFERENCE/DOCKET NUMBER: 31,705
; TELEPHONE: 203 321 2719
; TELEFAX: 203 321 2971
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4046 base pairs listed
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-07-793-961A-1

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Query Match 12.0%; Score 37.6; DB 1; Length 4046;
Best Local Similarity 49.2%; Pred. No. 0.52;
Matches 97; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 90 CCGTGGCACTCGGGCAGGTGGCTTCTGCACGCCCCCGCTATATGAGCTGCTCGGGGATGC 149
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 462 CCGGGGGTCACTGAGGGCCACCTCCAGCTGCCCAACCGCTGACATGGCTCAGTGTCC 403

QY 150 AGAGCCACCCAGCCGCCCTCGGGGCCCCCTCGGTGCCCTGGCAGGATGACGCCCTT 209
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 402 TCGAAGCCAGGGCCAGCCGCCAGCCAGCTCGGTGCCCTGGCGGGGCTCTC 343

QY 210 CATCCGGAGGGCGGCCCAAGCAAGAACTGGGGCTGCGGGCAGTGGCCCTGGG 269
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 342 CGGATGAAGGCTCATCTCTGCCAGGGCCACCGAGGGGGAGCCGACGGGTGGGACTGGG 283

QY 270 CTTCAAGATACCGAG 286
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 282 GGCTGCGCATCCGGAG 266

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RESULT 9
US-08-240-357-1/c
; Sequence 1, Application US/08240357
; Patent No. 5578481
; GENERAL INFORMATION:
; APPLICANT: Ishikawa, Yoshihiro
; TITLE OF INVENTION: Cloning and Characterization of a
; TITLE OF INVENTION: Cardiac Adenyllyl Cyclase
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/240,357
; FILING DATE: 10-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gordon, Alan M.
; REGISTRATION NUMBER: 30,637
; REFERENCE/DOCKET NUMBER: 31,705-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3244
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4046 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 131..3625
; US-08-240-357-1

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Query Match 12.0%; Score 37.6; DB 1; Length 4046;
Best Local Similarity 49.2%; Pred. No. 0.52;
Matches 97; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 90 CCGTGGCACTCGGGCAGGTGGCTTCTGCACGCCCCCGCTATATGAGCTGCTCGGGGATGC 149
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 462 CCGGGGGTCACTGAGGGCCACCTCCAGCTGCCCAACCGCTGACATGGCTCAGTGTCC 403

QY 150 AGAGCCACCCAGCCGCCCTCGGGGCCCCCTCGGTGCCCTGGCAGGATGACGCCCTT 209
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 402 TCGAAGCCAGGGCCAGCCGCCAGCCAGCTCGGTGCCCTGGCGGGGCTCTC 343

QY 210 CATCCGGAGGGCGGCCCAAGCAAGAACTGGGGCTGCGGGCAGTGGCCCTGGG 269
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 342 CGGATGAAGGCTCATCTCTGCCAGGGCCACCGAGGGGGAGCCGACGGGTGGGACTGGG 283

QY 270 CTTCAAGATACCGAG 286
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 282 GGCTGCGCATCCGGAG 266

```

```

RESULT 10
5498529-5
; Patent No. 5498529
; APPLICANT: BERKA, THOMAS R.; FERNWALD, JAMES A.; CORNIAK,
; JOSEFINA G.; ROSENBERG, MARTIN; STRICKLER, JAMES E.; TAYLOR, DEAN P.
; TITLE OF INVENTION: PROTEIN PROTEASE INHIBITORS FROM
; STREPTOMYCES
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,506
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 894,167
; FILING DATE: 03-JUN-1992
; APPLICATION NUMBER: 346,119
; FILING DATE: 16-FEB-1989
; APPLICATION NUMBER: 897,245
; FILING DATE: 18-AUG-1986
; SEQ ID NO: 5
; LENGTH: 668
5498529-5

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Query Match 11.8%; Score 37.2; DB 6; Length 668;
Best Local Similarity 49.4%; Pred. No. 0.49;
Matches 126; Conservative 0; Mismatches 121; Indels 8; Gaps 1;

QY 57 GGGTGAACCAATGGCAGAAAGGTTTCGGGGCGCCCTGGCAGTTCGGGCGAGGTGCTTCG 116
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 130 GGATGCACACAATGCGGAACACCGCGCTGGGCGACCCACCTCGCCCTCAGGCCACCG 189

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QY 117 CAGCGCCGCTATATGAGTGGCTCCGGGATGAGAGCCACCCAGCCACCCCTGCGGG 176  
Db 190 CGGTCTGCG-----GACCCCTCACCGAGCGCGCTCGCCACCCCGCGCTGCTGG 241  
QY 177 CCCCCCTGGTCCCTGGCAGGATGAGCCCTTATCCGGAGGGGCGGCCCAAGCAAGG 236  
Db 242 GGCCTCGCTCTACGCCCTCGGCGCTGGCTGCTACCGCTCGCGCCACGCGCACAAAGCGCGC 301  
QY 237 CAAGGAACCTGGGCTCGGGGAGTGGCCCTGGCTTCCGAAGATACCGAAGTGACAAACGAC 296  
Db 302 CCCCCGCGCGCTCGCGGCGGTACCCCTGAATGCGCGCCGAGCGGCTCCGGGAACCCA 361  
QY 297 ACCGGCGGACCGCT 311  
Db 362 TCCGCGCGCGNGCNT 376

RESULT 11  
US-08-928-069-5/c  
; Sequence 5, Application US/08928069  
; Patent No. 6462176  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; TITLE OF INVENTION: Apo-3 POLYPEPTIDE  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/928,069  
; FILING DATE: 11-Sep-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/026943  
; FILING DATE: 09/23/1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Marschang, Diane L.  
; REGISTRATION NUMBER: 35,600  
; REFERENCE/DOCKET NUMBER: P1052R1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5416  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1438 base pairs  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
US-08-928-069-5

Query Match 11.8%; Score 37.2; DB 4; Length 1438;  
Best Local Similarity 47.6%; Pred. No. 0.55;  
Matches 108; Conservative 0; Mismatches 119; Indels 0; Gaps 0;  
QY 78 CGGTTCCGGCGCGCTGACCTCGGCGAGTGGCTTCTGCACGCCCGCTATATGAGCTG 137  
Db 392 GCGCGCGCTGCTCCATAGCCCTCCGACGGGGCCCGAGGGGTTCCCGGCTCCGTCCTC 333  
QY 138 CTTCCGGGATGAGAGCCACCGCCACCCCTCGCGGCCCGCTCGGTGCCCTGCGCA 197  
Db 332 TGCCGCTGCTGTTCCGCTTACAGCCCGCGCCGCGCGCGCGCGCGCTCGAGA 273  
QY 198 GGATGAGCCCTTATCCCGAGGGGGCGCCANGCAAGGCAAGGAGTGGGCTCGGGC 257  
Db 272 AGGGCCCGCTTATCCCGAGGGGGGAGGCGGCGCGCGCGCGCGCGCTCGAGCA 213  
QY 258 AGTGGCCCTGCGCTCGAAGATACCGAAGTGACACGACACCGCGCG 304  
Db 212 GTGCCCCCTCTGCTCGGCGCTAGACCTGAGCTCAATTAGCGCGCAGCGG 166

Db 272 AGGCGCCCGCTGCGGGCGGGGAGGGGCGGCCCGAGCCCAACCGAGTCCGACGAC 213  
QY 258 AGTGGCCCTGCGCTCGAAGATACCGAAGTGACACGACACCGCGCG 304  
Db 212 GTGCCCCCTCTGCTCGGCGCTAGACCTGAGCTCAATTAGCGCGCAGCGG 166  
RESULT 12  
US-08-828-683A-5/c  
; Sequence 5, Application US/08828683A  
; Patent No. 6469144  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/828,683A  
; FILING DATE: 31-Mar-1997  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/625328  
; FILING DATE: 1-Apr-1996  
; APPLICATION NUMBER: 08/710802  
; FILING DATE: 23-Sep-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Marschang, Diane L.  
; REGISTRATION NUMBER: 35,600  
; REFERENCE/DOCKET NUMBER: P1007P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5416  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1438 base pairs  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-08-828-683A-5

Query Match 11.8%; Score 37.2; DB 4; Length 1438;  
Best Local Similarity 47.6%; Pred. No. 0.55;  
Matches 108; Conservative 0; Mismatches 119; Indels 0; Gaps 0;  
QY 78 CGGTTCCGGCGCGCTGACCTCGGCGAGTGGCTTCTGCACGCCCGCTATATGAGCTG 137  
Db 392 GCGCGCGCTGCTCCATAGCCCTCCGACGGGGCCCGAGGGGTTCCCGGCTCCGTCCTC 333  
QY 138 CTTCCGGGATGAGAGCCACCGCCACCCCTCGCGGCCCGCTCGGTGCCCTGCGCA 197  
Db 332 TGCCGCTGCTGTTCCGCTTACAGCCCGCGCCGCGCGCGCGCGCTCGAGA 273  
QY 198 GGATGAGCCCTTATCCCGAGGGGGCGCCANGCAAGGCAAGGAGTGGGCTCGGGC 257  
Db 272 AGGGCCCGCTTATCCCGAGGGGGGAGGCGGCGCGCGCGCGCGCTCGAGCA 213  
QY 258 AGTGGCCCTGCGCTCGAAGATACCGAAGTGACACGACACCGCGCG 304  
Db 212 GTGCCCCCTCTGCTCGGCGCTAGACCTGAGCTCAATTAGCGCGCAGCGG 166

US-08-828-683A-5  
Query Match 11.8%; Score 37.2; DB 4; Length 1438;  
Best Local Similarity 47.6%; Pred. No. 0.55;  
Matches 108; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

Db 2686 CAGCGGGGGCGGTGCACCCAGCGGGCACCAGCTG 2651

RESULT 14  
US-08-486-273A-44/C  
; Sequence 44, Application US/08486273A  
; Patent No. 5985586  
; GENERAL INFORMATION:  
; APPLICANT: Daggett, Lorrie P.  
; APPLICANT: Ellis, Steven B.  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lu, Chin-Chun  
; TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR SUBUNITS, DNA  
; TITLE OF INVENTION: ENCODING SAME AND USES THEREFOR  
; NUMBER OF SEQUENCES: 63  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 92101-2926  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/486,273A  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/231,193  
; FILING DATE: 20-APR-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seidman, Stephanie  
; REGISTRATION NUMBER: 33,779  
; REFERENCE/DOCKET NUMBER: 6362-9383B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-238-0999  
; TELEFAX: 619-238-0062  
; INFORMATION FOR SEQ ID NO: 44:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3243 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: CDNA  
; FEATURE:  
; NAME/KEY: Coding Sequence  
; LOCATION: 1...3243  
US-08-486-273A-44

		Query Match	11.7%;	Score 36.6;	DB 2;	Length 3243;
		Best Local Similarity	.45.7%;	Pred. No.	0.89;	
		Matches 126;	Conservative	0;	Mismatches 150;	Indels 0; Gaps 0;
Qy	13	AGTGGCTCTCTGTGTCCTAAAGTGATGAACGGAAACACGCCTGGCGTGACGCCAATTGGG	72			
Db	2926	AGAGGCCCCCAGGCGCCGGAGAGCCAGGAGCCGTGGCTGTCAAGSGTTGGAAGTGAAGA	2867			
Qy	73	CAGAAAGGCTTTCGGCGGCCCTTGGCACATCGGSCAGGTGGCTTCTCAGCGCCCGCTATATG	132			
Db	2866	CAGACAGCCCCCAGCACAAATGGCAGGTGGGCGTGGCGTGCAGGCAGACGTGCTGCTG	2807			
Qy	133	AGCTGCGCTCGGGATGCAGACCACCCAGCCCACCCCTCGGGGCCCCCTCGGTGCCCC	192			
Db	2806	TGCTGCCAGGGGGGGGCCCTTCCTGCTCGCCCCCTTCGGCAGGGCTCTCCCGGTAGATCGG	2747			
Qy	193	TGGCAGGATCAGCGCTTTCATCCGGAGGGGGGCCCAANGCAAAGGCCAAGAACCTGGGGCTG	252			
Db	2746	AAGCACATTCGACTCGCGCTTGCACAAGCGCTGCAGAGCCAGGTGGCGCGTCTGGGGCGGGCG	2687			





|||||  
Db 1 ATGTCATGTTTAGTGGCTCCTGGTCCCTAAAGTGGATGAACGAAACAGCCTGGGGT 60  
QY 61 GAACGCAATGGGACAGAGCGTTCCGGCGCGTGGCACTCGGCAGGTGGCTTCTGCACG 120  
Db 61 GAACGCAATGGGACAGAGCGTTCCGGCGCGTGGCACTCGGCAGGTGGCTTCTGCACG 120  
QY 121 CCCGCTATATAGTGGCTCCGGGATGCAGAGCCACCCAGCCACCCCTGCGGGCCCC 180  
Db 121 CCCGCTATATAGTGGCTCCGGGATGCAGAGCCACCCAGCCACCCCTGCGGGCCCC 180  
QY 181 CCTCGGTGCCCTGGCAGATGACGCCCTTTCATCCGGAGGGCGGCCANGCAAGGCAAG 240  
Db 181 CCTCGGTGCCCTGGCAGATGACGCCCTTTCATCCGGAGGGCGGCCANGCAAGGCAAG 240  
QY 241 GAACCTGGGGCTCGGGCAGTGGCCCTTTCAGAGTACCAACGACACCG 300  
Db 241 GAACCTGGGGCTCGGGCAGTGGCCCTTTCAGAGTACCAACGACACCG 300  
QY 301 GCGGGACCGCTGAA 314  
Db 301 GCGGGACCGCTGAA 314

RESULT 2  
US-09-750-240-5  
; Sequence 5, Application US/09750240  
; Patent No. US20020103147A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammon, H. K.  
; APPLICANT: Insel, P. A.  
; APPLICANT: Ping, P.  
; APPLICANT: Post, S. R.  
; APPLICANT: Gao, M.  
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART  
; FILE REFERENCE: 220002056723  
; CURRENT APPLICATION NUMBER: US/09/750,240  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 09/472,667  
; PRIOR FILING DATE: 1999-12-27  
; PRIOR APPLICATION NUMBER: US 09/008,097  
; PRIOR FILING DATE: 1998-01-16  
; PRIOR APPLICATION NUMBER: US 08/924,757  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: US 60/048,933  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: US 08/708,661  
; PRIOR FILING DATE: 1996-09-05  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 3549  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-750-240-5

Query Match 94.0%; Score 295.2; DB 10; Length 3549;  
Best Local Similarity 97.1%; Pred. No. 1.6e-68;  
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 1 ATGTCATGTTTAGTGGCTCCTGGTCCCTAAAGTGGATGAACGAAACAGCCTGGGGT 60  
Db 1 ATGTCATGTTTAGTGGCTCCTGGTCCCTAAAGTGGATGAACGAAACAGCCTGGGGT 60  
QY 61 GAACGCAATGGGACAGAGCGTTCCGGCGCGTGGCACTCGGCAGGTGGCTTCTGCACG 120  
Db 61 GAACGCAATGGGACAGAGCGTTCCGGCGCGTGGCACTCGGCAGGTGGCTTCTGCACG 120  
QY 121 CCCGCTATATAGTGGCTCCGGGATGCAGAGCCACCCAGCCACCCCTGCGGGCCCC 180  
Db 121 CCCGCTATATAGTGGCTCCGGGATGCAGAGCCACCCAGCCACCCCTGCGGGCCCC 180

QY 181 CCTCGGTGCCCTGGCAGATGACGCCCTTTCATCCGGAGGGCGGCCANGCAAGGCAAG 240  
Db 181 CCTCGGTGCCCTGGCAGATGACGCCCTTTCATCCGGAGGGCGGCCANGCAAGGCAAG 240  
QY 241 GAACCTGGGGCTCGGGCAGTGGCCCTTTCAGAGTACCAACGACACCG 300  
Db 241 GAGCTGGGGCTCGGGCAGTGGCCCTTTCAGAGTACCAACGACACCG 300  
QY 301 GCGGGACCG 309  
Db 301 GCGGGACCG 309  
RESULT 3  
US-09-750-240-10  
; Sequence 10, Application US/09750240  
; Patent No. US20020103147A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammon, H. K.  
; APPLICANT: Insel, P. A.  
; APPLICANT: Ping, P.  
; APPLICANT: Post, S. R.  
; APPLICANT: Gao, M.  
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART  
; FILE REFERENCE: 220002056723  
; CURRENT APPLICATION NUMBER: US/09/750,240  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 09/472,667  
; PRIOR FILING DATE: 1999-12-27  
; PRIOR APPLICATION NUMBER: US 09/008,097  
; PRIOR FILING DATE: 1998-01-16  
; PRIOR APPLICATION NUMBER: US 08/924,757  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: US 60/048,933  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: US 08/708,661  
; PRIOR FILING DATE: 1996-09-05  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 3552  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-750-240-10

Query Match 94.0%; Score 295.2; DB 10; Length 3552;  
Best Local Similarity 97.1%; Pred. No. 1.6e-68;  
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 1 ATGTCATGTTTAGTGGCTCCTGGTCCCTAAAGTGGATGAACGAAACAGCCTGGGGT 60  
Db 1 ATGTCATGTTTAGTGGCTCCTGGTCCCTAAAGTGGATGAACGAAACAGCCTGGGGT 60  
QY 61 GAACGCAATGGGACAGAGCGTTCCGGCGCGTGGCACTCGGCAGGTGGCTTCTGCACG 120  
Db 61 GAACGCAATGGGACAGAGCGTTCCGGCGCGTGGCACTCGGCAGGTGGCTTCTGCACG 120  
QY 121 CCCGCTATATAGTGGCTCCGGGATGCAGAGCCACCCAGCCACCCCTGCGGGCCCC 180  
Db 121 CCCGCTATATAGTGGCTCCGGGATGCAGAGCCACCCAGCCACCCCTGCGGGCCCC 180  
QY 181 CCTCGGTGCCCTGGCAGATGACGCCCTTTCATCCGGAGGGCGGCCANGCAAGGCAAG 240  
Db 181 CCTCGGTGCCCTGGCAGATGACGCCCTTTCATCCGGAGGGCGGCCANGCAAGGCAAG 240  
QY 241 GAACCTGGGGCTCGGGCAGTGGCCCTTTCAGAGTACCAACGACACCG 300  
Db 241 GAGCTGGGGCTCGGGCAGTGGCCCTTTCAGAGTACCAACGACACCG 300  
QY 301 GCGGGACCG 309  
Db 301 GCGGGACCG 309

; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
; TITLE OF INVENTION: CYCLASE
; FILE REFERENCE: 44481-5028-01-US
; CURRENT APPLICATION NUMBER: US/10/201,000
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: US/09/474,076
; PRIOR FILING DATE: 1999-12-12
; PRIOR APPLICATION NUMBER: PCT/US98/13694
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 607870,904
; PRIOR FILING DATE: 1997-07-01
; PRIOR APPLICATION NUMBER: 08/866,550
; PRIOR FILING DATE: 1997-07-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4942
; TYPE: DNA
; ORGANISM: human type VI adenylyl cyclase
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (145)..(3648)
US-10-201-000-1

Query Match 94.0%; Score 295.2; DB 9; Length 4942;
Best Local Similarity 97.1%; Pred. No. 1.7e-68;
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ATGTCATGTTTAGTGGCTCTCGTCCCTAAAGTGGATGAACGGAACACAGCCTGGGGT 60
Db 145 ATGTCATGTTTAGTGGCTCTCGTCCCTAAAGTGGATGAACGGAACACAGCCTGGGGT 204

QY 61 GAACGCAATGGGCAAGCGTTCCGGGCGCCGCTGGCACTCGGCGAGGTGCTTCTGCACG 120
Db 205 GAACGCAATGGGCAAGCGTTCCGGGCGCCGCTGGCACTCGGCGAGGTGCTTCTGCACG 264

QY 121 CCCCGCTATATGAGTGCCTCCGGGATGCAGAGCCACCCAGCCACCCCTGCGGGCCCC 180
Db 265 CCCCGCTATATGAGTGCCTCCGGGATGCAGAGCCACCCAGCCACCCCTGCGGGCCCC 324

QY 181 CTCGGTGCCTCGGAGGATGACGCTTCATCCCGAGGGGGGGCCCAANGCAAGGCAAG 240
Db 325 CTCGGTGCCTCGGAGGATGACGCTTCATCCCGAGGGGGGGCCCAANGCAAGGCAAG 384

QY 241 GAACTGGGCTCGGCGAGTGGCCCTCGGCTTCGAGATACCAAGTGACACGACACG 300
Db 385 GAACTGGGCTCGGCGAGTGGCCCTCGGCTTCGAGATACCAAGTGACACGACACG 444

QY 301 GCGGGACCG 309
Db 445 GCGGGACG 453

RESULT 6
US-09-933-797-165
; Sequence 165, Application US/09933797
; Patent No. US20020155119A1
; GENERAL INFORMATION:
; APPLICANT: Robert A. Sikes et al.
; TITLE OF INVENTION: Isolation and Use of Fetal Urogenital
; TITLE OF INVENTION: Sinus Expressed Sequences
; FILE REFERENCE: 9901-007-999
; CURRENT APPLICATION NUMBER: US/09/933,797
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US/09/482,933
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: PCT/US99/10746
; PRIOR FILING DATE: 1999-05/14
; PRIOR APPLICATION NUMBER: 60/085,383
; PRIOR FILING DATE: 1998-05-14
; NUMBER OF SEQ ID NOS: 811
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 165

US-09-750-240-12
; Sequence 12, Application US/09750240
; Patent No. US20020103147A1
; GENERAL INFORMATION:
; APPLICANT: Hammon, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P. R.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; TITLE OF INVENTION: FAILURE
; FILE REFERENCE: 220002056723
; CURRENT APPLICATION NUMBER: US/09/750,240
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 3582
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Modified AC-VI
US-09-750-240-12

Query Match 94.0%; Score 295.2; DB 10; Length 3582;
Best Local Similarity 97.1%; Pred. No. 1.6e-68;
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ATGTCATGTTTAGTGGCTCTCGTCCCTAAAGTGGATGAACGGAACACAGCCTGGGGT 60
Db 22 ATGTCATGTTTAGTGGCTCTCGTCCCTAAAGTGGATGAACGGAACACAGCCTGGGGT 81

QY 61 GAACGCAATGGGCAAGCGTTCCGGGCGCCGCTGGCACTCGGCGAGGTGCTTCTGCACG 120
Db 82 GAACGCAATGGGCAAGCGTTCCGGGCGCCGCTGGCACTCGGCGAGGTGCTTCTGCACG 141

QY 121 CCCCGCTATATGAGTGCCTCCGGGATGCAGAGCCACCCAGCCACCCCTGCGGGCCCC 180
Db 142 CCCCGCTATATGAGTGCCTCCGGGATGCAGAGCCACCCAGCCACCCCTGCGGGCCCC 201

QY 181 CTCGGTGCCTCGGAGGATGACGCTTCATCCCGAGGGGGGGCCCAANGCAAGGCAAG 240
Db 202 CTCGGTGCCTCGGAGGATGACGCTTCATCCCGAGGGGGGGCCCAANGCAAGGCAAG 261

QY 241 GAACTGGGCTCGGCGAGTGGCCCTCGGCTTCGAGATACCAAGTGACACGACACG 300
Db 262 GAACTGGGCTCGGCGAGTGGCCCTCGGCTTCGAGATACCAAGTGACACGACACG 321

QY 301 GCGGGACCG 309
Db 322 GCGGGACG 330

RESULT 5
US-10-201-000-1
; Sequence 1, Application US/10201000
; Publication No. US20020187540A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, James E.
; APPLICANT: COR Therapeutics, Inc.

```
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Murine
US-09-933-797-165

Query Match      52.0%; Score 163.4; DB 9; Length 358;
Best Local Similarity 83.1%; Pred. No. 3.7e-34;
Matches 196; Conservative 2; Mismatches 35; Indels 3; Gaps 1;

Qy 1 ATGTCATGTTTAGTGGCTCTCTGCTCCCTAAAGTGGATGAACGAAACAGCCTGGGGT 60
   |||||
Db 123 ATGTCATGTTTAGTGGCTCTCTGCTCCCAAGTGGATGAACGAAACAGCCTGGGGG 182
   |||||

Qy 61 GAACCAATGGGAGAACGCTTCGGCGCGGTGCACTCGGCGAGGTGGCTTCTGCACG 120
   |||||
Db 183 GAACCAATGGGAGAACGCG--CCACGCCACGCGAATGAGCCAGTGGCTTCTGCVCA 239
   |||||

Qy 121 CCCGCTATATGAGTGCCTCGGGGATGCAAGCCAGCCAGCCACCCCTGGGGCCCC 180
   |||||
Db 240 CTTGCTATATGAGTGCCTCAAGAATGCGGAGCCACCCAGCCCTCTCTGCAGCTCAC 299
   |||||

Qy 181 CTTGCTGTCCTCGGAGGATGACGCTTCATCCGGAGGGGCGGCCCAAGAGGG 236
   |||||
Db 300 ACTCGGTGCCCTSCAGATGAAGCCTTCATCAGGAGGGCGGCCCGGCGAGGG 355

RESULT 7
US-09-728-445-487
; Sequence 487, Application US/09728445
; Patent No. US20020102543A1
; GENERAL INFORMATION:
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020102543alel Mutated Mammalian Cells and
; TITLE OF INVENTION: Animals
; FILE REFERENCE: LEX-0102-USA
; CURRENT APPLICATION NUMBER: US/09/728,445
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/168,358
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 891
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 487
; LENGTH: 220
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-728-445-487

Query Match      30.1%; Score 94.6; DB 10; Length 220;
Best Local Similarity 84.4%; Pred. No. 3.6e-16;
Matches 119; Conservative 0; Mismatches 19; Indels 3; Gaps 1;

Qy 1 ATGTCATGTTTAGTGGCTCTCTGCTCCCTAAAGTGGATGAACGAAACAGCCTGGGGT 60
   |||||
Db 67 ATGTCATGTTTAGTGGCTCTCTGCTCCCAAGTGGATGAACGAAACAGCCTGGGGG 126
   |||||

Qy 61 GAACCAATGGGAGAACGCTTCGGCGCGGTGCACTCGGCGAGGTGGCTTCTGCACG 120
   |||||
Db 127 GAACCAATGGGAGAACGCG--CCACGCCACGCGAATGAGCCAGTGGCTTCTGCACA 183
   |||||

Qy 121 CCCGCTATATGAGTGCCTC 141
   |||||
Db 184 CTTGCTATATGAGTGCCTC 204
   |||||

RESULT 8
US-09-935-541-12/c
; Sequence 12, Application US/09935541
; Patent No. US20020150911A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
```

```
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 6503
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-935-541-12

Query Match      12.3%; Score 38.6; DB 10; Length 6503;
Best Local Similarity 55.2%; Pred. No. 0.31;
Matches 74; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Qy 141 CCGGGATGACAGGACACCCAGCCGCCCTGCGGGGCCCCCTCGGTGCGCCCTGGCAGGA 200
   |||||
Db 173 CCGGGTGGAGAGGACCCCGCGCCCGCCGCGCCCTCGGATTCGCGGATCAGCT 114
   |||||

Qy 201 TGACGCTTTCATCCGAGGAGGCGGCCGCGCCAGCAAGGCAAGAACTGGGGCTGGCGGCACT 260
   |||||
Db 113 GCGGCCCGGGGAGGAGGAGCGGCGATGACAGGCGGGCGGCCCGCGGGCGCGGCCAT 54
   |||||

Qy 261 GGCCTGGGCTTCG 274
   |||||
Db 53 GCGGGCGGGTCCG 40
   |||||

RESULT 9
US-10-081-280-5/c
; Sequence 5, Application US/10081280
; Patent No. US20020165157A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/081,280
; FILING DATE: 21-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,270
; FILING DATE: 31-Mar-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5416
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1438 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
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Db 332 TGCCGCTGCTGCTTCCGCTTACAGCCCGCGCCGAGGGCCCGCCGCGCTCGAGA 273  
QY 198 GGATGACGCGCTTCATCCGAGGCGGCGCCANGCAGGCAAGTGGGCTCGGGC 257  
Db 272 AGGGCCGCGCTGGCGGCGGGGAGGGGCGCCCGGAGCCCAACCGAGTCCGACCAG 213  
QY 258 AGTGGCGCTGGCTTCGAGATACGAAGTGACACGACACCGCGCG 304  
Db 212 GTGCCCCCTCTCTCGGCTAGACCTGAGCTCATTTAGGCGGAGCGG 166

RESULT 12  
US-09-884-733-5/c  
; Sequence 5, Application US/09884733  
; Patent No. US20020123116A1  
; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.  
; TITLE OF INVENTION: Apo-2 Ligand Inhibitor  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/884,733  
; FILING DATE: 19-Jun-2001  
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/304,003

; FILING DATE: 14-JUNE-2000

; ATTORNEY/AGENT INFORMATION:

; NAME: Marschang, Diane L.

; REGISTRATION NUMBER: 35,600

; REFERENCE/DOCKET NUMBER: P1007

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-5416

; TELEFAX: 415/952-9881

; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1438 base pairs

; TYPE: Nucleic Acid

; STRANDEDNESS: Single

; TOPOLOGY: Linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-884-733-5

Query Match 11.8%; Score 37.2; DB 10; Length 1438;  
Best Local Similarity 47.6%; Pred. No. 0.55;  
Matches 108; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

QY 78 GCGTTTCGGCGCCCTGCGACTCGGGCAGGTGGCTTCTGCAGCCCGCTATATAGCTG 137  
Db 392 GCGGCGCTGTCTCCATAGCCCTCCGACGGGCGCCAGGGGCTTCCCGGCTCGTCTCTC 333  
QY 138 CTCCGGGATGACAGACCCACCCACCCCTCGGGGCCCCCTCGGTGCCCCCTGGCA 197  
Db 332 TGCCCGTGTGTTCCGCTTCAGCCCGCGCGCCGCGCGCCGCGCTCGAGA 273  
QY 198 GGATGACGCGCTTCATCCGAGGCGGCGCCANGCAGGCAAGTGGGCTCGGGC 257  
Db 272 AGGGCCCGCTGGCGGCGGGGAGGGGCGCCCGGAGCCCAACCGAGTCCGACCAG 213  
QY 258 AGTGGCGCTGGCTTCGAGATACCGAAGTGACACGACACCGCGCG 304

RESULT 14

US-09-945-901-44/c

; Sequence 44, Application US/09945901

; Patent No. US20020161215A1

Db 212 GTGCCCCCTCTCTCGGCTAGACCTGAGCTCATTTAGGCGGAGCGG 166

RESULT 13

US-09-993-234-5/c

; Sequence 5, Application US/09993234

; Patent No. US20020146768A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/993,234

; FILING DATE: 19-No. US20020146768A1-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/828,683

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Marschang, Diane L.

; REGISTRATION NUMBER: 35,600

; REFERENCE/DOCKET NUMBER: P1007P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-5416

; TELEFAX: 415/952-9881

; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1438 base pairs

; TYPE: Nucleic Acid

; STRANDEDNESS: Single

; TOPOLOGY: Linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-993-234-5

Query Match 11.8%; Score 37.2; DB 10; Length 1438;  
Best Local Similarity 47.6%; Pred. No. 0.55;  
Matches 108; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

QY 78 GCGTTTCGGCGCCCTGCGACTCGGGCAGGTGGCTTCTGCAGCCCGCTATATAGCTG 137  
Db 392 GCGGCGCTGTCTCCATAGCCCTCCGACGGGCGCCAGGGGCTTCCCGGCTCGTCTCTC 333  
QY 138 CTCCGGGATGACAGACCCACCCACCCCTCGGGGCCCCCTCGGTGCCCCCTGGCA 197  
Db 332 TGCCCGTGTGTTCCGCTTCAGCCCGCGCGCCGCGCGCCGCGCTCGAGA 273  
QY 198 GGATGACGCGCTTCATCCGAGGCGGCGCCANGCAGGCAAGTGGGCTCGGGC 257  
Db 272 AGGGCCCGCTGGCGGCGGGGAGGGGCGCCCGGAGCCCAACCGAGTCCGACCAG 213  
QY 258 AGTGGCGCTGGCTTCGAGATACCGAAGTGACACGACACCGGGCG 304  
Db 212 GTGCCCCCTCTCTCGGCTAGACCTGAGCTCATTTAGGCGGAGCGG 166

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	Query Match	11.7%;	Score 36.6;	DB 9;	Length 3243;
	Best Local Similarity	45.7%;	Pred. No. 0.92;		
	Matches 126;	Conservative 0;	Mismatches 150;	Indels 0;	Gaps 0;
Qy	13	AGTGGCCTCTCGTCCCTAAAGTGATCAACGGAAACAGCCTGGGGTGAACCAATGGG	72		
Db	2926	AGAGGCCCCCAAGGCCCGGAGGAGCAGGACCGTGGCTGTACAGGGTGGAGGTGAGGA	2867		
Qy	73	CAGAAAGCGTTTCGCGGGCGCGTGGCACTCGGCGAGGTGGCTTCTGCACGCCCGCTATATG	132		
Db	2866	CAGACAGCCCCACAGCAATGGCAGGTGGCGTGGGGCGTCAGGCACACGTGCTGTCTG	2807		
Qy	133	AGCTGCCTCGCGGATGAGAGCCACCCAGCCCCACCCCTGCGGGGCCCCCTTCGGTGGCCCC	192		
Db	2806	TGCTGCCAGGCGGGGGCCCTGCTGTGCGCCCTCCCTGGCAGGCCTCCCGGTAGATCGCC	2747		

Qy	193	TGGCAGATGACCCCTTCATCCGAGGGGCGCCACCAAGGCAGGAACCTGGGCTG	252
Db	2746	AGCCACATCAGCTGCGCCCTGCGCCCAAGCGCTGTCAGGCCGAGTGGCCGTGGGGCGGGCG	2687
Qy	253	CGGGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTG	288
Db	2686	CAGCGGGGCGGCTGCACCCAGCGGCGCAGCAGCTG	2651

Search completed: March 1, 2003, 09:03:39  
Job time : 19.892 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2003, 23:39:42 ; Search time 46.5329 Seconds  
(without alignments)  
11498.584 Million cell updates/sec

Title: US-09-750-240-1

Perfect score: 314

Sequence: 1 atgtcatgttttagtgctt.....acacggcgggaccgctgaa 314

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3936061 seqs, 852009584 residues

Total number of hits satisfying chosen parameters: 7872122

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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5: /cgn2\_6/ptodata/2/pna/US09\_NEW\_COMB.seq.\*  
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7: /cgn2\_6/ptodata/2/pna/US60\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	295.2	94.0	1386	1	PCT-US02-36759-83
2	199.2	63.4	5826	6	US-10-144-771-5921
3	39.8	12.7	36303	6	US-10-152-724-24
4	39.8	12.7	36303	6	US-10-152-724A-24
5	38.2	12.2	1878	5	US-09-724-676-33617
6	38.2	12.2	1878	5	US-09-724-676A-33617
7	38.2	12.2	3174	6	US-10-218-140-5849
8	38.2	12.2	3182	5	US-09-724-676A-33618
9	38.2	12.2	3182	5	US-09-724-676-33618
10	36.6	11.7	1542	1	PCT-US02-38526-349
11	36.6	11.7	2216	1	PCT-US02-38526-347
12	36.4	11.6	485	5	US-09-585-645A-59
13	36	11.5	22118	6	US-10-287-313-16
14	35.8	11.4	1824	5	US-09-724-676-45770
15	35.8	11.4	1824	5	US-09-724-676A-45770
16	35.2	11.2	2883	6	US-10-125-923A-157
17	35.2	11.2	2883	6	US-10-205-892-157
18	35.2	11.2	2883	6	US-10-174-575-157
19	35.2	11.2	2883	6	US-10-174-575A-157
20	35.2	11.2	2883	6	US-10-015-610A-23
21	35.2	11.2	2883	6	US-10-226-254A-23
22	35.2	11.2	2883	6	US-10-187-755-157
23	35.2	11.2	2883	6	US-10-187-749-157
24	35.2	11.2	2883	6	US-10-017-253A-23
25	35.2	11.2	2883	6	US-10-199-672-157
26	35.2	11.2	2883	6	US-10-194-486-157

Sequence 3, Appli  
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Sequence 65, Appl  
Sequence 21648, A  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 23402, A  
Sequence 319, App  
Sequence 179, App  
Sequence 179, App  
Sequence 66, Appl  
Sequence 17257, A  
Sequence 26872, A  
Sequence 143, App  
Sequence 143, App  
Sequence 1374, Ap  
Sequence 14604, A  
Sequence 14604, A

#### ALIGNMENTS

RESULT 1  
PCT-US02-36759-83  
; Sequence 83, Application PC/TUS0236759  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: DUGGAN, Brendan M.  
; APPLICANT: YANG, Junming  
; APPLICANT: GIETZEN, Kimberly J.  
; APPLICANT: LEE, Soo Yeun  
; APPLICANT: TANG, Y. Tom  
; APPLICANT: AZIMZAI, Yalda  
; APPLICANT: WALIA, Narinder K.  
; APPLICANT: WARREN, Bridget A.  
; APPLICANT: BARROSO, Ines  
; APPLICANT: BECHA, Shanya D.  
; APPLICANT: YUE, Henry  
; APPLICANT: LEHR-MASON, Patricia M.  
; APPLICANT: THANGAVELU, Kavitha  
; APPLICANT: LEE, Sally  
; APPLICANT: EMERLING, Brooke M.  
; APPLICANT: KABLE, Amy E.  
; APPLICANT: KHARE, Reena  
; APPLICANT: BAUGHN, Mariah R.  
; APPLICANT: GANDHI, Ameena R.  
; APPLICANT: TRAN, Uyen K.  
; APPLICANT: RICHARDSON, Thomas W.  
; APPLICANT: MARQUIS, Joseph P.  
; APPLICANT: LAL, Preeti G.  
; APPLICANT: FORSYTHE, Ian J.  
; APPLICANT: LEE, Ernestine A.  
; APPLICANT: SWARNAKAR, Anita.  
; APPLICANT: KALLICK, Deborah A.  
; APPLICANT: GRIFFIN, Jennifer A.  
; APPLICANT: ELLIOTT, Vicki S.  
; APPLICANT: GORVAD, Ann E.  
; APPLICANT: HAFALIA, April J.A.  
; APPLICANT: ISON, Craig H.  
; APPLICANT: JIN, Pei  
; APPLICANT: JIANG, Xin  
; APPLICANT: JACKSON, Alan  
; APPLICANT: BHATIA, Umesh  
; APPLICANT: BURRILL, John D.  
; APPLICANT: BLAKE, Julie J.  
; APPLICANT: HO, Ann  
; APPLICANT: ZHENG, Wenjin  
; APPLICANT: GAO, Jing  
; TITLE OF INVENTION: RECEPTORS AND MEMBRANE-ASSOCIATED PROTEINS  
; FILE REFERENCE: PF-1279 PCT  
; CURRENT APPLICATION NUMBER: PCT/US02/36759



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; FILE REFERENCE: P22378
; CURRENT APPLICATION NUMBER: US/10/152,724A
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: Australian App No PQ 4348
; PRIOR FILING DATE: 1999-11-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 36303
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-152-724A-24

Query Match      12.7%; Score 39.8; DB 6; Length 36303;
Best Local Similarity 55.4%; Pred. No. 1.4;
Matches 77; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 78 GCCTTCGGCGCGCGTGGCACTCGGCAGGTGGCTTCTGCACGCCCGCGTATATGAGCTG 137
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 34505 GAGTGGCGGCGCGCGGAGTGGCGGAGCCTCCCTTACCCCTCGCCCGACCGGCAG 34446

QY 138 CTTCCGGGATGACAGACCCAGCCACCCCTCGGGGCCCCCTCGGTGGCCCTGGCA 197
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 34445 CCTACGGCGCGAGCTCTCTCTCGCCCTCTCTTCGCGCGGACGGGGAGTCCCGGCC 34386

QY 198 GGATGACGCTTCATCCGG 216
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Db 34385 TCTCGGCTCTCTCTCCGG 34367

RESULT 5
US-09-724-676-33617/c
; Sequence 33617, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33617
; LENGTH: 1878
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-33617

Query Match      12.2%; Score 38.2; DB 5; Length 1878;
Best Local Similarity 46.0%; Pred. No. 1.9;
Matches 127; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

QY 13 AGTGGCCTCTGTGCTCCCTAAAGTGGATGAACGGAACACACCCCTGGGGTGAACGCAATGGG 72
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1319 AGAGGCCCCCAGGCCCCCGAGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260

QY 73 CAGAAGCGTTTCGGGGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACGCCCGCCCTATATG 132
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1259 CAGACAGCCCCCAGCAAAATGGCAGGTGGCGGTGCGAGGACAGCTGCTGTCTG 1200

QY 133 AGTGCCTTCGGGATCAGAGCCACCCAGCCCGCCCTCGGGGCCCCCTCGGTGGCCCC 192
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1199 TGCTGCCAGGCGGGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140

QY 193 TGGCAGGATGACCCCTTCATCCGAGGGGGGGGCCCAAGGCAAGGCAAGTGGGGCTG 252
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1139 AAGCACATGACGTGCGCCTGCGCCAAAGCGCCTGCAGCGCAGTGGCGGTGGGGCGGCG 1080

QY 253 CGGGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTG 288
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Db 1079 CAGCGGGCGCGGTGCACCCAGCGGCGAGCTG 1044

RESULT 6
US-10-218-140-5849
; Sequence 5849, Application US/10218140
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES
; FILE REFERENCE: 15966-543 CON
; CURRENT APPLICATION NUMBER: US/10/218,140
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 09/340,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/127,728
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 60/127,636
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/127,607
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 6322
; SOFTWARE: Curanator Version 1.0
; SEQ ID NO 5849
; LENGTH: 3174
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1870)..(2332)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: "n" = "a", "c", "t" or "g"
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (961)..(961)
; OTHER INFORMATION: "n" = "a", "c", "t" or "g"
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; LOCATION: (1191)..(1191)
; OTHER INFORMATION: "n" = "a", "c", "t" or "g"
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1193)..(1193)
; OTHER INFORMATION: "n" = "a", "c", "t" or "g"
US-218-140-5849

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[illegible]

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RESULT 8
US-09-724-676-33618/c
; Sequence 33618, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: CompuGen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 CompuGen
; CURRENT APPLICATION NUMBER: US/09724, 676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33618
; LENGTH: 3182
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-33618

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Query Match	12.2%	Score 38.2;	DB 5;	Length 3182;
Best Local Similarity	46.0%;	Pred. No. 2.1;		
Matches 127; Conservative	0;	Mismatches 149;	Indels	0; Gaps 0;
QY	13	AGTGGCCTCTGTGCTCCCTAAAGTGGATGAACGGAAAAACAGCCTCTGGGTGAACGCAATGGG	72	
Db	2623	AGAGCCCCCAGGCCCGGAGAGCCGAGAGCCGTGGCTGGCACAGGCTGGAAGGTGAGGA	2564	
QY	73	CAGAAAGGTTTCGGGGCGCGTGGCACTCGGCGAGGTGGCTTCTCGACGCCCGCGTATATG	132	
Db	2563	CAGACAGCCCCCAGCAAAAATGGCAGTGGCGTGGGGCGTCAGGCAGACAGTGTGCTGTG	2504	
QY	133	AGTGCTCTCCGGGATGCAGAGCCACCCAGGCCCCACCCTCGCGGGCCCCCTCGGTGCCCC	192	
Db	2503	TGCTGCCAGCGGGGGGCCCTCGCTGCTCGGCCCTCTGGCAGGCCCTCCCGGTAGATCGCC	2444	
QY	193	TGCGAGGATCAGCGCTTCATCCGAGGGGGGGCCCCANGCAGGCGCAAGGAACCTGGGGCTG	252	
Db	2443	ARGCACAATGACTCGCCCTGGGCCAAGCCCTTCGAGGCCGAGTGGCCCTCGGGGCGGGCG	2384	
QY	253	CGGGCACTGGCCCTGGGCTTCGAAGATACCGAAGTG	288	
Db	2383	CAGCGGGGGCGGCTGCAACCCAGCGGGCGCAGCGAGCTG	2348	

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RESULT 9
US-09-724-676A-33618/c
; Sequence 33618, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: CompuGen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 CompuGen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33618
; LENGTH: 3182
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-724-676A-33618

Query Match      12.2%; Score 38.2; DB 5; Length 3182;
Best Local Similarity 46.0%; Pred. No. 2.1;
Matches 127; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

QY      13  AGTGGCCCTCTGTTCCTTAAAGTGGATGACGGAAACACAGCTGGGGTGACGCAATGGG 72
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      2623  AGAGGCCCCCAGGCCCGGAGAGCAGGAGCCGTGGCTGGCAGAGGGTGGAAAGGTGAGGA 2564

QY      73  CAGAAAGGTTTCGGGGGCCCTTGCACCTCGGGCAGGTGGCTTCTGCAGCCCCCGCTATATG 132
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      2563  CAGACAGCCCCCAGCAAAAATGGCAGTGGGCGTGGGCGTGCAGGCAGACGTGCTGTCTG 2504

QY      133  AGCTGCTCCGGGATGCAGAGCCACCCAGGCCACCCCTCGGGGCCCCCTCGGTGCCCC 192
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      2503  TGTGCCAGCGGGGGGCCCTTCTGCTCGCCCTCTCTGGCAGGCCTCCCGGTAGATCGGC 2444

QY      193  TGCAGGATGACGCTTCATCCGGAGGGGGGCCCAANGCAAGGSCAAGAACTGGGGCTG 252
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      2443  AAGCACATGACTGGGCTCGGCCAAGCGCTGCAGCCGAGTGGCCGTGGGGCGGGCG 2384

QY      253  CGGGCAGTGGCCCTGGGCTTCGAAGATACCGAGTG 288
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      2383  CAGCGGGGGCGGTGCACCCAGGGGGGCGAGGAGCTG 2348

```

```

RESULT 10
PCT-US02-38526-349/c
/ Sequence 349, Application PC/TUS0238526
/ GENERAL INFORMATION:
/ APPLICANT: Ghosh, Malabika
/ APPLICANT: Tang, Y. Tom
/ APPLICANT: Wang, Jian-Rui
/ APPLICANT: Wang, Zhiwei
/ APPLICANT: Zhao, Qing
/ APPLICANT: Xu, Chongjun
/ APPLICANT: Mulero, Julio J.
/ APPLICANT: Boyle, Bryan J.
/ TITLE OF INVENTION: METHODS AND MATERIALS
/ FILE REFERENCE: HYS-BI/PCT
/ CURRENT APPLICATION NUMBER: PCT/US02/38526
/ CURRENT FILING DATE: 2002-12-03
/ PRIOR APPLICATION NUMBER: US 09/488,725
/ PRIOR FILING DATE: 2000-01-21
/ PRIOR APPLICATION NUMBER: US 09/552,317
/ PRIOR FILING DATE: 2000-04-25
/ PRIOR APPLICATION NUMBER: PCT/US00/35017
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: US 09/620,312
/ PRIOR FILING DATE: 2000-07-19
/ PRIOR APPLICATION NUMBER: PCT/US00/34263
/ PRIOR FILING DATE: 2000-12-26
/ PRIOR APPLICATION NUMBER: US 09/496,914
/ PRIOR FILING DATE: 2000-02-03
/ PRIOR APPLICATION NUMBER: US 09/560,875
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: PCT/US01/03800

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; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/598,075
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/04098
; PRIOR FILING DATE: 2001-02-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: PatentIn version 3.1
; NUMBER OF SEQ ID NOS: 653
; SEQ ID NO 349
; LENGTH: 1542
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38526-349

Query Match      11.7%; Score 36.6; DB 1; Length 1542;
Best Local Similarity 47.0%; Pred. No. 4.6;
Matches 111; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

QY 70 GGCACAGAGCTTCGGCGGCCCTGGCACTCGGCGAGGTGGCTTCGACGCCCGCGCTAT 129
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Db 821 GGGCGCTGGCGCTCGGCGGGCGGCTCGGCTGCGAGGGCTCTTCGGGGCTCTGGG 762

QY 130 ATGAGTGCCTCGGATGATGAGAGCACCAGAGCCACCCAGCCCTGCGGGCCCCCTCGGTGC 189
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 761 GCGGGGGGGGCGAGGGCGGCTCGTCTGAACACACTCTCTGCGGGGGCCCCACGGCCT 702

QY 190 CCTGTGGCAGTACGCTTCATCCGAGGGGGCGCCCAAGCAAGGCAAGCACTGGGG 249
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 701 CTCGGGGCTCGGAGGACCTCGCGGGGGCGCCAGGGCTGCGGGAGCGCTGAG 642

QY 250 CTGCGGGCAGTGGCCCTGGGCTTCGAGATACCGAAGTGACACAGCAGCGCGGG 305
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 641 GAGGGCTCAGGCTCCACGAGGGCGCGCCACAGCGCCACGTCGCCAGCGGAAG 586

RESULT 11
PCT-US02-38526-347/c
; Sequence 347, Application PC/TUS0238526
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Malabika
; APPLICANT: Tang, Y. Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wang, Zhiwei
; APPLICANT: Zhao, Qing
; APPLICANT: Xu, Chongjun
; APPLICANT: Mulero, Julio J
; APPLICANT: Boyle, Bryan J
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; FILE REFERENCE: HYS-BI/PCT
; CURRENT APPLICATION NUMBER: PCT/US02/38526
; CURRENT FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: PCT/US00/34263
; PRIOR FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/598,075
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/04098
; PRIOR FILING DATE: 2001-02-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 653
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 347
; LENGTH: 2216
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1542)
; OTHER INFORMATION:
PCT-US02-38526-347

Query Match      11.7%; Score 36.6; DB 1; Length 2216;
Best Local Similarity 47.0%; Pred. No. 5;
Matches 111; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

QY 70 GGCACAGAGCTTCGGCGGCCCTGGCACTCGGCGAGGTGGCTTCGACGCCCGCGCTAT 129
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 821 GGGCGCTGGCGCTCGGCGGGCGGCTCGGCTGCGAGGGCTCTTCGGGGCTCTGGG 762

QY 130 ATGAGTGCCTCGGATGATGAGAGCACCAGAGCCACCCAGCCCTGCGGGCCCCCTCGGTGC 189
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 761 GCGGGGGGGGCGAGGGCGGCTCGTCTGAACACACTCTCTGCGGGGGCCCCACGGCCT 702

QY 190 CCTGTGGCAGTACGCTTCATCCGAGGGGGCGCCCAAGCAAGGCAAGCACTGGGG 249
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 701 CTCGGGGCTCGGAGGACCTCGCGGGGGCGCCAGGGCTGCGGGAGCGCTGAG 642

QY 250 CTGCGGGCAGTGGCCCTGGGCTTCGAGATACCGAAGTGACACAGCAGCGCGGG 305
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 641 GAGGGCTCAGGCTCCACGAGGGCGCGCCACAGCGCCACGTCGCCAGCGGAAG 586

RESULT 12
US-09-585-645A-59/c
; Sequence 59, Application US/09585645A
; GENERAL INFORMATION:
; APPLICANT: Zoghbi, Huda
; APPLICANT: Bellen, Hugo
; APPLICANT: Bermingham, Nessim
; APPLICANT: Hassen, Bessam
; APPLICANT: Ben-Arie, Nissim
; TITLE OF INVENTION: Compositions and Methods for Therapeutic Use of Abnormal Association of Abnormal Cell Proliferation
; FILE REFERENCE: P01899US2
; CURRENT APPLICATION NUMBER: US/09/585,645A
; CURRENT FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/137,060
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: US 60/176,993
; PRIOR FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 485
; TYPE: DNA
; ORGANISM: CHICKEN
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (147)..(147)
; OTHER INFORMATION: n can be any nucleotide
US-09-585-645A-59

Query Match      11.6%; Score 36.4; DB 5; Length 485;
Best Local Similarity 54.7%; Pred. No. 4;
Matches 70; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 110 GCTTCTGCAGCGCCCGCTATATGAGTGCCTCGGGATGAGAGCCAGCCAGCCACCC 169
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 253 GCTTCTGCAGCGCGCTACCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 194

QY 170 CTGCGGGCCCCCTCGGTGCCCTGCGAGGATGACGCTTCATCCGAGGGGGCGGCCAN 229
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 193 CGCGCGCGCGCGCGCTCCCGCGGGCTCTCCCGCGGAGCGCGNGCGCGCGCGCG 134
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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2003, 21:14:01 ; Search time 301.551 Seconds  
(without alignments)  
16864.108 Million cell updates/sec

Title: US-09-750-240-1  
Perfect score: 314  
Sequence: 1 atgtcatgttttagtgctt.....acacgggggacgcgtgaa 314

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 16154066 seqs, 8097743376 residues  
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match	Description
1	199.2	63.4	618 10 BB866520
2	180	57.3	631 10 BB866451
3	60.2	19.2	1011 17 CNS02STX
4	58.8	18.7	941 13 BG916212
5	51.4	16.4	925 17 CNS0091P
6	50.4	16.1	1009 17 CNS010EW

7	43.4	13.8	846	17	CNS010RJ	AL099337 Drosophil
8	43	13.7	932	17	CNS0072Q	AL066742 Drosophil
9	43	13.7	950	14	BQ948546	BQ948546 AGENCOURT
c 10	42.4	13.5	778	14	BQ892531	BQ892531 AGENCOURT
c 11	42.4	13.5	925	17	CNS0091P	AL053013 Drosophil
c 12	42.4	13.5	1065	17	CNS0108S	AL098862 Drosophil
c 13	41.8	13.3	935	17	CNS006XK	AL098861 Drosophil
c 14	41.8	13.3	968	17	AG030603	AG030603 Pan trogl
c 15	41.4	13.2	1075	17	AG073983	AG073983 Pan trogl
c 16	41.2	13.1	1010	14	BQ064125	BQ064125 AGENCOURT
c 17	41.2	13.1	1203	17	CNS015Y4	AL106054 Drosophil
c 18	40.6	12.9	884	17	CNS018NP	AL109567 Drosophil
c 19	40.6	12.9	948	14	BQ646304	BQ646304 AGENCOURT
c 20	40.4	12.9	846	10	BE233788	BE233788 140263 MA
c 21	40.4	12.9	894	17	CNS0159I	AL105168 Drosophil
c 22	40.4	12.9	1612	13	BM455541	BM455541 AGENCOURT
c 23	40.2	12.8	1101	17	CNS0150D	AL104839 Drosophil
c 24	40	12.7	844	17	CNS0052P	AL056652 Drosophil
c 25	40	12.7	844	17	CNS0052P	AL056652 Drosophil
c 26	40	12.7	932	17	CNS0072Q	AL066742 Drosophil
c 27	40	12.7	935	17	CNS006XK	AL066051 Drosophil
c 28	40	12.7	1125	17	AG073746	AG073746 Pan trogl
c 29	39.8	12.7	906	17	AG081338	AG081338 Pan trogl
c 30	39.6	12.6	731	17	AG061169	AG061169 Pan trogl
c 31	39.6	12.6	935	17	AG073949	AG073949 Pan trogl
c 32	39.6	12.6	1538	17	AG030607	AG030607 Pan trogl
c 33	39.4	12.5	717	17	CNS011IL	AL100311 Drosophil
c 34	39.2	12.5	858	12	BG481980	BG481980 602527810
c 35	39.2	12.5	877	17	CNS025CS	AL211694 Tetraodon
c 36	39.2	12.5	1003	14	BQ886908	BQ886908 AGENCOURT
c 37	39	12.4	635	10	BG656840	BB656840 BB656840
c 38	38.8	12.4	447	13	BI403012	BI403012 MI-P-CP1-
c 39	38.8	12.4	481	10	BE233791	BE233791 140269 MA
c 40	38.8	12.4	587	13	BI399585	BI399585 MI-P-AVL-
c 41	38.8	12.4	588	13	BI402027	BI402027 MI-P-CF0-
c 42	38.8	12.4	687	13	BI182737	BI182737 UNL-P-FN-
c 43	38.8	12.4	725	13	BI181902	BI181902 UNL-P-FN-
c 44	38.8	12.4	839	17	CNS004NB	AL054280 Drosophil
c 45	38.6	12.3	504	13	BI669206	BI669206 603295447

ALIGNMENTS

RESULT 1	BB866520	618 bp	linear	EST 27-NOV-2001
LOCUS	BB866520	RIKEN full-length enriched, colon RCB-0549 C1e-H3 cDNA Mus		
DEFINITION	musculus cDNA clone G431005N18 5', mRNA sequence.			
ACCESSION	BB866520			
VERSION	BB866520.1	GI:17112730		
KEYWORDS	EST.			
SOURCE	house mouse.			
ORGANISM	Mus musculus			
REFERENCE	1 (bases 1 to 618)			
AUTHORS	Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imocani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y., et al.			
TITLE	RIKEN Encyclopedia of Mouse Full-length cDNAs (AKIMURA, T., et al. 2001)			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan			



(tissue\_type=bladder, cell\_line=RCB-0544 MBT-2),  
(tissue\_type=bone marrow, cell\_type=stroma cell,  
cell\_line=CRL-2028 SR-4987), (tissue\_type=colon,  
cell\_line=RCB-0549 CLe-H3), (tissue\_type=kidney,  
cell\_line=CCL-142 RAG), (tissue\_type=submandibular gland,  
cell\_line=CRL-1734 SCA-9 clone 15), (strain=BALB/C,  
cell\_type=B cells, cell\_line=CRL-1669 BCL1 Clone 13.20-3B3  
, (strain=C3H, tissue\_type=brain, cell\_line=CRL-1443  
BC3H1)"

BASE COUNT 90 a 217 c 174 g 150 t  
ORIGIN

Query Match 57.3%; Score 180; DB 10; Length 631;  
Best Local Similarity 78.2%; Pred. No. 1.9e-34;  
Matches 229; Conservative 0; Mismatches 61; Indels 3; Gaps 1;

QY 1 ATGTCATGTTTGTAGTCCCTCCCTGCTTCCCTAAAGTGGATGAACGGAACAGCCTGGGT 60  
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Db 37 ATGTCATGTTTGTAGTCCCTCCCTGCTTCCCTACAGTGGATGAACGGAACAGCCTGGGG 96  
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QY 61 GAACGCAATGGGCGAGAGGTTTCGGCGCGCGCTGGGCACCTGGGCAGGTGCTTCTGCACG 120  
|||||  
Db 97 GAACCTTTGGGCGAGAGCG---CCACGCCAGCGCTAATCGAGCCAGTGGCTTCTGCAGC 153  
|||||  
QY 121 CCCCCTATATAGTGCCTTCGGGATGAGAGCCACCAGCCCCCACCCTCGCGGCCCC 180  
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Db 154 CTTTGCTACTTGTAGCTGCCCTCCCGACTGGGGAGCCACCAGCCCCCCTCTGCTGTAC 213  
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QY 181 CFTCGTGCCCTGGCAGATGACGCTTCATCCGGAGGGGGCGCCCAAGCGGCAAG 240  
|||||  
Db 214 ACTTGGTGCCCTTGGCAGATGAAGCTTCATCAAGAGGGCCGCCCGGGGGGGTGTG 273  
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QY 241 GAATCGGGCTGGCGGCGAGTGGCCCTGGGCTTCGAAGATACCGAAGTGACAAC 293  
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Db 274 GATCTGGGCTGGCGGCGAGTGGCCCTCGGTTGCGAGCAGCTGTGCTGAGCAC 326  
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RESULT 3  
CNS02STX/c  
LOCUS  
DEFINITION  
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone  
162f16 of library G from Tetraodon nigroviridis, genomic survey  
sequence.  
1011 bp DNA linear GSS 15-MAY-2000  
CNS02STX  
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone  
162f16 of library G from Tetraodon nigroviridis, genomic survey  
sequence.  
1011 bp DNA linear GSS 15-MAY-2000  
CNS02STX/c  
AL212334.1 GI:7871153  
GSS: genome survey sequence.  
KEYWORDS  
Tetraodon nigroviridis.  
SOURCE  
Tetraodon nigroviridis  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
Tetraodontidae; Tetraodon.  
REFERENCE  
1 (bases 1 to 1011)  
Roest-Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,  
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,  
Saurin,W. and Weissenbach,J.  
Human gene number estimate provided by genome wide analysis using  
Tetraodon nigroviridis DNA sequence  
Unpublished  
JOURNAL  
Tetraodon nigroviridis  
AUTHORS  
2 (bases 1 to 1011)  
Roest-Crolius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,  
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and  
Weissenbach,J.  
Characterization and repeat analysis of the compact genome of the  
freshwater pufferfish Tetraodon nigroviridis  
Unpublished  
JOURNAL  
Tetraodon nigroviridis  
AUTHORS  
3 (bases 1 to 1011)  
Roest-Crolius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,  
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and  
Weissenbach,J.  
Direct Submission  
Submitted (12-APR-2000)  
Genoscope.  
TITLE  
This sequence is a single read and was generated as part of a large  
scale clone-end sequencing project of the Tetraodon nigroviridis  
genome. For more information, please take a look at

http://www.genoscope.cns.fr/Tetraodon.

FEATURES  
Source

Location/Qualifiers  
1..1011  
/organism="Tetraodon nigroviridis"  
/db\_xref="taxon:99883"  
/clone="162F16"  
/clone\_lib="G"  
/note="Genoscope sequence ID : C0AG162BC08SP1-end ;  
PUC-Ori"  
BASE COUNT 191 a 297 c 324 g 175 t 24 others  
ORIGIN

Query Match 19.2%; Score 60.2; DB 17; Length 1011;  
Best Local Similarity 63.1%; Pred. No. 9.1e-05;  
Matches 128; Conservative 1; Mismatches 64; Indels 10; Gaps 2;

QY 1 ATGTCATGTTTGTAGTCCCTCCCTGCTTCCCTAAAGTGGATGAACGGAACAGCCTGGGT 60  
|||||  
Db 283 ATGTCCTGTTTCAAGTGGTTTCTAGTGGCAGAGTGGACGACGAAAGAGCGCTGGGG 224  
|||||  
QY 61 GAACGCAATGGGCGAGAGGTTTCGGCGCGCGCTGGGCACCTGGGCAGGTGCTTCTGCACG 120  
|||||  
Db 223 GACGCAATGGGCGAGAGGTTTCGGCGCGCGCTGGGCAGGTGCTTCTGCACG 173  
|||||  
QY 121 CCCCCTATATAGTGCCTTCGGGATGAGAGCCACCAGCCCCCACCCTCGCGGCCCC 179  
|||||  
Db 172 CCCCCTWACATGAGTGCCTTCGGGAGCCCGACGACCATGGAGCCCCCTCCGGAGGCC 113  
|||||  
QY 180 CCTCTCGTGGCTTCGCAGGATG 202  
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Db 112 CTCCATCAGCACCACCGCGGAGG 90  
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RESULT 4  
BG916212  
LOCUS

602814927F1 NCI\_CGAP\_Mam4 Mus musculus cDNA clone IMAGE:4937095 5',  
mRNA sequence.  
941 bp mRNA linear EST 05-JUN-2001  
BG916212  
BG916212.1 GI:14296688  
EST.  
house mouse.  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NIH-MGC http://mgc.nci.nih.gov/  
1 (bases 1 to 941)  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth  
Ph.D.

cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM10870 row: f column: 08  
High quality sequence stop: 151.  
Location/Qualifiers  
1..941  
/organism="Mus musculus"  
/strain="NMRI"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4937095"  
/clone\_lib="NCI\_CGAP\_Mam4"  
/tissue\_type="tumor, gross tissue"  
/dev\_stage="5 months"  
/lab\_host="DH10B"

FEATURES  
source

Location/Qualifiers  
1..941  
/organism="Mus musculus"  
/strain="NMRI"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4937095"  
/clone\_lib="NCI\_CGAP\_Mam4"  
/tissue\_type="tumor, gross tissue"  
/dev\_stage="5 months"  
/lab\_host="DH10B"  
/note="Organ: mammary; Vector: pCMV-SPORT6; Site\_1: SalI;  
Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt.









NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of *Drosophila* DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

## FEATURES

source

1. .925  
/organism="Drosophila melanogaster"  
/db\_xref="taxon:7227"  
/clone="BACR19D16"  
/clone\_lib="RPCI-98"  
/note="end : TET3"

BASE COUNT 120 a 61 c 61 g 172 t 511 others

## ORIGIN

Query Match 13.5%; Score 42.4; DB 17; Length 925;

Best Local Similarity 10.4%; Pred. No. 2.2;

Matches 31; Conservative 146; Mismatches 120; Indels 0; Gaps 0;

QY 14 GTGGCTCTCGTCCCTAAGTCGATGACGGAACAGCCCTGGGTGAACGCAATGGGC 73

Db 628 GTSCSSSSSSSSSTSSSTSSSTSSSTSSSTSSSTSSSTSSSTSSSTSSSTSSSTSS 687

QY 74 AGAAGCGTTTCGGCGCGCGTGCACCTCGGCAGGTGCTTCTGCACGCCCGCTATATGA 133

Db 688 GSGTGSTSSSSSSSTSSSTSSSTSSSTSSSTSSSTSSSTSSSTSSSTSSSTSSSTSS 747

QY 134 GTGCTCTCGGGATGACGACCCACCCACCCCTCGGCGCCCGCTCGGTGCCCT 193

Db 748 SSSSYSSSTSCCTCCSYSSSTSSSTSSSTSSSTSSSTSSSTSSSTSSSTSSSTSSST 807

QY 194 GCAGATGACGCTTCATCCGAGGGGGCCCGCCGAGCAAGGCAAGCAACTGGCGTCG 253

Db 808 CTTCTCCCTTTCCTTCGCGCGSSSSGKGTTCGCGCGSSSTNGMBGTSSACSSS 867

QY 254 GGCAGTGGCCCTCGAGATACCAAGTACCAACGACACCGCGCGGACCGC 310

Db 868 SSCSS 924

RESULT 12

CNS0108S/c

LOCUS

DEFINITION

Drosophila melanogaster genome survey sequence T7 end of BAC

BACN03J03 of DrosBAC library from *Drosophila melanogaster* (fruit

fly), genomic survey sequence.

ACCESSION AL098662.1 GI:5610273

VERSION

KEYWORDS

SOURCE

ORGANISM

Drosophila melanogaster.

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; *Drosophila*.

1 (bases 1 to 1065)

Genoscope.

Direct Submission

Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : [seqref@genoscope.cns.fr](mailto:seqref@genoscope.cns.fr))- Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a

collaboration with the European *Drosophila* Genome Project (EDGP) -<http://www.edgp.ebi.ac.uk>. This *Drosophila melanogaster* BAC

library (Dros BAC) was made by Alain Billaud at CEPH (Centre

d'Etude du Polymorphisme Humain) with funding provided by a MRC

project grant. The DNA was prepared from embryos by Alain Bucheton

and Genevieve Payan. It has been constructed in the vector

pBelOBAC11.

Location/Qualifiers

1. .1065

/organism="Drosophila melanogaster"

FEATURES

source

1. .1065

/organism="Drosophila melanogaster"

BASE COUNT

ORIGIN

257 a 170 c 162 g 96 t 250 others

/db\_xref="taxon:7227"  
/clone="BACN03J03"  
/clone\_lib="DrosBAC"  
/plasmid="pBelOBAC11"  
/note="end : T7"

BASE COUNT 121 a 225 c 252 g 313 t 154 others

## ORIGIN

Query Match

Best Local Similarity 13.5%; Score 42.4; DB 17; Length 1065;

Matches 73; Conservative 58; Mismatches 107; Indels 0; Gaps 0;

QY 75 GAAGCGTTTCGGCGCGCGTGCACCTCGGCAGGTGCTTCTGCACGCCCGCTATATGAG 134

Db 1028 GRCCCSRCGGSAGKXVACAGCCGGGGGRCCTCCSMSAGACMCSCSCCCACAC 969

QY 135 CTGCTTCGGGATGACAGCCACCCAGCCCGCCCTGCGGGCCCGCTCGGTGCCCTG 194

Db 968 AAKGVCCSMCYCSGCCCGCCACSCGSCCMGTMBCMAGCSCSSSCSSSCSSCAMSGG 909

QY 195 GCAGGATGAGCCCTTCATCGGAGGGCGGCCGANGCAAGGCAAGAACTGGGCTGCG 254

Db 908 MGAGGSS 849

QY 255 GGCAGTGGCGCTGGGCTTCAAGATACCAAGTACCAACGACACCGCGCGGACCGCTG 312

Db 848 GGGGRRGCCCGGGAACGACMACVAAAGGTGACMCCSCSMVSSCVSSSSSCMCGG 791

RESULT 13

CNS006XK

LOCUS

DEFINITION

Drosophila melanogaster genome survey sequence T7 end of BAC #

BACR14N09 of RPCI-98 library from *Drosophila melanogaster* (fruit

fly), genomic survey sequence.

ACCESSION AL066051

VERSION

KEYWORDS

SOURCE

ORGANISM

Drosophila melanogaster.

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; *Drosophila*.

1 (bases 1 to 935)

Genoscope.

Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : [seqref@genoscope.cns.fr](mailto:seqref@genoscope.cns.fr))- Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a

collaboration with the Berkeley *Drosophila* Genome Project (BDGP).The BDGP is constructing a physical map of the *Drosophila**melanogaster* genome using these BACs. For further informationplease see <http://www.fruitfly.org> The BDGP *Drosophila**melanogaster* BAC library was prepared by Kazutoyo Osogawa and

Aaron Mamoser in Pieter de Jong's laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,

NY. The library is named RPCI-98 and was constructed by partial

EcoRI digestion of *Drosophila* DNA provided by the BDGP from the

isogenic strain y2; cn bw sp, the same strain used for the BDGP's

p1 and EST libraries. A more detailed description of the library

and how to order individual BAC clones, the entire library, or

filters for hybridization from the BACPAC Resource Center can be

found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

Location/Qualifiers

1. .935

/organism="Drosophila melanogaster"

/db\_xref="taxon:7227"

/clone="BACR14N09"

/clone\_lib="RPCI-98"

/note="end : T7"

BASE COUNT

ORIGIN

257 a 170 c 162 g 96 t 250 others

Query Match	13.3%;	Score 41.8;	DB 17;	Length 935;	
Best Local Similarity	36.7%;	Pred. No. 3.2;			
Matches	69;	Conservative	45;	Mismatches	73;
				Indels	1;
				Gaps	1;
QY	83	CGCGGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACGCCCGCGTATATGAGCTGCCTCC	142		
Db	682	CGCGSCGGCGSCGCGGCGGGGCGGCGCGSCSGCGSCGCGSGSGSCGCCSC	741		
QY	143	GGGATCAGAGCCACCCAGCCACCCCTGCGGGGCCCTCGGTGCCCTGGCAGGATG	202		
Db	742	CGSCSCSSSGSCCGCGCGMSGCGSGGSCGCCSGC-CGCSGCCGCGCGCGCG	800		
QY	203	ACGCTTCATCGGAGGGCGGCCANGCAAGGCAAGAACTGGGGTGTGGCGCAGTGG	262		
Db	801	GC CGCGSGCGCGGSGSGSGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	860		
QY	263	CCTCTGGGC	270		
Db	861	CGSGGCGS	868		
RESULT 14					
AG030603		968 bp	DNA	linear	GSS 01-NOV-2001
LOCUS		Pan troglodytes DNA, clone: PTB-003A16.F, genomic survey sequence.			
DEFINITION		Pan troglodytes DNA, clone: PTB-003A16.F, genomic survey sequence.			
ACCESSION		AG030603			
VERSION		AG030603.1	GI:16557476		
KEYWORDS		GSS.			
SOURCE		Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male			
ORGANISM		BAC Library clone:PTB-003A16.F.			
REFERENCE					
AUTHORS		Totoki,Y., Watanabe,H. and Sakaki,Y.			
TITLE		BAC end sequences of Library PTB			
JOURNAL		Unpublished			
REFERENCE					
AUTHORS		Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,			
TITLE		Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical			
JOURNAL		and Chemical Research (RIKEN), Genomic Sciences Center (GSC);			
COMMENT		Clones are derived from the chimpanzee BAC library PTB This BAC end			
		clone tracking errors.			
PRIMERS					
LIBRARY		Sequencing: -21M13			
Vector		: pKS145			
R.Site 1		: SacI			
R.Site 2		: SacI.			
Location/Qualifiers					
1..968					
/organism="Pan troglodytes"					
/db_xref="taxon:9598"					
/clone="PTB-003A16.F"					
/sex="male"					
/cell_type="lymphoblast"					
/clone_lib="PTB Chimpanzee Male BAC Library"					
BASE COUNT		40 a	361 c	474 g	16 t
ORIGIN					
Query Match		13.3%;	Score 41.8;	DB 17;	Length 968;
Best Local Similarity		48.8%;	Pred. No. 3.2;		
Matches		106;	Conservative	0;	Mismatches
				111;	Indels
				0;	Gaps
QY	83	CGCGGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACGCCCGCGTATATGAGCTGCCTCC	142		





GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus\_p2n model  
Run On: March 1, 2003, 04:06:12 ; Search time 2156 Seconds  
(without alignments)  
1403.846 Million cell updates/sec

Title: US-09-750-240-2  
Perfect score: 570  
Sequence: 1 MSWFGSLVLPVKDKRTAWG.....RAVALGFEDTEVTTTPAGPL 104

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters: -DEV=xlh  
-MODE=frame+p2n.model -DEV=xlh  
-Q/cgn2\_1/USPTO.spool/US09750240/runat\_25022003\_103941\_24963/app\_query.fasta\_1.263  
-DB=GenEmbl -QFMT=fastap -SUFFIX=rg -MINMATCH=0.1 -LOOPL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09750240.@Cgn\_1\_1\_1616@runat\_25022003\_103941\_24963 -NCPU=6 -ICPU=3  
-NO\_XLPXY -NO\_MMALP -LARGEQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl: \*  
1: gb.ba.\*  
2: gb.htg.\*  
3: gb.in.\*  
4: gb.om.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.sts.\*  
12: gb.sy.\*  
13: gb.un.\*  
14: gb.vi.\*  
15: em.ba.\*  
16: em.fun.\*  
17: em.hum.\*  
18: em.in.\*  
19: em.mu.\*  
20: em.om.\*  
21: em.or.\*  
22: em.ov.\*  
23: em.pat.\*  
24: em.ph.\*  
25: em.pl.\*  
26: em.ro.\*  
27: em.sts.\*  
28: em.un.\*

29: em.vi.\*  
30: em.htg\_hum.\*  
31: em.htg\_inv.\*  
32: em.htg\_other.\*  
33: em.htg\_mus.\*  
34: em.htg\_pln.\*  
35: em.htg\_rod.\*  
36: em.htg\_mam.\*  
37: em.htg\_vrt.\*  
38: em\_sy.\*  
39: em\_htgo\_hum.\*  
40: em\_htgo\_mus.\*  
41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	568	99.6	314	6	AR174471	AR174471 Sequence
2	568	99.6	314	6	AX189757	AX189757 Sequence
3	545	95.6	3549	6	AR174473	AR174473 Sequence
4	545	95.6	3549	6	AX189761	AX189761 Sequence
5	545	95.6	3552	6	AX189766	AX189766 Sequence
6	545	95.6	3582	6	AX189768	AX189768 Sequence
7	545	95.6	5877	9	AB007882	AB007882 Homo sapi
8	545	95.6	6463	9	AF250226	AF250226 Homo sapi
9	545	95.6	193283	2	AC021647	AC021647 Homo sapi
10	545	95.6	205248	2	AC117498	AC117498 Homo sapi
11	518	90.9	171345	2	AC025557	AC025557 Homo sapi
12	472.5	82.9	4046	4	DOGADENCYC	M94968 Canis fami
13	472.5	82.9	4046	6	I29958	I29958 Sequence 1
14	432	75.8	4131	6	AR106659	AR106659 Sequence
15	432	75.8	4131	10	RATADCYB	M96160 Rattus norv
16	432	75.8	5841	6	AX305965	AX305965 Sequence
17	432	75.8	5841	10	MUSADCYC	M93422 Mouse adeny
18	428	75.1	6036	10	RATADC	AC074028 Mus muscu
19	426	74.7	151706	2	AC129405	L0115 Rattus norv
20	426	70.5	108689	2	AC096835	AC129405 Rattus no
21	395	69.3	3465	10	MUSADNLCYC	AC096835 Rattus no
22	258	45.3	61901	5	U72484	M96553 Mus musculu
23	109	19.1	206934	2	AC126672	U72484 Fugu rubrip
24	105.5	18.5	110000	2	AC098456	AC126672 Mus muscu
25	103.5	18.2	8366	1	AF072709	AC098456 Rattus no
26	103.5	18.2	17228	1	SC3F60	AF072709 Streptomy
27	103.5	18.2	210215	2	AC097157	AL445945 Streptomy
28	103	18.1	6536	10	MUSALCR01	AC097157 Rattus no
29	103	18.1	179362	10	AC115355	L36825 Mus Musculu
30	100.5	17.6	129778	8	AC091123	AC115355 Mus muscu
31	100.5	17.5	148102	8	AP003328	AC091123 Oryza sat
32	100	17.5	148102	8	AP003328	AP003328 Oryza sat
33	100	17.5	148762	8	AP002843	AP002843 Oryza sat
34	99.5	17.5	14676	1	AE006014	AE006014 Caulobact
35	99	17.4	431	14	HEHS03	V00462 Herpes simp
36	99	17.4	2391	1	AF288483	AF288483 Azospirill
37	99	17.4	2560	14	HS1IEM5G	J02220 Herpes simp
38	99	17.4	13037	1	AF157643	AF157643 Mycobacte
39	99	17.4	98092	2	AC099455	AC099455 Rattus no
40	99	17.4	148120	9	AC090051	AC099455 Rattus no
41	98.5	17.3	65190	2	B1011H02	AC090051 Homo sapi
42	98.5	17.3	139807	8	OSJN00183	AL442109 Oryza sat
43	98.5	17.3	171557	8	OSJN00177	AL662984 Oryza sat
44	98	17.2	13036	1	AE005839	AL662976 Oryza sat
45	98	17.2	201050	1	AL646064	AE005839 Caulobact
						AL646064 Ralstonia

# ALIGNMENTS

RESULT 1

AR174471	AR174471	314 bp	DNA	linear	PAT 17-DEC-2001
LOCUS	Sequence 1 from patent US 6306830.				
DEFINITION	AR174471				
ACCESSION	AR174471				
VERSION	AR174471.1	GI:17914791			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 314)				
TITLE	Hammond,H.Kirk., Insel,P.A., Ping,P., Post,S.R. and Gao,M.				
JOURNAL	Gene therapy for congestive heart failure				
FEATURES	Patent: US 6306830-A 1 23-OCT-2001;				
source	Location/Qualifiers				
	1..314				
	/organism="unknown"				
BASE COUNT	60 a 98 c 108 g	47 t		1 others	
ORIGIN					
Alignment Scores:					
Pred. No.:	3.27e-29	Length:	314		
Score:	568.00	Matches:	104		
Percent Similarity:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	99.65%	Indels:	0		
DB:	6	Gaps:	0		
US-09-750-240-2 (1-104) x AR174471 (1-314)					
Qy	1 MetSerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGly	20			
Db	1 ATGTCATGTTTACTGGCTCTCTGTCCTCCCTAACTGGATGAACGAAACAGCCTGGGT	60			
Qy	21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyPheCysThr	40			
Db	61 GAACGCAATGGCGAAGACGTTCCGCGCGCGTGGCACTCGGGACAGGTGGCTTCTGCACG	120			
Qy	41 ProArgTyrMetSerCysLeuArgAspAlaGluProSerProThrProAlaGlyPro	60			
Db	121 CCGCGCTATATGAGCTGCCCTCCGGATGCGAGCCACCCAGCCCTCCGGGGCCCC	180			
Qy	61 ProArgCysProTrpGlnAspAspAlaPheIleArgArgGlyGlyPro**LysGlyLys	80			
Db	181 CCTCGGTGCCCTGGCAGGATGAGCCCTTCATCGGAGGGCGGCCGANGCAGGGCAAG	240			
Qy	81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro	100			
Db	241 GAACGGGGTGGCGGAGTGGCCCTGGCTTCGAGATACCGAAGTGACACACACCG	300			
Qy	101 AlaGlyProLeu 104				
Db	301 GCGGGACCGCTG 312				
RESULT 2					
AX189757					
LOCUS	AX189757	314 bp	DNA	linear	PAT 08-AUG-2001
DEFINITION	Sequence 1 from Patent WO0148164.				
ACCESSION	AX189757				
VERSION	AX189757.1	GI:15143133			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
TITLE	1 (bases 1 to 314)				
JOURNAL	Hammond,H.K. and Gao,M.				
FEATURES	Gene therapy for congestive heart failure				
source	Patent: WO 0148164-A 1 05-JUL-2001;				
	THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)				
	Location/Qualifiers				
	1..314				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				



Db 61 GAACGCAATGGCGAGAGGCTTCGGCGCGCCCTGGCACTGGGCAAGTGGCTTCTGCACG 120

QY 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60  
|||||  
Db 121 CCCCGTATATAGCTGCTCCGGGATGCAGACCCACCCAGCCCTCGCGGCCCC 180

QY 61 ProArgCysProTrpGlnAspAlaPheIleArgArgGlyGlyPro\*\*\*LysGlyLys 80  
|||||  
Db 181 CCTCGTGGCCCTGGCAGGATGACGCTTCATCCGAGGGGGCGGCCAGGCAAG 240

QY 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100  
|||||  
Db 241 GAGCTGGGCTGGGCGAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACACGACAGCG 300

QY 101 AlaGly 102  
|||

Db 301 GGCGGG 306

RESULT 4  
AXI89761

LOCUS AXI89761 3549 bp DNA linear PAT 08-AUG-2001

DEFINITION Sequence 5 from Patent WO0148164.

ACCESSION AXI89761

VERSION AXI89761.1 GI:15143135

KEYWORDS human.

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3549)

AUTHORS Hammond, H.K. and Gao, M.

TITLE Gene therapy for congestive heart failure

JOURNAL Patent: WO 0148164-A 5 05-JUL-2001;

FEATURES  
source Location/Qualifiers  
1..3549  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"

BASE COUNT 699 a 1025 c 1061 g 764 t

ORIGIN

Alignment Scores:  
Pred. No.: 8.64e-27 Length: 3549  
Score: 545.00 Matches: 99  
Percent Similarity: 97.06% Conservative: 0  
Best Local Similarity: 97.06% Mismatches: 3  
Query Match: 95.61% Indels: 0  
DB: 6 Gaps: 0

US-09-750-240-2 (1-104) x AXI89761 (1-3549)

QY 1 MetSerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGly 20  
|||||  
Db 1 ATGTCATGTTAGTGGCTCCGTCCTAAAGTGGATGAACGGAACAGCCTGGGGT 60

QY 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40  
|||||  
Db 61 GAACGCAATGGCGAGAGGCTTCGGCGCGCCCTGGCACTGGGCAAGTGGCTTCTGCACG 120

QY 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60  
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Db 121 CCCCGTATATAGCTGCTCCGGGATGCAGACCCACCCAGCCCTCGCGGCCCC 180

QY 61 ProArgCysProTrpGlnAspAlaPheIleArgArgGlyGlyPro\*\*\*LysGlyLys 80  
|||||  
Db 181 CCTCGTGGCCCTGGCAGGATGACGCTTCATCCGAGGGGGCGGCCAGGCAAG 240

US-09-750-240-2 (1-104) x AXI89761 (1-3549)

QY 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100  
|||||  
Db 241 GAGCTGGGCTGGGCGAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACACGACAGCG 300

QY 101 AlaGly 102  
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Db 301 GGCGGG 306

RESULT 6  
AXI89768

LOCUS AXI89768 3582 bp DNA linear PAT 08-AUG-2001

DEFINITION Sequence 12 from Patent WO0148164.

ACCESSION AXI89768

VERSION AXI89768.1 GI:15143140

KEYWORDS synthetic construct.

SOURCE artificial sequences.

ORGANISM 1 (bases 1 to 3582)

REFERENCE Hammond, H.K. and Gao, M.

AUTHORS Hammond, H.K. and Gao, M.

TITLE Gene therapy for congestive heart failure

JOURNAL Patent: WO 0148164-A 12 05-JUL-2001;

Db 301 GGCGGG 306

RESULT 5  
AXI89766

LOCUS AXI89766 3552 bp DNA linear PAT 08-AUG-2001

DEFINITION Sequence 10 from Patent WO0148164.

ACCESSION AXI89766

VERSION AXI89766.1 GI:15143139

KEYWORDS human.

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3552)

AUTHORS Hammond, H.K. and Gao, M.

TITLE Gene therapy for congestive heart failure

JOURNAL Patent: WO 0148164-A 10 05-JUL-2001;

FEATURES  
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BASE COUNT 686 a 1037 c 1068 g 761 t

ORIGIN

Alignment Scores:  
Pred. No.: 8.65e-27 Length: 3552  
Score: 545.00 Matches: 99  
Percent Similarity: 97.06% Conservative: 0  
Best Local Similarity: 97.06% Mismatches: 3  
Query Match: 95.61% Indels: 0  
DB: 6 Gaps: 0

US-09-750-240-2 (1-104) x AXI89766 (1-3552)

QY 1 MetSerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGly 20  
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QY 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40  
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Db 61 GAACGCAATGGCGAGAGGCTTCGGCGCGCCCTGGCACTGGGCAAGTGGCTTCTGCACG 120

QY 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60  
|||||  
Db 121 CCCCGTATATAGCTGCTCCGGGATGCAGACCCACCCAGCCCTCGCGGCCCC 180

QY 61 ProArgCysProTrpGlnAspAlaPheIleArgArgGlyGlyPro\*\*\*LysGlyLys 80  
|||||  
Db 181 CCTCGTGGCCCTGGCAGGATGACGCTTCATCCGAGGGGGCGGCCAGGCAAG 240

US-09-750-240-2 (1-104) x AXI89766 (1-3552)

QY 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100  
|||||  
Db 241 GAGCTGGGCTGGGCGAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACACGACAGCG 300

QY 101 AlaGly 102  
|||

Db 301 GGCGGG 306

RESULT 6  
AXI89768

LOCUS AXI89768 3582 bp DNA linear PAT 08-AUG-2001

DEFINITION Sequence 12 from Patent WO0148164.

ACCESSION AXI89768

VERSION AXI89768.1 GI:15143140

KEYWORDS synthetic construct.

SOURCE artificial sequences.

ORGANISM 1 (bases 1 to 3582)

REFERENCE Hammond, H.K. and Gao, M.

AUTHORS Hammond, H.K. and Gao, M.

TITLE Gene therapy for congestive heart failure

JOURNAL Patent: WO 0148164-A 12 05-JUL-2001;

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[illegible]

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QY 101 AlaGly 102
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Db 437 GCGGG 442

RESULT 8
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LOCUS Homo sapiens adenylyl cyclase type VI mRNA, complete cds.
DEFINITION Homo sapiens adenylyl cyclase type VI mRNA, complete cds.
ACCESSION AF250226
VERSION AF250226.1 GI:9049782
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 6463)
AUTHORS Wicker,R., Catalan,A.G., Cailleux,A., Starenki,D., Stengel,D.,
Sarasin,A. and Suarez,H.G.
Cloning and expression of human adenylyl cyclase type VI in normal
thyroid tissues
Biochim. Biophys. Acta 1493 (1-2), 279-283 (2000)
JOURNAL
MEDLINE 20435313
PubMed 10978539
REFERENCE 2 (bases 1 to 6463)
Wicker,R., Gascon Catalan,A., Cailleux,A.-F., Starenki,D.,
Stengel,D., Sarasin,A. and Suarez,H.G.
Direct Submission
Submitted (28-MAR-2000) Lab Etude des Relations - Instabilite
genetique et Cancer UPR 2169, Institut de Recherches sur le Cancer
CNRS IFR 1221, 7 rue Guy Moquet, Villejuif 94801, France
FEATURES
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KITGTYTGAAGSINATYDQVGRSHITALADYAMRLMEQMKHINSHSFNNFQMKIGLN
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GVVKKVGKEMTYTFLNGPSS"
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BASE COUNT 1264 a 1795 c 1871 g 1533 t

ORIGIN

Alignment Scores:

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Pred. No.: 1.47e-26 Length: 6463
Score: 545.00 Matches: 99
Percent Similarity: 97.06% Conservative: 0
Best Local Similarity: 97.06% Mismatches: 3
Query Match: 95.61% Indels: 0
DB: 9 Gaps: 0

US-09-750-240-2 (1-104) x AF250226 (1-6463)

QY 1 MetSerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTatPgly 20
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Db 695 ATGTCATGTTTACTGCGCTCTCTGGTCCCTTAAAGTGGATGAACGAAACAGCCTGGGGC 754
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QY 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40
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Db 755 GAACCAATGGGCGAGAAAGCTTCGCGGCGCGTGGCACTCGGCAGGTGCTTCTGCACG 814
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QY 41 ProArgTyrMetSerCysLeuArgAspAlaGluProSerProThrProAlaGlyPro 60
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Db 815 CCCCGTATATGAGCTGCCTCCGGGATGCAGAGCCACCCAGCCCACTCCGCGCCCC 874
    |||

QY 61 ProArgCysProTrpGlnAspAspAlaPheIleArgArgGlyGlyPro**LysGlyLys 80
    |||
Db 875 CCTCGGTGCCCTGGCAGGATGACGCTTCATCCGAGGGCGGCCGCCAGGCGGCAAG 934
    |||

QY 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100
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Db 935 GACCTGGGCTGCGGGCAGTGCGCTTCGAGGATACCGAGGTGACACGACGACGCG 994
    |||

QY 101 AlaGly 102
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Db 995 GCGGG 1000

RESULT 9
AC021647/c AC021647 193283 bp DNA linear HTG 09-MAY-2002
LOCUS Homo sapiens chromosome 12 clone RP11-455I22, WORKING DRAFT
DEFINITION SEQUENCE, 8 unordered pieces.
ACCESSION AC021647
VERSION AC021647.18 GI:20335444
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 193283)
AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaralunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carton,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
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Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hoques,M., Holloway,C., Hollins,B.,
Homs,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlisson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,D.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
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Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newtonson,J., Newtonson,N., Nguyen,A., Nguyen,N.,
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Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rivers, M., Rojas, A., Rojokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shoostari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Woodson, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.

Direct Submission  
Unpublished  
2 (bases 1 to 193283)  
Worley, K.C.

Direct Submission  
Submitted (19-JAN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 193283)  
Worley, K.C.

Direct Submission  
Submitted (09-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On Apr 28, 2002 this sequence version replaced gi:15809061.

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Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
-----  
Project Information  
Center project name: HAAF  
Center clone name: RP11-455122  
-----  
Summary Statistics  
Sequencing vector: Plasmid;  
Chemistry: Dye-terminator Big Dye; 2% of reads  
Chemistry: Dye-terminator Big Dye; 98% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 219180 bases at least Q40  
Consensus quality: 233400 bases at least Q30  
Consensus quality: 243367 bases at least Q20  
Estimated insert size: 209025; sum-of-contigs estimation  
Quality coverage: 10x in Q20 bases; sum-of-contigs estimation  
-----

\* NOTE: Estimated insert size may differ from sequence length  
(see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 8 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

\* 1 2133: contig of 2133 bp in length  
\* 2134 2233: gap of unknown length  
\* 2234 5400: contig of 3167 bp in length  
\* 5401 5500: gap of unknown length  
\* 5501 7889: contig of 2389 bp in length  
\* 7890 7989: gap of unknown length  
\* 7990 35656: contig of 27667 bp in length  
\* 35657 35756: gap of unknown length  
\* 35757 65617: contig of 29861 bp in length  
\* 65618 65717: gap of unknown length  
\* 65718 104448: contig of 38731 bp in length  
\* 104449 104548: gap of unknown length  
\* 104549 145966: contig of 41418 bp in length  
\* 145967 146066: gap of unknown length  
\* 146067 193283: contig of 47217 bp in length.

FEATURES  
source 1. 193283  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="12"  
/clone="RP11-455122"  
BASE COUNT 49273 a 48888 c 46863 g 47544 t 715 others  
ORIGIN  
Alignment Scores: 3.01e-25 Length: 193283  
Pred. No.: 545.00 Matches: 99  
Score: 97.06% Conservative: 0  
Percent Similarity: 97.06% Mismatches: 3  
Best Local Similarity: 95.61% Indels: 0  
Query Match: 2 Gaps: 0  
DB: 2  
US-09-750-240-2 (1-104) x AC021647 (1-193283)  
QY 1 MetSerTTPpHeSerGlyLeuLeuValProTysValAspGluArgLysThrAlaTyrGly 20  
Db 74771 ATGTCATGTTTAGTGGCTCTCTGTCCTAAAGTGGATGAACGGAACACACCTGGGGT 74712  
QY 21 GluArgASngLgLnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40  
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QY 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60  
Db 74651 CCCCGTATATAGCTGCTCCGGGATGCAGAGCCACCCAGCCCTCGGGGCCCC 74592  
QY 61 ProArgCysProTTPGlnAspAspAlaPheIleArgArgGlyGlyPro\*\*LysGlyLys 80  
Db 74591 CTTGGTCCCTTGGCAGGATGACGCCCTCATCGGAGGGGGCGCCAGGAGGCAAG 74532  
QY 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100  
Db 74531 GAGCTGGGGCTCGGGCAGTGGCCCTTGGGCTTCGAGGATACCGAGGTGACACGACGAGG 74472  
QY 101 AlaGly 102  
Db 74471 GCGGG 74466  
RESULT 10  
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LOCUS AC117498 205248 bp DNA linear HTG 31-JUL-2002  
DEFINITION Homo sapiens clone RP11-422021, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 20  
unordered pieces.  
ACCESSION AC117498  
VERSION AC117498.4 GI:22002346  
KEYWORDS HTG; HTGS\_PHASE1.  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 205248)  
AUTHORS Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayale, M., Banks, T., Barbara, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brivaw, M., Brown, E., Brown, M., Bryant, N.P., Buha, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleaveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Din, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hoques, M., Holloway, C., Hollins, B.,

Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E.,  
 Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,  
 Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,  
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 Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louise, H.,  
 Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,  
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 Scherer, S., Scott, G., Shen, H., Shoostari, N., Sisson, I.,  
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 Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K.,  
 Wu, C., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,  
 Weinstein, G., and Gibbs, R.  
 Direct Submission  
 Unpublished  
 2 (bases 1 to 205248)  
 Worley, K.C.  
 Direct Submission  
 Submitted (10-APR-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 3 (bases 1 to 205248)  
 Worley, K.C.  
 Direct Submission  
 Submitted (31-JUL-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 On Jul 29, 2002 this sequence version replaced gi:21956504.  
 ----- Genome Center  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: <http://www.hgsc.bcm.tmc.edu/>  
 Drafting Center Code: WUGSC  
 Contact: hgsc-help@bcm.tmc.edu  
 ----- Project Information  
 Center project name: HEAU  
 Center clone name: RP11-422021  
 ----- Summary Statistics  
 Sequencing vector: Plasmid;  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.990329  
 Consensus quality: 216840 bases at least Q40  
 Consensus quality: 220255 bases at least Q30  
 Consensus quality: 222408 bases at least Q20  
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 \* NOTE: Estimated insert size may differ from sequence length  
 \* (see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)).  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 20 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
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 \* 1 2025: contig of 2025 bp in length  
 \* 2026 2125: gap of unknown length  
 \* 2126 4437: contig of 2312 bp in length  
 \* 4438 4537: gap of unknown length  
 \* 4538 6633: contig of 2096 bp in length  
 \* 6634 6733: gap of unknown length  
 \* 6734 9148: contig of 2415 bp in length  
 \* 9149 9248: gap of unknown length

\* 9249 11635: contig of 2387 bp in length  
 \* 11636 11735: gap of unknown length  
 \* 11736 13780: contig of 2045 bp in length  
 \* 13781 13880: gap of unknown length  
 \* 13881 16997: contig of 2817 bp in length  
 \* 16998 16997: gap of unknown length  
 \* 16998 20089: contig of 3292 bp in length  
 \* 20090 20189: gap of unknown length  
 \* 20190 23014: contig of 2825 bp in length  
 \* 23015 23114: gap of unknown length  
 \* 23115 25345: contig of 2231 bp in length  
 \* 25346 25445: gap of unknown length  
 \* 25446 31033: contig of 5588 bp in length  
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 \* 31134 35863: contig of 4730 bp in length  
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 \* 49815 49914: gap of unknown length  
 \* 49915 64385: contig of 14471 bp in length  
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 \* 81201 97966: contig of 16766 bp in length  
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 \* 115534 115633: gap of unknown length  
 \* 115634 139873: contig of 24240 bp in length  
 \* 139874 139973: gap of unknown length  
 \* 139974 175364: contig of 35391 bp in length  
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 Alignment Scores:  
 Pred. No.: 3.17e-25 Length: 205248  
 Score: 545.00 Matches: 99  
 Percent Similarity: 97.06% Conservative: 0  
 Best Local Similarity: 97.06% Mismatches: 3  
 Query Match: 95.61% Indels: 0  
 DB: 2 Gaps: 0  
 US-09-750-240-2 (1-104) x AC117498 (1-205248)  
 QY 1 MetSerTripphSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGly 20  
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 QY 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100  
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 QY 101 AlaGly 102  
 Db 168819 GCGGG 168814

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RESULT 11
AC025557/c
LOCUS      171945 bp      DNA      linear      HTG 07-JUL-2000
DEFINITION Homo sapiens chromosome 12 clone RP11-579D7, WORKING DRAFT
SEQUENCE, 17 unordered pieces.
ACCESSION AC025557
VERSION    4
KEYWORDS   HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            Waterston,R.H.
            The sequence of Homo sapiens clone
            Unpublished
            2 (bases 1 to 171945)
            Waterston,R.H.
            Direct Submission
            Submitted (10-MAR-2000) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
            On Apr 27, 2000 this sequence version replaced gi:7574970.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H.NH0579D7
----- Summary Statistics -----
Sequencing vector: M13; 100%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 166140 bases at least Q40
Consensus quality: 167959 bases at least Q30
Consensus quality: 168924 bases at least Q20
Insert size: 177000; agarose-fp
Insert size: 170345; sum-of-ctnigs
Quality coverage: 5.62 in Q20 bases; agarose-fp
Quality coverage: 5.86 in Q20 bases; sum-of-ctnigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 17 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 1862: contig of 1862 bp in length
* 1863 1962: gap of unknown length
* 1963 3736: contig of 1774 bp in length
* 3737 3836: gap of unknown length
* 3837 6925: contig of 3089 bp in length
* 6926 7025: gap of unknown length
* 7026 11773: contig of 4748 bp in length
* 11774 11873: gap of unknown length
* 11874 19405: contig of 7532 bp in length
* 19406 19505: gap of unknown length
* 19506 26329: contig of 6824 bp in length
* 26330 26429: gap of unknown length
* 26430 33594: contig of 7165 bp in length
* 33595 33694: gap of unknown length
* 33695 42148: contig of 8454 bp in length
* 42149 42249: gap of unknown length
* 42249 52390: contig of 10142 bp in length
* 52391 52491: gap of unknown length
* 52491 62388: contig of 9898 bp in length
* 62389 62488: gap of unknown length
* 62489 72408: contig of 9920 bp in length

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* 72409 72508: gap of unknown length
* 72509 84743: contig of 12235 bp in length
* 84744 84843: gap of unknown length
* 84844 97522: contig of 12679 bp in length
* 97523 97622: gap of unknown length
* 97623 110884: contig of 13262 bp in length
* 110885 110984: gap of unknown length
* 110985 126977: contig of 15993 bp in length
* 126978 127077: gap of unknown length
* 127078 146137: contig of 19060 bp in length
* 146138 146237: gap of unknown length
* 146238 171945: contig of 25708 bp in length.
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        3837. 6925
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        7026. 11773
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        26430. 33594
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            /note="assembly_name:Contig13"
        52491. 62388
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        84844. 97522
            /note="assembly_name:Contig17"
        97623. 110884
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        110985. 126977
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BASE COUNT 43195 a 42962 c 41369 g 42818 t 1601 others
ORIGIN
Alignment Scores:
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Score:          518.00      Matches:      98
Percent Similarity: 96.08%      Conservative: 0
Best Local Similarity: 96.08%      Mismatches: 4
Query Match:      90.88%      Indels:      1
DB:              2          Gaps:      0
US-09-750-240-2 (1-104) x AC025557 (1-171945)
Qy 1 MetSerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGly 20
Db 79560 ATGTCATGGTTTACTGGCCCTCTGTCCTCTAAAGTGGATGAACGAAACACCTGGGGT 79501

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QY 21 GluArgAsnGlyClnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40
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Db 79500 GAACGCAATGGCAGAGCGTTCCGCGCGCTGGGACACTCGGCAGTGGCTTCGCACG 79441

QY 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60
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Db 79440 CCCCCTATATAGTGCCTCCGGGATGCAGAGCCACCCAGCCACCCTGC-GGCCCC 79382

QY 61 ProArgCysProTrpClnAspAlaPheIleArgArgGlyGlyPro***LysGlyLys 80
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Db 79381 CTTGGTGGCCCTGGCAGGATGAGCGCTTCATCCGGAGGGGGGCCAGGCAAGGGCAAG 79322

QY 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100
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Db 79321 GAGCTGGGCTGGGGCAGTGGCCCTGGCTTCGAGGATACCGAGGTGACACGACAGCG 79262

QY 101 AlaGly 102
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Db 79261 GCGGG 79256

RESULT 12
LOCUS DOGADENCYC 4046 bp mRNA linear MAM 27-APR-1993
DEFINITION Canis familiaris adenylyl cyclase type VI mRNA sequence.
ACCESSION M94968
VERSION M94968.1 GI:163896
KEYWORDS adenylyl cyclase type VI.
SOURCE Canis familiaris cardiac muscle cDNA to mRNA.
ORGANISM Canis familiaris

REFERENCE
1 (bases 1 to 4046)
AUTHORS Katsushika, S., Chen, L., Kawabe, J., Nilakantan, R., Halnon, N.J.,
Honey, C.J. and Ishikawa, Y.
TITLE Cloning and characterization of a sixth adenylyl cyclase isoform:
types V and VI constitute a subgroup within the mammalian adenylyl
cyclase family
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (18), 8774-8778 (1992)
MEDLINE 92409599
PubMed 1528892
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Location/Qualifiers
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/organism="Canis familiaris"
/db_xref="taxon:9615"
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source
Location/Qualifiers
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/tissue.type="cardiac muscle"
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source
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Best Local Similarity: 83.18% Mismatches: 11
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Db 131 ATGTCGTGTTAGTGGCTCTCTGTCCTCCCAAGTGATGAACGGAAGACAGCTGGGT 190

QY 21 GluArgAsnGlyClnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40
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Db 191 GAACGCAATGGCAGAGCGTCCA---CGCCGGGAGACTCGGACCACTGGCTTCTGCACG 247

QY 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60
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Db 248 CCCCCTATATAGTGCCTCCGGGATGCAGAGCCACCCAGTCCACCTCGCGCTCC 307

QY 61 ProArgCysProTrpClnAspAlaPheIleArgArgGlyGlyPro***LysGlyLys 80
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QY 97 ThrThrThrProAlaGlyPro 103
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Db 428 GGGCAGCTGGAGGTGGCCCT 448

RESULT 14
LOCUS AR106659 4131 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 11 from patent-US 610706.
ACCESSION AR106659
VERSION AR106659.1 GI:12821189
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

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QY 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGlu-----Val 96
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RESULT 13
LOCUS I29958 4046 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 1 from patent US 5578481.
ACCESSION I29958
VERSION I29958.1 GI:1820749
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 4046)
AUTHORS Ishikawa, Y.
TITLE Cloning and characterization of a cardiac adenylyl cyclase
JOURNAL Patent: US 5578481-A 1 26-NOV-1996;
FEATURES Location/Qualifiers
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/organism="unknown"
BASE COUNT 743 a 1202 c 1257 g 844 t
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source
Alignment Scores:
Pred. No.: 4.7e-22 Length: 4046
Score: 472.50 Matches: 89
Percent Similarity: 85.05% Conservative: 2
Best Local Similarity: 83.18% Mismatches: 11
Query Match: 82.89% Indels: 5
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QY 21 GluArgAsnGlyClnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40
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Db 191 GAACGCAATGGCAGAGCGTCCA---CGCCGGGAGACTCGGACCACTGGCTTCTGCACG 247

QY 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60
|||
Db 248 CCCCCTATATAGTGCCTCCGGGATGCAGAGCCACCCAGTCCACCTCGCGCTCC 307

QY 61 ProArgCysProTrpClnAspAlaPheIleArgArgGlyGlyPro***LysGlyLys 80
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Db 308 CCTCGTGGCCCTGGCAGGATGAGCGCTTCATCCGAGAGGGCGGCCGCAAGGGCAGC 367

QY 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGlu-----Val 96
|||
Db 368 GAGCTGGGCTGGGGCGGTGGCCCTGGCTTCGAGGACACTGAGGCCATGTCAGCGGTT 427

QY 97 ThrThrThrProAlaGlyPro 103
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Db 428 GGGCAGCTGGAGGTGGCCCT 448

RESULT 14
LOCUS AR106659 4131 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 11 from patent-US 610706.
ACCESSION AR106659
VERSION AR106659.1 GI:12821189
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

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REFERENCE 1 (bases 1 to 4131)  
AUTHORS Tang,W.-J. and Gilman,A.G.  
TITLE Soluble mammalian adenylyl cyclase and uses therefor  
JOURNAL Patent: US 6107076-A 11 22-AUG-2000;  
FEATURES Location/Qualifiers  
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/organism="unknown"

BASE COUNT 835 a 1190 c 1182 g 924 t  
ORIGIN

Alignment Scores:  
Pred. No.: 1.99e-19 Length: 4131  
Score: 432.00 Matches: 81  
Percent Similarity: 86.27% Conservative: 7  
Best Local Similarity: 79.41% Mismatches: 12  
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US-09-750-240-2 (1-104) x AR106659 (1-4131)

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Qy 101 AlaGly 102  
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Db 350 ATGGGG 355

RESULT 15  
RATADCYB 4131 bp mRNA linear ROD 27-APR-1993  
LOCUS  
DEFINITION Rattus norvegicus adenylyl cyclase type VI mRNA, complete cds.  
ACCESSION M96160  
VERSION M96160.1 GI:202718  
KEYWORDS adenylylate cyclase; adenylyl cyclase type VI.  
SOURCE Rattus norvegicus (strain Sprague-Dawley) adult liver, kidney,  
heart cDNA to mRNA.

ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
1 (bases 1 to 4131)  
Premont, R.T.  
TITLE Multiple mechanisms underlying desensitization of the liver  
adenylyl cyclase system. Structure and cAMP regulation of liver  
adenylyl cyclases  
Thesis (1992)

REFERENCE 2 (bases 1 to 4131)  
AUTHORS Premont, R.T., Chen, J., Ma, H.W., Ponnappalli, M. and Iyengar, R.  
TITLE Two members of a widely expressed subfamily of hormone-stimulated  
adenylyl cyclases  
Proc. Natl. Acad. Sci. U.S.A. 89 (20), 9809-9813 (1992)  
JOURNAL MEDLINE 93028552  
PUBMED 1409703

FEATURES Location/Qualifiers  
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/strain="Sprague-Dawley"  
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BASE COUNT 835 a 1190 c 1182 g 924 t  
ORIGIN

Alignment Scores:  
Pred. No.: 1.99e-19 Length: 4131  
Score: 432.00 Matches: 81  
Percent Similarity: 86.27% Conservative: 7  
Best Local Similarity: 79.41% Mismatches: 12  
Query Match: 75.79% Indels: 2  
DB: 6 Gaps: 2

US-09-750-240-2 (1-104) x RATADCYB (1-4131)

Qy 1 MetSerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGly 20  
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Db 56 ATGTCATGTTTAGCGGCTCTGTTCCCAAGTGGATGACGAAACAGCCTGGGCG 115  
Qy 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40  
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Db 116 GAACGCAATGACAGACGCGCCCA---CGCCAGCGCGACCCGCGGCTTCTGCGCG 172  
Qy 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60  
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Db 173 CCCGCTACATGAGCTGCTCAAGAATGTGGAGCCACCCAGCCGCTCTGCGCTGCG 232  
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Db 233 ACTGGTCCCTGGCAGGATGAGCCTTCATCAGGAGGCGTGGCCCGGAAGGGGTGTG 292  
Qy 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100  
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Db 293 GAGCTGGGCTGCGGTCACTAGTGGCTTGGGTTTGTATGACACTGAGGTG---ACCACACCG 349  
Qy 101 AlaGly 102  
|||  
Db 350 ATGGGG 355

Search completed: March 1, 2003, 11:05:22







GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 1, 2003, 03:53:43 ; Search time 219 Seconds  
(without alignments)  
1069.442 Million cell updates/sec

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Perfect score: 570  
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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
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Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0  
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Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	568	99.6	2127	19	AAV23246 Human adenylyl cycl
3	545	95.6	3549	22	AA080563 Human cardiac aden
4	545	95.6	3552	22	AA080567 Human cardiac aden
5	545	95.6	3582	22	AA080568 Human modified car
6	545	95.6	4942	20	AA000461 Human type VI aden
7	472.5	82.9	4046	14	AAQ42525 Cardiac adenylyl c
8	432	75.8	4131	21	AA53923 Type VI adenylyl c
9	432	75.8	5841	24	ABT196680 Mouse ischaemic co
10	94	16.5	1533	23	AA554118 Pseudomonas aerugi
11	94	16.5	2312	14	AAQ35141 smrk coding sequen
12	92.5	16.2	2622	22	AAH16074 Human cDNA sequenc
13	91.5	16.1	3474	9	AAH80908 Sequence of Herpes
14	91.5	16.1	4257	19	AAV68520 The nucleotide seq
15	91.5	16.1	4257	19	AAV10362 Infected cell prot
16	91.5	16.1	12001	16	AAQ76213 HSV L/ST region.
17	90.5	15.9	1173	21	AAZ94583 Maize cyclin D Zmc
18	90.5	15.9	1932	20	AAZ19961 Corn cyclin delta-
19	90	15.8	777	22	AAH04121 Human cDNA clone (
20	90	15.8	2612	22	AAH17215 Human cDNA sequenc
21	90	15.8	3465	12	AAQ14478 HSVgB gene. Herpe
22	89.5	15.7	1182	19	AAV50488 Streptomyces clavu
23	89.5	15.7	1879	12	AAQ11126 Sequence encoding
24	89.5	15.7	7193	19	AAV50431 Streptomyces clavu
25	89	15.6	3642	6	AAH50364 DNA fragment encod
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28	88.5	15.5	3394	22	AAI58433 Human polynucleoti
29	88.5	15.5	4098	23	ABL41555 Fusion gene of tre
30	88.5	15.5	12749	20	AAQ78032 Human Huntington's
31	88	15.4	1974	24	ABQ90272 M. capsulatus gene
32	88	15.4	3472	14	AAQ48497 Glycoprotein B (gB
33	88	15.4	3473	18	AAAT93651 Herpes simplex vir
34	88	15.4	10982	22	ABA20509 Human nervous syst
35	88	15.4	10982	22	ABA20510 Human nervous syst
36	88	15.4	49634	24	ABL68647 Kidney cancer rela
37	88	15.4	53789	19	AAV21187 Amycolatopsis medi
38	87.5	15.4	2127	23	ABA95459 Thermus thermophil
39	87	15.3	1544	20	AAV80747 Human secreted pro
40	87	15.3	1622	22	AAH98204 Human EST-derived
41	87	15.3	2241	21	AAZ51469 Vector pVGRXR enco
42	87	15.3	2295	21	AAZ51470 Vector pVGRXR-5A/5
43	87	15.3	2301	21	AAZ51471 Control vector pVg
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ALIGNMENTS

RESULT 1

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ID AAD08561 standard; cDNA; 314 BP.  
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AC AAD08561;  
XX  
DT 04-SEP-2001 (first entry)  
XX

Human partial cardiac adenylylase VI (ACVI) isoform #1 cDNA.

Human; cardiant; beta-adrenergic signalling protein; beta-ASP;  
myocardium; gene therapy; beta-adrenergic receptor; beta-AR;  
adenylylase; adenylylase; adenylylase; cAMP synthetase;  
G-protein receptor kinase; GRK; heart disease; congestive heart failure;  
cardiac adenylylase VI; ACVI isoform; beta-ASP transgene; ss.  
Homo sapiens.  
XX  
XX



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Alignment Scores:
Pred. No.: 1,86e-35 Length: 2127
Score: 568.00 Matches: 104
Percent Similarity: 100.00% Conservatives: 0
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Query Match: 99.65% Indels: 0
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US-09-750-240-2 (1-104) x AAV23246 (1-2127)
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DQ 61 GAACGCAATGGGCGAGAGGCTTCGCGCGCGCTGGGCACTCGGCGAGTGGCTTCTGCACG 120
QY 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60
DQ 121 CCCCCTATATAGCTGCTCCGGGATGAGAGCCACCCAGCCCTCGCGGCGCC 180
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ID AAD08563 standard; DNA; 3549 BP.
AC AAD08563;
XX
DT 04-SEP-2001 (first entry)
DE Human cardiac adenylylase VI (ACVI) isoform #1 DNA.
KW Human; cardiant; beta-adrenergic signalling protein; beta-ASP;
KW myocardium; gene therapy; beta-adrenergic receptor; beta-AR;
KW adenylylase; adenylylase; adenylylase; CAMP synthetase;
KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;
KW cardiac adenylylase VI; ACVI isoform; beta-ASP transgene; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
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PN WO200148164-A2.
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PD 05-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US35411.
XX
PR 27-DEC-1999; 99US-0472667.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Hammond HK, Gao M;
XX
XX WPI; 2001-418260/44.
DR P-PSDB; AAE04310.
```

```
XX
PT Novel polynucleotide encoding a modified adenylylase polypeptide
PT useful for enhancing cardiac function in mammalian hearts, and for
PT treating heart disease, especially congestive heart failure -
XX
PS Example 5; Page 122-129; 153pp; English.
XX
CC The present invention relates to methods and compositions for enhancing
CC cardiac function in mammalian hearts by inserting transgenes encoding
CC beta-adrenergic signalling proteins (beta-ASP) which increase
CC beta-adrenergic responsiveness within the myocardium using in vivo
CC gene therapy. The beta-ASPs of the invention include beta-adrenergic
CC receptors (beta-AR), adenylylases (also referred to as adenylylase,
CC adenylylase and CAMP synthetase) and G-protein receptor kinase
CC (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function
CC in mammalian hearts and for treating heart disease, especially
CC congestive heart failure. The present DNA sequence encodes human
CC cardiac adenylylase VI (ACVI) isoform which is used for generating
CC a third beta-ASP transgene, used in the exemplification
XX of the invention.
XX
SQ Sequence 3549 BP; 699 A; 1025 C; 1061 G; 764 T; 0 other;

Alignment Scores:
Pred. No.: 1,91e-33 Length: 3549
Score: 545.00 Matches: 99
Percent Similarity: 97.06% Conservatives: 0
Best Local Similarity: 97.06% Mismatches: 3
Query Match: 95.61% Indels: 0
DB: 22 Gaps: 0

US-09-750-240-2 (1-104) x AAD08563 (1-3549)
QY 1 MetSerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGly 20
DQ 1 ATGTCATGGTTAGTGGCTCCCTGCTCCCTAAAGTGGATGAACGGAACACAGCCTGGGT 60
QY 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40
DQ 61 GAACGCAATGGGCGAGAGGCTTCGCGCGCGCTGGGCACTCGGCGAGTGGCTTCTGCACG 120
QY 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60
DQ 121 CCCCCTATATAGCTGCTCCGGGATGAGAGCCACCCAGCCCTCGCGGCGCC 180
QY 61 ProArgCysProTrpGlnAspAlaPheIleArgArgGlyGlyPro***LysGlyLys 80
DQ 181 CCTCGTGCCCTGGCAGGATGAGCTTCATCCGAGGGGGCGCCANGCAAGGCAAG 240
QY 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100
DQ 241 GAGCTGGGGTGGGGCAGTGGGCTTGGGCTTGAAGATACCGAAGTGACACGACACG 300
QY 101 AlaGly 102
DQ 301 GCGGG 306
RESULT 4
AAD08567
ID AAD08567 standard; DNA; 3552 BP.
XX
AC AAD08567;
XX
DT 04-SEP-2001 (first entry)
DE Human cardiac adenylylase VI (ACVI) isoform #2 DNA.
KW Human; cardiant; beta-adrenergic signalling protein; beta-ASP;
KW myocardium; gene therapy; beta-adrenergic receptor; beta-AR;
KW adenylylase; adenylylase; adenylylase; CAMP synthetase;
KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;
KW cardiac adenylylase VI; ACVI isoform; beta-ASP transgene; ds.
XX
```

OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT 1..3507  
FT /\*tag= a  
FT /product= "Human cardiac adenylylase VI isoform #2"  
FT /EC\_number= "4.6.1.1"  
XX  
PN WO200148164-A2.  
XX  
XX 05-JUL-2001.  
XX  
XX 26-DEC-2000; 2000WO-US35411.  
XX  
XX 27-DEC-1999; 99US-0472667.  
XX  
XX (REGC ) UNIV CALIFORNIA.  
XX  
XX Hammond HK, Gao M;  
XX WPI; 2001-418260/44.  
XX P-PSDB; AAE04311.  
XX  
XX Novel polynucleotide encoding a modified adenylylase polypeptide  
XX useful for enhancing cardiac function in mammalian hearts, and for  
XX treating heart disease, especially congestive heart failure -  
XX  
XX Claim 6; Page 134-140; 153pp; English.  
XX  
XX The present invention relates to methods and compositions for enhancing  
XX cardiac function in mammalian hearts by inserting transgenes encoding  
XX beta-adrenergic signalling proteins (beta-ASP) which increase  
XX beta-adrenergic responsiveness within the myocardium using in vivo  
XX gene therapy. The beta-ASPs of the invention include beta-adrenergic  
XX receptors (beta-AR), adenylylases (also referred as adenylylase,  
XX adenylylase and G-protein receptor kinase) and G-protein receptor kinase  
XX (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function  
XX in mammalian hearts and for treating heart disease, especially  
XX congestive heart failure. The present DNA sequence encodes human  
XX cardiac adenylylase VI (ACVI) isoform which is used for generating  
XX a fourth beta-ASP transgene, used in the exemplification  
XX of the invention.  
XX  
SQ Sequence 3552 BP; 686 A; 1037 C; 1068 G; 761 T; 0 other;  
  
Alignment Scores:  
Pred. No.: 1.91e-33 Length: 3552  
Score: 545.00 Matches: 99  
Percent Similarity: 97.06% Conservative: 0  
Best Local Similarity: 97.06% Mismatches: 3  
Query Match: 95.61% Indels: 0  
DB: 22 Gaps: 0  
  
US-09-750-240-2 (1-104) x AAD08567 (1-3552)  
  
Qy 1 MetSerTrpSerGlyLeuValProLysValAspGluArgLysThrAlaTrpGly 20  
Db 1 ATGTGATGTTTAGTGGCTCTCTGTCTCTTAAGTGGATGAACGAAACACCTGGGGT 60  
Qy 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40  
Db 61 GAACGCAATGGGCAAGAACGCTCGGGGCGGTGGCACTCGGCGAGGTGCTTGCACG 120  
Qy 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60  
Db 121 CCCCGTATATAGCTGCTCCGGATGACAGAGCCACCCACCCCTGGGGCCCC 180  
Qy 61 ProArgCysProTrpGlnAspAlaPheIleArgArgGlyGlyPro\*\*\*LysGlyLys 80  
Db 181 CCTCGGTCCCTGGCAGGATGACGCTTCATCCGGAGGGCGGCCACGAGGCAAG 240  
Qy 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100  
|||||

Db 241 GAGCTGGGGTGGGGGAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACACGACGCG 300  
Qy 101 AlaGly 102  
|||  
Db 301 GCGGG 306  
RESULT 5  
AAD08568  
ID AAD08568 standard; cDNA; 3582 BP.  
XX  
XX AAD08568;  
XX  
XX 04-SEP-2001 (first entry)  
XX  
XX Human modified cardiac adenylylase VI (ACVI) isoform cDNA.  
XX  
XX Human; cardiac; beta-adrenergic signalling protein; beta-ASP;  
XX myocardium; gene therapy; beta-adrenergic receptor; beta-AR;  
XX adenylylase; adenylylase; adenylylase; adenylylase;  
XX G-protein receptor kinase; GRK; heart disease; congestive heart failure;  
XX cardiac adenylylase VI; ACVI isoform; beta-ASP transgene; ss.  
XX  
XX Homo sapiens.  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
XX CDS 22..3525  
XX /\*tag= a  
XX /product= "Human modified cardiac ACVI isoform"  
XX  
XX WO200148164-A2.  
XX  
XX 05-JUL-2001.  
XX  
XX 26-DEC-2000; 2000WO-US35411.  
XX  
XX 27-DEC-1999; 99US-0472667.  
XX  
XX (REGC ) UNIV CALIFORNIA.  
XX  
XX Hammond HK, Gao M;  
XX  
XX WPI; 2001-418260/44.  
XX P-PSDB; AAE04312.  
XX  
XX Novel polynucleotide encoding a modified adenylylase polypeptide  
XX useful for enhancing cardiac function in mammalian hearts, and for  
XX treating heart disease, especially congestive heart failure -  
XX  
XX Claim 4; Page 143-150; 153pp; English.  
XX  
XX The present invention relates to methods and compositions for enhancing  
XX cardiac function in mammalian hearts by inserting transgenes encoding  
XX beta-adrenergic signalling proteins (beta-ASP) which increase  
XX beta-adrenergic responsiveness within the myocardium using in vivo  
XX gene therapy. The beta-ASPs of the invention include beta-adrenergic  
XX receptors (beta-AR), adenylylases (also referred as adenylylase,  
XX adenylylase and G-protein receptor kinase) and G-protein receptor kinase  
XX (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function  
XX in mammalian hearts and for treating heart disease, especially  
XX congestive heart failure. The present cDNA sequence encodes human  
XX modified cardiac adenylylase VI (ACVI) isoform which is used for  
XX generating a beta-ASP transgene, used in the exemplification of the  
XX invention.  
XX  
SQ Sequence 3582 BP; 703 A; 1036 C; 1067 G; 776 T; 0 other;  
  
Alignment Scores:  
Pred. No.: 1.93e-33 Length: 3582  
Score: 545.00 Matches: 99  
Percent Similarity: 97.06% Conservative: 0  
Best Local Similarity: 97.06% Mismatches: 3  
Query Match: 95.61% Indels: 0

```

DB:                22                Gaps:                0
US-09-750-240-2 (1-104) x AAD08568 (1-3582)
QY 1 MetSerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGly 20
   |||
Db 22 ATCTCATGGTTTGTAGTGGCTCTCTGGTCCCTAAAGTGGATGAACGGAACAGCCTGGGT 81
QY 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40
   |||
Db 82 GAACGCAATGGGCAAGAGCTTCGCGCGCGGTGGCACTCGGGCAGTGGCTTCTGCACG 141
QY 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60
   |||
Db 142 CCCCGCTATATGAGCTCCCTCCGGGATGCAGAGCCACCCAGCCCTGGGGCCCC 201
QY 61 ProArgCysProTrpGlnAspAspAlaPheIleArgArgGlyGlyPro***LysGlyLys 80
   |||
Db 202 CCTCGTGGCCCTGGCAGGATGACGCTTCATCCGGAGGGCGGCCGCAAGGCAAG 261
QY 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100
   |||
Db 262 GAGCTGGGCTGGGGCAGTGGCCCTTCGAGGATACCGAGGTGACACGACAGCG 321
QY 101 AlaGly 102
   |||
Db 322 GCGGG 327

RESULT 6
AAX00461
ID AAX00461 standard; cDNA; 4942 BP.
XX
AC AAX00461;
XX
DT 21-MAY-1999 (first entry)
XX
DE Human type VI adenylyl cyclase cDNA.
XX
KW Adenylyl cyclase type VI; human; hAC6; therapy; diagnosis; ds.
XX
OS Homo sapiens.
XX
FH Key
FT CDS
FT FT
FT FT
PN WO9901547-A1.
XX
PD 14-JAN-1999.
XX
XX 01-JUL-1998; 98WO-US13694.
XX
PR 01-JUL-1997; 97US-0886550.
PR 01-JUL-1997; 97US-0070904.
XX
PA (CORT-) COR THERAPEUTICS INC.
XX
PI Tomlinson JA;
XX
DR WPI; 1999-106049/09.
DR P-PSDB; AAW30599.
XX
PT Newly isolated and purified human type VI adenylyl cyclase (hAC6)
PT polypeptide - useful for identifying potential therapeutic agents
PT that modulate hAC6 activity, and for the diagnosis of
PT hAC6-associated diseases and disorders
XX
PS Claim 3; Fig 1A-I; 42pp; English.
XX
CC This DNA sequence encodes human type VI adenylyl cyclase (hAC6), see
CC AAW30599) that is expressed mainly in the heart and brain. hAC6 has
CC a similar putative structure to other adenylyl cyclase isoforms
CC but, like type V, is distinguishable in that it has a larger

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CC N-terminus and a relatively shorter C-terminus as it lacks the C2b
CC region. hAC6 cDNA was initially isolated from a human heart cDNA
CC library using an adenylyl cyclase PCR fragment as probe. It was
CC used to design primers that were used in a PCR-based RACE to obtain
CC the full-length cDNA sequence. The invention relates to the hAC6
CC gene, methods for the recombinant production of purified hAC6 and
CC the proteins made by these methods, antibodies against hAC6,
CC vectors, probes and host cells (especially HEK-293) transformed by
CC genes encoding polypeptides having hAC6 activity, along with
CC diagnostic and therapeutic uses for these various reagents. hAC6
CC can be used as a tool to screen for agonists and antagonists that
CC stimulate/inhibit hAC6. Such compounds have therapeutic utility
CC in treating diseases caused by aberrant activity of this enzyme.
CC and diseases whose symptoms can be ameliorated by stimulating or
CC inhibiting the activity of hAC6.
XX
SQ Sequence 4942 BP; 953 A; 1404 C; 1512 G; 1073 T; 0 other;

Alignment Scores:
Pred. No.:      2,66e-33      Length:      4942
Score:          545.00      Matches:    99
Percent Similarity: 97.06%      Conservative: 0
Best Local Similarity: 97.06%      Mismatches: 3
Query Match:      95.61%      Indels:    0
DB:              20          Gaps:      0

US-09-750-240-2 (1-104) x AAX00461 (1-4942)
QY 1 MetSerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGly 20
   |||
Db 145 ATGTCATGGTTTGTAGTGGCTCTCTGGTCCCTAAAGTGGATGAACGGAACAGCCTGGGT 204
QY 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40
   |||
Db 205 GAACGCAATGGGCAAGAGCTTCGCGCGCGGTGGCACTCGGGCAGTGGCTTCTGCACG 264
QY 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60
   |||
Db 265 CCCCGCTATATGAGCTCCCTCCGGGATGCAGAGCCACCCAGCCCTGGGGCCCC 324
QY 61 ProArgCysProTrpGlnAspAspAlaPheIleArgArgGlyGlyPro***LysGlyLys 80
   |||
Db 325 CCTCGTGGCCCTGGCAGGATGACGCTTCATCCGGAGGGCGGCCGCAAGGCAAG 384
QY 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100
   |||
Db 385 GAGCTGGGCTGGGGCAGTGGCCCTTCGAGGATACCGAGGTGACACGACAGCG 444
QY 101 AlaGly 102
   |||
Db 445 GCGGG 450

RESULT 7
AAX042525
ID AAX042525 standard; DNA; 4046 BP.
XX
AC AAX042525;
XX
DT 14-SEP-1993 (first entry)
XX
DE Cardiac adenylyl cyclase gene.
XX
KW Regulation; cardiac function; heart; heart failure; ss.
XX
OS Canis familiaris.
XX
FH Key
FT CDS
FT FT
FT FT
PN EP543137-A.
XX
XX 26-MAY-1993.

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XX PF 12-OCT-1992; 92EP-0117374.
XX XX
PR 18-NOV-1991; 91US-0793961.
XX XX
PA (AMCY ) AMERICAN CYANAMID CO.
XX XX
PI Ishikawa Y;
XX XX
DR WPI: 1993-168873/21.
DR P-PSDB; AAR37309.
XX XX
PT Purified DNA encoding cardiac adenyl cyclase - useful to screen
PT for cpds. which stimulate activity of the cyclase
XX XX
PS Claim 1; Fig 2; 34pp; English.
XX XX
CC A canine heart cDNA library was constructed in lambda gt10 and was
CC screened with a 970 bp AatI-HincII fragment from type I adenyl
CC cyclase cDNA probe (encodes the first cytoplasmic domain of adenyl
CC cyclase, which has significant homology to other previously known
CC types of adenyl cyclase). One positive clone, of 5.4 kb was obtd.
CC Positive colonies were subcloned into pUC18 and further subcloned
CC and sequenced bidirectionally. The 5.4 kb clone was used to
CC rescreen the library and on overlapping clone contg. the 5' end of
CC the gene was isolated. Together the two clones cover the complete
CC canine cardiac adenyl cyclase gene. The gene is suspected of
CC being involved in the regulation of cardiac function and it is thought
CC that decreased activity of adenyl cyclase in the heart may be a
CC major factor in the development of heart failure. Thus the adenyl
CC cyclase gene is useful to screen cpds. which stimulate the activity
CC of the cyclase.
XX XX
SQ Sequence 4046 BP; 743 A; 1206 C; 1254 G; 843 T; 0 other;

Alignment Scores:
Pred. No.: 9,62e-28 Length: 4046
Score: 472.50 Matches: 89
Percent Similarity: 85.05% Conservative: 2
Best Local Similarity: 83.18% Mismatches: 11
Query Match: 82.89% Indels: 5
DB: 14 Gaps: 2

US-09-750-240-2 (1-104) x AAQ42525 (1-4046)
QY 1 MetSerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGly 20
Db 131 ATGTCGTGTTTGTAGTGGCTCTCTGTCCTCCCAAGTGGATGAACGAGACACGCCCTGGGGT 190
QY 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40
Db 191 GAACGCAATGGCAGACAGGTTCCA--CGCCGCGGACTCGGACCATGGCTTCGTGCAGC 247
QY 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60
Db 248 CCCGCTATATAGTGTCCGCGGATGCGAGCCGCCAGTCCACGCCCTCGCGCTCCC 307
QY 61 ProArgCysProTrpGlnAspAlaPheIleArgArgGlyGlyPro***LysGlyLys 80
Db 308 CCTCGGTGCCCTGGCAGATGAGGCTTCATCCGGAGAGCGGCCCGCGGCAAGGCGACG 367
QY 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGlu-----Val 96
Db 368 GAGCTGGGGCTCGGGCGGTGGCCCTGGGCTTCGAGGACACTGAGGCCATGTCACGGGTT 427
QY 97 ThrThrThrProAlaGlyPro 103
Db 428 GGGCAGCTGGAGGTGGCCCT 448

RESULT 8
AAA53923
ID AAA53923 standard; cDNA; 4131 BP.
XX

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```

-AC AAA53923;
XX XX
DT 03-JAN-2001 (first entry)
XX XX
DE Type VI adenyl cyclase coding sequence.
XX XX
KW Adenyl cyclase; type I; type II; recombinant; enzyme; CAMP;
KW cyclic AMP; adenosine monophosphate; screening; stimulation;
KW inhibition; treatment; cholera; pituitary tumour; heart failure;
KW ischaemia; endocrine disorder; cell necrosis;
KW pseudohypoparathyroidism; endocrine deficiency; human; ss.
XX OS Homo sapiens.
XX XX
FH Key Location/Qualifiers
FT CDS 14..3536
FT /*tag= a
FT /product= Type VI adenyl cyclase
XX XX
PN US6107076-A.
XX XX
PD 22-AUG-2000.
XX XX
PF 04-OCT-1996; 96US-0726214.
XX XX
PR 04-OCT-1995; 95US-0005498.
XX (TEXA ) UNIV TEXAS SYSTEM.
XX Gilman AG, Tang W;
XX WPI: 2000-578539/54.
DR P-PSDB; AAB02010.
XX XX
PT Novel soluble mammalian polypeptide composition comprising adenyl
PT cyclase activity for screening stimulators and inhibitors of adenyl
PT cyclase, is activated by Gsalpha
XX XX
PS Disclosure; Columns 75-78; 73pp; English.
XX CC
CC A recombinant Adenyl cyclase is described which lacks membrane
CC bound domains. Separation and purification of the recombinant
CC enzyme is much easier compared with wild type enzymes and the
CC recombinant enzyme is more stable than the wild type enzyme which
CC allows easier screening of compounds that stimulate and inhibit
CC Adenyl cyclase activity. The recombinant adenyl cyclase comprises
CC a chimera of adenyl cyclase C_1 and C_2 domains linked covalently.
CC The domains may be linked by a linker peptide. The recombinant
CC adenyl cyclase is useful for screening inhibitors and stimulators
CC of adenyl cyclase activity. Inhibitors of the enzyme are useful for
CC treating cholera, pituitary tumors, heart failure, ischaemia,
CC endocrine disorders and cell necrosis. Stimulators of adenyl
CC cyclase are useful for treating pseudohypoparathyroidism and other
CC endocrine deficiencies.
XX SQ
SQ Sequence 4131 BP; 835 A; 1190 C; 1182 G; 924 T; 0 other;

Alignment Scores:
Pred. No.: 1.4e-24 Length: 4131
Score: 432.00 Matches: 81
Percent Similarity: 86.27% Conservative: 7
Best Local Similarity: 79.41% Mismatches: 12
Query Match: 75.79% Indels: 2
DB: 21 Gaps: 2

US-09-750-240-2 (1-104) x AAA53923 (1-4131)
QY 1 MetSerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGly 20
Db 56 ATGTCATGTTTAGCGGCTCTCTGTTCCCAAGTGGATGAACGAGAACACCCCTGGGCG 115
QY 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40

```



Db 116 GAGCAATGAGCAGAGCCGCCA---CGCCAGCGCAGCCCGCTGGCTTCTCGCG 172

QY 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60  
|||||  
Db 173 CCCCCTACATGAGCTGCCTCAGATGTGGAGCCACCCAGCCCTCTCTGAGCTCGC 232

QY 61 ProArgCysProTrpGlnAspAlaPheIleArgGlyGlyPro\*\*\*LysGlyLys 80  
|||||  
Db 233 ACTCGTGCCCTGGCAGGATGAAGCTTCATCAGGAGGCTGCGCCGGAAGGGTGTG 292

QY 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100  
|||||  
Db 293 GAGCTGGGGTGGCTGAGTGGCTTGGGTTTGTGACACTGAGGTG---ACCACACCG 349

QY 101 AlaGly 102  
|||

Db 350 ATGGGG 355

RESULT 9

ABI99680

ID ABI99680 standard; cDNA; 5841 BP.

XX

AC ABI99680;

XX

DT 07-MAR-2002 (first entry)

XX

DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:716.

XX

KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;

KW vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.

XX

OS Mus musculus.

XX

PN WO200118188-A2.

XX

PD 22-NOV-2001.

XX

PF 18-MAY-2001; 2001WO-JP04192.

XX

PR 18-MAY-2000; 2000JP-0145977.

XX

PA (UYNI-) UNIV NTHON SCHOOL JURIDICAL PERSON.

XX

PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;

XX

DR WPI: 2002-034733/04.

DR P-PSDB; ABB57257.

XX

PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring

PT expression levels of particular genes defined in the specification or

PT by determining the expression profile of a gene group comprising these

PT genes -

XX

PS Claim 2; Page 1771-1780; 2690pp; English.

XX

CC The present invention describes a method for examining ischaemic

CC conditions, comprising measuring the expression levels of particular

CC genes (1) in a test sample or determining the expression profile of a

CC gene group in the sample comprising genes selected from (1). The method

CC is useful for examining the ischaemic condition (e.g. compressive

CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring

CC expression levels of particular genes (ABI99202 to ABI99912, encoding

CC the protein sequences in ABB57020 to ABB57374) or by determining the

CC expression profile of a gene group comprising these genes. The

CC expression levels or expression profiles produced by these genes are

CC used as an indicator when screening for ischaemic condition-improving

CC drugs or therapeutics for ischaemic diseases. ABI99913 and ABI99914

CC represent PCR primers for a mouse ischaemic condition related sequence,

CC which are used in the exemplification of the present invention.

XX

SQ Sequence 5841 BP; 1214 A; 1558 C; 1673 G; 1396 T; 0 other;

Alignment Scores:

Pred. No.: 1.98e-24 Length: 5841

Score: 432.00 Matches: 81

Percent Similarity: 85.29% Conservative: 6

Best Local Similarity: 79.41% Mismatches: 13

Query Match: 75.79% Indels: 2

DB: Gaps: 2

US-09-750-240-2 (1-104) x ABI99680 (1-5841)

QY 1 MetSerTrpPheSerGlyLeuValProLysValAspGluArgLysThrAlaTrpGly 20  
|||||

Db 96 ATGTCATGTTAGTGGCTCCTGGTTCCAAAGTGGATGAACGAAACAGCTTGGGG 155

QY 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyPheCysThr 40  
|||||

Db 156 GAAGCAATGGCAGAGCGCCCA---CGCCAGCGAATCGAGCCAGCTTCTCGGCA 212

QY 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60  
|||||

Db 213 CTTGCTACATGAGTGCCTCAAGAATGCGGAGCCACCCAGCCCTCTCTGAGCTCAC 272

QY 61 ProArgCysProTrpGlnAspAlaPheIleArgGlyGlyPro\*\*\*LysGlyLys 80  
|||||

Db 273 ACTCGTGCCCTGGCAGGATGAAGCTTCATCAGGAGGCGCGCGGCGGTGTG 332

QY 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100  
|||||

Db 333 GAGCTGGGGTGGCTGAGTGGCTTGGGTTTGTGACACACTGAGGTG---ACCACACCG 389

QY 101 AlaGly 102  
|||

Db 390 ATGGGC 395

RESULT 10

AAS54118/c

ID AAS54118 standard; DNA; 1533 BP.

XX

AC AAS54118;

XX

DT 13-FEB-2002 (first entry)

XX

DE Pseudomonas aeruginosa DNA for cellular proliferation protein #249.

XX

KW Antisense; ds; prokaryotic cellular proliferation gene;

KW antibiotic; antibacterial; drug design.

XX

OS Pseudomonas aeruginosa.

XX

PN WO200170955-A2.

XX

PD 27-SEP-2001.

XX

PF 21-MAR-2001; 2001WO-US09180.

XX

PR 21-MAR-2000; 2000US-191078P.

PR 23-MAY-2000; 2000US-206848P.

PR 26-MAY-2000; 2000US-207727P.

PR 23-OCT-2000; 2000US-242578P.

PR 27-NOV-2000; 2000US-253625P.

PR 22-DEC-2000; 2000US-257931P.

PR 16-FEB-2001; 2001US-269308P.

XX

PA (ELIT-) ELITRA PHARM INC.

XX

PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;

PI Yamamoto RT, Xu HH;

XX

XX WPI: 2001-611495/70.

DR P-PSDB; AAU36259.

XX

PT New polynucleotides for the identification and development of

PT antibiotics, comprise sequences of antisense nucleic acids -

XX





US-09-750-240-2 (1-104) x AAN80908 (1-3474)

```
Oy 15 ArgLysThrAlaTprGluArgAsnGlyGlnLysArgSerArgArgGlyThrArg 34
    ||| ||||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 506 CGGTGTCCTGGGCGCCCAAGGCGGCGCGCGCGAGTGGCAGGCGCCCGCTTCGC 447

Oy 35 AlaGlyGlyPheCysThrProArgTyrMetSerCysLeuArgAspAlaGluProProSer 54
    ||| ||||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 446 GCGCT-GGG---TCGCGCGCCGCGACCCCGAGCGTGCCTGGGGAACCTCGAGCGCCGACG 391

Oy 55 Pro-----ThrProAlaGlyProProArgCysProTrpGlnAspAlaPheIleArg 72
    ||| ||||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 390 CCACGAGACCCCGCGCTCAACCCCAAGCGGCC-----ATACGA 349

Oy 73 Arg-----GlyGlyPro**LysGlyLys----- 80
    ||| ||||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 348 CGAACCCGCGACCCCGCGCGCGCGCGCGCTGCGCGACTGCGGGGCGCCG 289

Oy 81 -----GluLeuGlyLeuArgAla-----ValAlaLeuGlyPheGlu 92
    ||| ||||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 288 TCGTGCCTCCCGTCAAGTAGCTGGGGCGGAGGTGCTGGAGGACCGAGTAGAGGATCGAG 229

Oy 93 AspThrGluVal-----ThrThrProAlaGlyProLeu 104
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Db 228 AAACGTCTCGTGTAGACACCGACCGACCGCGGGGCGCGATA 187
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## RESULT 14

AAV68520  
ID AAV68520 standard; DNA; 4257 BP.

XX AAV68520;

XX 29-JAN-1999 (first entry)

XX The nucleotide sequence of the Herpes simplex virus ICP4.

XX Herpes simplex virus ICP4; HSV ICP4; modulator; apoptosis;  
XX stimulation; inhibition; HSV infection; ss.

XX Herpes simplex virus.

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Key Location/Qualifiers
CDS 361..4257
    /*tag= a
    /product= "HSV ICP4 protein"
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XX WO9846637-A2.

XX 22-OCT-1998.

XX 16-APR-1998; 98WO-US07573.

XX 16-APR-1997; 97US-0843659.

XX (ARCH-) ARCH DEV CORP.

XX Leopardi R, Roizman B;

XX WPI; 1998-594559/50.

XX P-PSDB; AAW80810.

XX Use of herpes simplex virus U(s)3 polypeptide - for developing  
XX products for modulating apoptosis in cells and for identifying  
XX compounds which act as stimulators or inhibitors of apoptosis

XX Example 2; Pages 60-63; 85pp; English.

XX This is the nucleotide sequence of Herpes simplex virus ICP4 used in  
XX the method of the invention as modulators of apoptosis. The methods  
XX and products can be used to identify compounds which modulate  
XX (stimulate or inhibit) apoptosis in cells. They can be used to  
XX immortalise cells for the study of these cells or for growing cells  
XX in large numbers for the productions of proteins. They can also be

CC used for stimulating apoptosis in cells, e.g. for treating a subject  
CC with a HSV infection.  
XX  
SQ Sequence 4257 BP; 412 A; 1768 C; 1663 G; 414 T; 0 other;

## Alignment Scores:

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Pred. No.: 470 Length: 4257
Score: 91.50 Matches: 36
Percent Similarity: 42.86% Conservative: 6
Best Local Similarity: 36.73% Mismatches: 38
Query Match: 16.05% Indels: 18
DB: 19 Gaps: 5
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US-09-750-240-2 (1-104) x AAV68520 (1-4257)

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Oy 17 ThrAlaTrpGlyGluArgAsnGlyGlnLysArgSer-----ArgArg-ArgG1 32
    ||| ||||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 2786 ACCCCCTGGCGGTGGCGCGCGAGCCCGCGGCCCGCCAGCACACGCGCGCCGCG 2845

Oy 32 yThrArgAlaGlyGly-PheCysThrProArgTyrMetSerCysLeuArgAspAlaGluP 52
    ||| ||||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 2846 CCGCGCGCTGGAGCGCTACTGCTCCCGCGCGCGCGTGGCGGAGCTCAGGAC---CACC 2902

Oy 52 ro-ProSerProThrProAlaGlyProProArgCys-----ProTrpGlnAsp 67
    ||| ||||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 2903 CGCTGTTCCTCCGTCCTGGCGAGCGCGCTCATGTTTGACCGCGCGCGCTGGCTCGA 2962

Oy 68 AspAlaPheIleArgArgGlyGlyPro**LysGlyLysGluLeuGlyLeuArgAlaVal 87
    ||| ||||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 2963 TCGCGG-----CGCGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3013

Oy 88 AlaLeuGlyPheGluAspThrGluValThrThrProAlaGlyPro 103
    ||| ||||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 3014 GCG-----GGCAGCAGCAGCATACCCCGCGCGCGCGCGCGCGCGCGCGCG 3052
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## RESULT 15

AAV10362  
ID AAV10362 standard; cDNA; 4257 BP.

XX AAV10362;

XX 30-JUN-1998 (first entry)

XX Infected cell protein number 4 alpha-4 gene.

XX Infected cell protein number 4; ICP4; alpha-4; cell apoptosis;  
XX therapeutics; ss.

XX Herpes simplex virus.

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Key Location/Qualifiers
CDS 361..4257
    /*tag= a
    /product= "Infected cell protein"
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XX WO9804709-A2.

XX 05-FEB-1998.

XX 23-JUL-1997; 97WO-US12904.

XX 26-JUL-1996; 96US-0690473.

XX (ARCH-) ARCH DEV CORP.

XX Leopardi R, Roizman B;

XX WPI; 1998-130697/12.

XX P-PSDB; AAW40200.

XX Use of herpes simplex virus ICP4 polypeptide - useful for, e.g.  
XX blocking apoptosis in cells, production of proteins and gene therapy

PS Disclosure; Fig 2; 63pp; English.

XX The herpes simplex virus (HSV) alpha-4 gene encodes infected cell protein  
 CC number 4 (ICP4). Both the alpha-4 gene and ICP4 can be used to block  
 CC cell apoptosis. Similarly the administration of an agent that inhibits  
 CC ICP4 or the alpha-4 gene can induce apoptosis in HSV infected cells.  
 CC This can be used for the immortalisation of cells, production of  
 CC proteins, gene therapy, or inhibition of cell death induced in vivo.  
 CC They can also be used for production of therapeutics comprising  
 CC inhibitors of HSV ICP4 function, useful for treating HSV function.  
 XX

SQ Sequence 4257 BP; 412 A; 1768 C; 1663 G; 414 T; 0 other;

Alignment Scores:

Pred. No.:	470	Length:	4257
Score:	91.50	Matches:	36
Percent Similarity:	42.86%	Conservative:	6
Best Local Similarity:	36.73%	Mismatches:	38
Query Match:	16.05%	Indels:	18
DB:	19	Gaps:	5

US-09-750-240-2 (1-104) x AAV10362 (1-4257)

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QY	32	yThrArgAlaGlyGly-PheCysThrProArgTyrMetSerCysLeuArgAspAlaGluP	52
DB	2846	CCGCGCGCCCTGGAGGCGCTACTGTCCCGCGCGCGGTGGCCGAGCTCACGGAC---CACC	2902
QY	52	ro-ProSerProThrProAlaGlyProProArgCys-----ProTrpGlnAsp	67
DB	2903	CGCTGTTCCCGTCCCTGGCGACCGCCCTCATGTTTGACCCGCGGGCCCTGGCCTCGA	2962
QY	68	AspAlaPheIleArgArgGlyGlyPro***LysGlyLysGluLeuGlyLeuArgAlaVal	87
DB	2963	TCGCGG-----CGCGGTGGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG	3013
QY	88	AlaLeuGlyPheGluAspThrGluValThrThrProAlaGlyPro	103
DB	3014	GCG-----GCGAGGACGACGATAACCCACCCACCGGGGCGG	3052

Search completed: March 1, 2003, 09:07:43

Job time : 228 secs



GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 1, 2003, 09:01:49 ; Search time 44 Seconds  
(without alignments)  
724.872 Million cell updates/sec

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Perfect score: 570  
Sequence: 1 MSWFSGLLPVKVDKRTANG.....RAVALGFEDTEVTTTPAGPL 104

Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
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-O=/cgn2.1/USPTO.spool/US09750240/runat\_25022003\_103942\_24989/app\_query.fasta\_1.263  
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-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
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-NO\_XLPXY -NO\_MAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV\_TIMEOUT=120  
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Database : Issued\_Patents\_NA:\*  
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5: /cgn2.6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgn2.6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	568	99.6	314	4	US-09-008-097-1
2	545	95.6	3549	4	US-09-008-097-5
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4	472.5	82.9	4046	1	US-07-793-961A-1
5	472.5	82.9	4046	1	US-08-240-357-1
6	432	75.8	4131	3	US-08-726-214-11
7	94	16.5	2312	1	US-07-736-178C-1
8	91.5	16.1	4257	2	US-08-690-473-1
9	91.5	16.1	4257	4	US-09-259-821A-1
10	91.5	16.1	4257	4	US-08-843-659-1
11	91.5	16.1	12001	1	US-08-458-568A-11
12	89.5	15.7	1221	6	5212296-16

C 13	89.5	15.7	1879	6	5212296-5	Patent No. 5212296
C 14	88	15.4	3472	3	5244792-2	Patent No. 5244792
C 15	87	15.3	2241	3	US-09-144-759-17	Sequence 17, Appl
C 16	87	15.3	2295	3	US-09-144-759-19	Sequence 19, Appl
C 17	87	15.3	2301	3	US-09-144-759-21	Sequence 21, Appl
C 18	86.5	15.2	1078	4	US-09-452-239-41	Sequence 41, Appl
C 19	86	15.1	1108	5	PCT-US93-03035-1	Sequence 1, Appl
C 20	86	15.1	2368	3	US-09-032-365A-57	Sequence 57, Appl
C 21	85	14.9	4695	2	US-08-231-193A-57	Sequence 57, Appl
C 22	85	14.9	4695	2	US-08-486-272A-57	Sequence 57, Appl
C 23	85	14.9	4695	3	US-08-940-086A-57	Sequence 57, Appl
C 24	85	14.9	4695	4	US-08-940-035A-57	Sequence 57, Appl
C 25	85	14.9	4695	4	US-08-935-105A-57	Sequence 57, Appl
C 26	85	14.9	4695	4	US-09-648-797-57	Sequence 57, Appl
C 27	84.5	14.8	2728	3	US-09-188-930-213	Sequence 213, App
C 28	84	14.7	1656	3	US-08-659-188-17	Sequence 17, Appl
C 29	84	14.7	1856	3	US-08-655-227-17	Sequence 17, Appl
C 30	84	14.7	1856	3	US-08-655-241-17	Sequence 17, Appl
C 31	84	14.7	1656	4	US-09-398-326-17	Sequence 17, Appl
C 32	84	14.7	2970	5	PCT-US92-06391-1	Sequence 1, Appl
C 33	84	14.7	4800	3	US-09-106-638-1	Sequence 1, Appl
C 34	84	14.7	13953	4	US-09-738-884-3	Sequence 3, Appl
C 35	83	14.6	540	2	US-08-726-306A-182	Sequence 182, App
C 36	83	14.6	1430	4	US-09-492-985-1	Sequence 1, Appl
C 37	83	14.6	3624	1	US-07-951-715A-6	Sequence 6, Appl
C 38	83	14.6	3624	2	US-08-459-448A-6	Sequence 6, Appl
C 39	83	14.6	3624	3	US-08-459-595A-6	Sequence 6, Appl
C 40	83	14.6	3624	3	US-08-459-504B-6	Sequence 6, Appl
C 41	83	14.6	3624	3	US-08-459-444-6	Sequence 6, Appl
C 42	83	14.6	3624	3	US-09-053-549-7	Sequence 7, Appl
C 43	83	14.6	3624	4	US-09-547-422-6	Sequence 6, Appl
C 44	82.5	14.5	3060	1	US-08-714-991-26	Sequence 26, Appl
C 45	82.5	14.5	3090	1	US-08-102-942A-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1  
US-09-008-097-1  
; Sequence 1, Application US/09008097  
; Patent No. 6306830  
; GENERAL INFORMATION:  
; APPLICANT: Hammond, H. Kirk  
; APPLICANT: Insel, Paul A.  
; APPLICANT: Ping, Peipei  
; APPLICANT: Post, Steven R.  
; APPLICANT: Gao, Meihua  
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE  
; TITLE OF INVENTION: HEART FAILURE  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/008,097  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dylan, Tyler M  
; REGISTRATION NUMBER: 37,612  
; REFERENCE/DOCKET NUMBER: 22000-20567.21

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..312
; OTHER INFORMATION:
US-09-008-097-1

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Pred. No.: 314 Length: 314
Score: 568.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.65% Indels: 0
DB: 4 Gaps: 0

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Db 1 ATGTCATGTTTATGTCCTCTGCTTAAAGTGGATGAACGAAACAGCCTGGGGT 60
Qy 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40
Db 61 GAACCAATGGCAGAACGCTTCGGCGGCCCTGCGACTCGGCAGAGTGCTTCTGCACG 120
Qy 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60
Db 121 CCCCGCTATATGAGTCGCTCCGGATGCAGAGCCACCCAGCCGCCCTGGGGCCCC 180
Qy 61 ProArgCysProTrpGlnAspAlaPheIleArgArgGlyGlyPro**LysGlyLys 80
Db 181 CCTCGGTCCCCCTGGCAGATGACGCTTCAATCCGAGGGGGCGGCCCAAGGCGCAAG 240
Qy 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100
Db 241 GAACCTGGGCTCGCGCAGTGGCCCTGGGCTTCAAGATACCGAAGTCAACAACGACCG 300
Qy 101 AlaGlyProLeu 104
Db 301 GCGGACCCGCTG 312

RESULT 2
US-09-008-097-5
; Sequence 5, Application US/09008097
; Patent No. 6306830
; GENERAL INFORMATION:
; APPLICANT: Hammond, H. Kirk
; APPLICANT: Insel, Paul A.
; APPLICANT: Ping, Peipei
; APPLICANT: Post, Steven R.
; APPLICANT: Gao, Meihua
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE
; TITLE OF INVENTION: HEART FAILURE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/008,097
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dylan, Tyler M
; REGISTRATION NUMBER: 37,612
; REFERENCE/DOCKET NUMBER: 22000-20567.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3549 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..3501
; OTHER INFORMATION:
US-09-008-097-5

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Db 121 CCCCGCTATATGAGTCGCTCCGGATGCAGAGCCACCCAGCCGCCCTGGGGCCCC 180
Qy 61 ProArgCysProTrpGlnAspAlaPheIleArgArgGlyGlyPro**LysGlyLys 80
Db 181 CCTCGGTCCCCCTGGCAGATGACGCTTCAATCCGAGGGGGCGGCCCAAGGCGCAAG 240
Qy 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100
Db 241 GAGCTGGGCTGCGGCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGCAACACGACCG 300
Qy 101 AlaGly 102
Db 301 GCGGCG 306

RESULT 3
US-09-474-076-1
; Sequence 1, Application US/09474076
; Patent No. 6465237
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, James E.
; APPLICANT: COR Therapeutics, Inc.
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
; TITLE OF INVENTION: CYCLASE
; FILE REFERENCE: 44481-5028-01-US
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; COMPUTER: IBM PC AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: ASCII from DW4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/793,961A
; FILING DATE: 19911118
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gordon, Alan M.
; REGISTRATION NUMBER: 30,637
; REFERENCE/DOCKET NUMBER: 31,705
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203 321 2719
; TELEFAX: 203 321 2971
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4046 base pairs listed
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-793-961A-1

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Pred. No.:      8,9e-32          Length:      4046
Score:         472.50           Matches:     89
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Query Match:    82.89%          Indels:       5
DB:             1              Gaps:          2

US-09-750-240-2 (1-104) x US-07-793-961A-1 (1-4046)

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Db  131 ATGTCTGGTGTATTAGTGCCCTCCTGGTCCCCCAAGTGGATGAACGGAGACAGCGCTGGGGT 190
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QY  21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40
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Db  191 GAACGCATGGCAGAAGCGTCCA--CGCGCGGGGACTCGGACCAGTCGGCTTCTGCACG 247
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QY  41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60
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Db  308 CCTCGTGCCCTGGCAGGATGAGCCCTTCATCGGAGAGCGCGCCCGGCAAGGGCACG 367
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QY  81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGlu-----Val 96
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Db  368 GAGCTGGGGCTGCGGGGGTGGCCCTGGGCTTCGAGGACACTGAGGGCCATGTCAGCGGTT 427
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QY  97 ThrThrThrProAlaGlyPro 103
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Db  428 GGGCGAGCTGGAGTGGCCCT 448

RESULT 5
US-08-240-357-1
; Sequence 1, Application US/08240357
; Patent No. 5578481
; GENERAL INFORMATION:
; APPLICANT: Ishikawa, Yoshihiro
; TITLE OF INVENTION: Cloning and Characterization of a
; TITLE OF INVENTION: Cardiac Adenylyl Cyclase
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; STREET: One Cyanamid Company
; ADDRESS: American Cyanamid Plaza

```

CITY: Wayne  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07470-8426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/240,357  
FILING DATE: 10-MAY-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Gordon, Alan M.  
REGISTRATION NUMBER: 30,637  
REFERENCE/DOCKET NUMBER: 31,705-01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-831-3244  
TELEFAX: 201-831-3305  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4046 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 131..3625  
US-08-240-357-1

Alignment Scores:  
Pred. No.: 8.9e-32 Length: 4046  
Score: 472.50 Matches: 89  
Percent Similarity: 85.05% Conservative: 2  
Best Local Similarity: 83.18% Mismatches: 11  
Query Match: 82.89% Indels: 5  
DB: 1 Gaps: 2

US-09-750-240-2 (1-104) x US-08-240-357-1 (1-4046)

Qy 1 MetSerTrpPheSerGlyLeuValProLysValAspGluArgLysThrAlaTrpGly 20  
|||||  
Db 131 ATGTCGTGTTAGTGGCTCTGTCCTCCCAAGTGGATGAACGAGACAGCGCTGGGT 190  
Qy 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40  
|||||  
Db 191 GAACGCAATGGCAGAACGTCCTCAAGTGGATGAACGAGACAGCGCTGGGTTCGACG 247  
Qy 41 ProArgTrpMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60  
|||||  
Db 248 CCCGCTATATAGCTGCTCCGGATGCGAGTCCGAGCCGCCAGTCCACCCCTCGCGCTCC 307  
Qy 61 ProArgCysProTrpGlnAspAlaPheileArgArgGlyGlyPro\*\*\*LysGlyLys 80  
|||||  
Db 308 CTGCGTCCCTGTCAGGATGAGCGCTTCATCCGGAGAGCGCGCCGCGCAAGGGCAG 367  
Qy 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGlu-----Val 96  
|||||  
Db 368 GAGCTGGGGCTGCGGGCGGTGGCTTCGAGGACACTGAGGCCATGTCAGCGGTT 427  
Qy 97 ThrThrThrProAlaGlyPro 103  
|||||  
Db 428 GGGCAGCTGGAGGTGGCCCT 448  
RESULT 6  
us-08-726-214-11  
Sequence 11, Application US/08726214  
Patent No. 6107076  
GENERAL INFORMATION:  
APPLICANT: Tang, Wei-Jen  
APPLICANT: Gilman, Alfred G.

TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYL CYCLASE  
TITLE OF INVENTION: AND USES THEREFOR  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/726,214  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/005,498  
FILING DATE: 04-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L.  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: UTSD:450  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4131 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-726-214-11  
Alignment Scores:  
Pred. No.: 2.74e-28 Length: 4131  
Score: 432.00 Matches: 81  
Percent Similarity: 86.27% Conservative: 7  
Best Local Similarity: 79.41% Mismatches: 12  
Query Match: 75.79% Indels: 2  
DB: 3 Gaps: 2  
US-09-750-240-2 (1-104) x US-08-726-214-11 (1-4131)  
Qy 1 MetSerTrpPheSerGlyLeuValProLysValAspGluArgLysThrAlaTrpGly 20  
|||||  
Db 56 ATGTCATGTTAGCGGCTCTGTTCCAAAGTGGATGAACGAAACAGCGCTGGGGC 115  
Qy 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40  
|||||  
Db 116 GAACGCAATGACAGACAGCGGCCA---CGCCAGGCGACCCAGCGCTGCTGCGCG 172  
Qy 41 ProArgTrpMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60  
|||||  
Db 173 CCCGCTATATAGCTGCTCCGAAATGTGGAGCACCCAGCCACCTCTGACGCTGC 232  
Qy 61 ProArgCysProTrpGlnAspAlaPheileArgArgGlyGlyPro\*\*\*LysGlyLys 80  
|||||  
Db 233 ACTCGTGGCTGCGCGGATGAAGCTTCATCAGGAGGCTGCGCCCGGAAGGGGTGTG 292  
Qy 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100  
|||||  
Db 293 GAGCTGGGGCTGCGGTGCTGAGTGGCTTTGAGTACTGAGGTG---ACCACACCG 349  
Qy 101 AlaGly 102  
|||  
Db 350 ATGGG 355  
RESULT 7  
US-07-736-178C-1/c

[illegible]

Db 3014 GCG-----GCGAGCAGCAGATACACCCACCCACCCACCGGGCGG 3052

## RESULT 9

US-09-259-821A-1  
; Sequence 1, Application US/09259821A  
; Patent No. 6210926  
; GENERAL INFORMATION:  
; APPLICANT: LEOPARDI, ROSARIO  
; APPLICANT: ROIZMAN, BERNARD  
; TITLE OF INVENTION: HERPES SIMPLEX VIRUS ICP4 IS AN INHIBITOR OF APOPTOSIS  
; FILE REFERENCE: ARCD:317  
; CURRENT APPLICATION NUMBER: US/09/259,821A  
; CURRENT FILING DATE: 1999-03-01  
; PRIOR APPLICATION NUMBER: 08/690,473  
; PRIOR FILING DATE: 1996-07-26  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 4257  
; TYPE: DNA  
; ORGANISM: HERPES VIRUS, TYPE 1  
US-09-259-821A-1

Alignment Scores:  
Pred. No.: 48.6 Length: 4257  
Score: 91.50 Matches: 36  
Percent Similarity: 42.86% Conservative: 6  
Best Local Similarity: 36.73% Mismatches: 38  
Query Match: 16.05% Indels: 18  
DB: 4 Gaps: 5

US-09-750-240-2 (1-104) x US-09-259-821A-1 (1-4257)

QY 17 ThrAlaTrpGlyGluArgAsnGlyGlnLysArgSer-----ArgArg-ArgGl 32  
Db 2786 ACCCCTGGCGGCGTGGCGGCGAGCCCCCGGGCGCCAGCCACACGCGGCGCGCGG 2845  
QY 32 yThrArgAlaGlyGly-PheCysThrProArgTyrMetSerCysLeuArgAspAlaGluP 52  
Db 2846 CCGCGCGCGCTGGAGCGCTACTCTCCCGCGCGCGTGGCGGAGCTCAGGAC---CACC 2902  
QY 52 ro-ProSerProThrProAlaGlyProProArgCys-----ProTrpGlnAsp 67  
Db 2903 CGCTGTTCCTCCCTCGCGGCGGCGCTCATGTTGACCCGCGGCGCTCGA 2962  
QY 68 AspAlaPheIleArgArgGlyGlyPro\*\*\*LysGlyLysGluLeuGlyLeuArgAlaVal 87  
Db 2963 TCGCGG-----CGCGGTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3013  
QY 88 AlaLeuGlyPheGluAspThrGluValThrThrProAlaGlyPro 103  
Db 3014 GCG-----GCGAGCAGCAGATACACCCACCCACCGGGCGG 3052

## RESULT 10

US-08-843-659-1  
; Sequence 1, Application US/08843659  
; Patent No. 6218103  
; GENERAL INFORMATION:  
; APPLICANT: Leopardi, Rosario  
; APPLICANT: Roizman, Bernard  
; TITLE OF INVENTION: HERPES SIMPLEX VIRUS US3 AND ICP4 AS  
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/843,659  
; FILING DATE: Concurrently Herewith  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Highlander, Steven L.  
; REGISTRATION NUMBER: 37,642  
; REFERENCE/DOCKET NUMBER: ARSB:519  
; TELEPHONE: (512) 474-3000  
; TELEFAX: (512) 474-7577  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4257 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-843-659-1

Alignment Scores:  
Pred. No.: 48.6 Length: 4257  
Score: 91.50 Matches: 36  
Percent Similarity: 42.86% Conservative: 6  
Best Local Similarity: 36.73% Mismatches: 38  
Query Match: 16.05% Indels: 18  
DB: 4 Gaps: 5

US-09-750-240-2 (1-104) x US-08-843-659-1 (1-4257)

QY 17 ThrAlaTrpGlyGluArgAsnGlyGlnLysArgSer-----ArgArg-ArgGl 32  
Db 2786 ACCCCTGGCGGCGTGGCGGCGAGCCCCCGGGCGCCAGCCACACGCGGCGCGG 2845  
QY 32 yThrArgAlaGlyGly-PheCysThrProArgTyrMetSerCysLeuArgAspAlaGluP 52  
Db 2846 CCGCGCGCGCTGGAGCGCTACTCTCCCGCGCGCGTGGCGGAGCTCAGGAC---CACC 2902  
QY 52 ro-ProSerProThrProAlaGlyProProArgCys-----ProTrpGlnAsp 67  
Db 2903 CGCTGTTCCTCCCTCGCGGCGGCGCTCATGTTGACCCGCGGCGCTCGA 2962  
QY 68 AspAlaPheIleArgArgGlyGlyPro\*\*\*LysGlyLysGluLeuGlyLeuArgAlaVal 87  
Db 2963 TCGCGG-----CGCGGTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3013  
QY 88 AlaLeuGlyPheGluAspThrGluValThrThrProAlaGlyPro 103  
Db 3014 GCG-----GCGAGCAGCAGATACACCCACCCACCGGGCGG 3052

## RESULT 11

US-08-458-568A-11/c  
; Sequence 11, Application US/08458568A  
; Patent No. 5821339  
; GENERAL INFORMATION:  
; APPLICANT: Schaffer, Priscilla A.  
; APPLICANT: Yeh, Lily  
; TITLE OF INVENTION: Compositions and Methods for Treatment of Herpesvirus  
; TITLE OF INVENTION: Infections  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5821339rls  
; STREET: One Liberty place, 46th floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Wordperfect 5.1

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,568A
; FILING DATE: 02-JUNE-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: US 08/065,146
; FILING DATE: 05-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Leary Ph.D., Kathryn R.
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: DFCI-0029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12001 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Herpes simplex virus
; STRAIN: Herpes Simplex Virus Type 1
; US-08-458-568A-11

Alignment Scores:
Pred. No.: 157 Length: 12001
Score: 91.50 Matches: 36
Percent Similarity: 42.86% Conservative: 6
Best Local Similarity: 36.73% Mismatches: 38
Query Match: 16.05% Indels: 18
DB: 1 Gaps: 5

US-09-750-240-2 (1-104) x US-08-458-568A-11 (1-12001)
QY 17 ThrAlaTrpGlyLuArgAsnGlyGlnLysArgSer-----ArgArg-ArgGl 32
Db 3888 ACCCTGGGGGCTGGCGCGCGACGCCCGGGGCGCCAGCCACACGGCGCGCGCGG 3829
QY 32 yThrArgAlaGlyGly-PheCysThrProArgTyrMetSerCysLeuArgAspAlaGluP 52
Db 3828 CCGCCGCTGGAGGCTACTGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 3772
QY 52 ro-ProSerProThrProAlaGlyProProArgCys-----ProTrpGlnAsp 67
Db 3771 CGCTGTCCCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 3712
QY 68 AspAlaPheIleArgArgGlyGlyPro**LysGlyLysGluLeuGlyLeuArgAlaVal 87
Db 3711 TCGCCG-----CGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 3661
QY 88 AlaLeuGlyPheGluAspThrGluValThrThrThrProAlaGlyPro 103
Db 3660 GCG-----CGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGG 3622

RESULT 12
5212296-16/c
; Patent No. 5212296
; APPLICANT: DEAN, CAROLINE; HARDER, PATRICIA A.; LETO, KENNETH
; J.; O'KEEFE, DANIEL P.; OMER, CHARLES A.; ROMESSER, JAMES A.
; TEPPERMAN, JAMES M.
; TITLE OF INVENTION: EXPRESSION OF HERBICIDE METABOLIZING
; CYTOCHROMES
; NUMBER OF SEQUENCES: 19
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/569,781
; FILING DATE: 23-AUG-1990
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: 464,499
; FILING DATE: 12-JAN-1990
; APPLICATION NUMBER: 405,605
; FILING DATE: 11-SEP-1989
; SEQ ID NO: 5:
; LENGTH: 1879
5212296-5

Alignment Scores:
Pred. No.: 28.5 Length: 1879
Score: 89.50 Matches: 30
Percent Similarity: 44.44% Conservative: 6
Best Local Similarity: 37.04% Mismatches: 26
Query Match: 15.70% Indels: 19
DB: 6 Gaps: 5

US-09-750-240-2 (1-104) x 5212296-5 (1-1879)
QY 20 GlyLuArgAsnGlyGlnLysArgSerArgArg-----GlyThrArgAlaGlyGly 37
Db 1199 GGCCCCAGGCAGTGTGTCACGCCGAGCGGAGGTGTGTCGCGCGCGCGCGGTGGA 1140
QY 38 Phe-----CysThrProArgTyrMetSerCysLeuArg 48

; FILING DATE: 12-JAN-1990
; APPLICATION NUMBER: 405,605
; FILING DATE: 11-SEP-1989
; SEQ ID NO: 16:
; LENGTH: 1221
5212296-16

Alignment Scores:
Pred. No.: 17.5 Length: 1221
Score: 89.50 Matches: 30
Percent Similarity: 44.44% Conservative: 6
Best Local Similarity: 37.04% Mismatches: 26
Query Match: 15.70% Indels: 19
DB: 6 Gaps: 5

US-09-750-240-2 (1-104) x 5212296-16 (1-1221)
QY 20 GlyLuArgAsnGlyGlnLysArgSerArgArg-----GlyThrArgAlaGlyGly 37
Db 1072 GGCCCCAGGCAGTGTGTCACGCCGAGCGGAGGTGTGTCGCGCGCGCGCGGTGGA 1013
QY 38 Phe-----CysThrProArgTyrMetSerCysLeuArg 48
Db 1012 TGTCGAGGGGCTCCGGGTCTCTGTACACCGTGCCTCCCGTGTGCTATCGAGTTGACGA 953
QY 49 AspAlaGluProProSerProThrProAlaGlyPro---ProArgCys---ProTrpGln 66
Db 952 CGATCAGCCCTCGCGCGCGCGGATGAGTGCCCTCGACCTGATGTCGCGCGGTGG--- 896
QY 67 AspAlaPheIleArgArgGlyGlyPro**LysGlyLysGluLeuGlyLeuArgAla 86
Db 895 -----CGACGCGCGCGCGCGCGATGTCGCGGATGTCGCGGAGTAGCGGAGCA 851
QY 87 val 87
Db 850 GTT 848

RESULT 13
5212296-5/c
; Patent No. 5212296
; APPLICANT: DEAN, CAROLINE; HARDER, PATRICIA A.; LETO, KENNETH
; J.; O'KEEFE, DANIEL P.; OMER, CHARLES A.; ROMESSER, JAMES A.
; TEPPERMAN, JAMES M.
; TITLE OF INVENTION: EXPRESSION OF HERBICIDE METABOLIZING
; CYTOCHROMES
; NUMBER OF SEQUENCES: 19
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/569,781
; FILING DATE: 23-AUG-1990
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: 464,499
; FILING DATE: 12-JAN-1990
; APPLICATION NUMBER: 405,605
; FILING DATE: 11-SEP-1989
; SEQ ID NO: 5:
; LENGTH: 1879
5212296-5

Alignment Scores:
Pred. No.: 28.5 Length: 1879
Score: 89.50 Matches: 30
Percent Similarity: 44.44% Conservative: 6
Best Local Similarity: 37.04% Mismatches: 26
Query Match: 15.70% Indels: 19
DB: 6 Gaps: 5

US-09-750-240-2 (1-104) x 5212296-5 (1-1879)
QY 20 GlyLuArgAsnGlyGlnLysArgSerArgArg-----GlyThrArgAlaGlyGly 37
Db 1199 GGCCCCAGGCAGTGTGTCACGCCGAGCGGAGGTGTGTCGCGCGCGCGCGGTGGA 1140
QY 38 Phe-----CysThrProArgTyrMetSerCysLeuArg 48
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```
Db 1139 TCTCAGGCGCTCCGGTCTCGTACACGTCCTCCGCTGCGGTTCGATPCGAGTTGACGA 1080
QY 49 AspaLaGluProSerProThrProAlaGlyPro---ProArgCys---ProTrpGln 66
Db 1079 CGATCAGCCCTCGCGCGCGGAGGTGAGTGCCTCGACCTCGATGTCGCGCGTGG--- 1023
QY 67 AspaAlaPheIleArgArgGlyGlyPro***LysGlyLysGluLeuGlyLeuArgAla 86
Db 1022 -----CGAGCGCGCGCGCGGATGTCGCGGATGCGGAGGTAGCGGAGCA 978
QY 87 Val 87
Db 977 GTT 975

RESULT 14
5244792-2/c
; Patent No. 5244792
; APPLICANT: BURKE, RAE L.; PACHL, CAROL; VALENZUELA, PABLO D.T.
; TITLE OF INVENTION: EXPRESSION OF RECOMBINANT GLYOPROTEIN
; B FROM HERPES SIMPLEX VIRUS
; NUMBER OF SEQUENCES: 19
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/587,179
; FILING DATE: 20-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 921,730
; FILING DATE: 20-OCT-1986
; APPLICATION NUMBER: 597,784
; FILING DATE: 06-APR-1984
; SEQ ID NO:2:
; LENGTH: 3472
5244792-2

Alignment Scores:
Pred. No.: 77 Length: 3472
Score: 88.00 Matches: 33
Percent Similarity: 39.45% Conservative: 10
Best Local Similarity: 30.28% Mismatches: 36
Query Match: 15.44% Indels: 30
DB: 6 Gaps: 6

US-09-750-240-2 (1-104) x 5244792-2 (1-3472)
QY 20 GlyGluArgAsnGlyGlnLysArgSerArgArgArgGlyThrArgAlaGlyGlyPheCys 39
Db 495 GGGCGCGCCAGGCGCGCGCGCGGAGTGGCAGGCGCCCGTTCGCGCGCTGGGTGG 436
QY 40 ThrProArgTyrMetSerCysLeuArgAspAlaGluProProSerPro-----ThrPro 57
Db 435 CGGCGCGCACCCAGCGCGTGGCGGGGAACCTCGGAGCGCGGACGCCACCGAGGCCCA 376
QY 58 AlaGlyProProArgCysProTrpGlnAspAlaPheIleArg-----GlyGly 75
Db 375 GCGTCAACCCCAAGAGCGCCC-----ATACGACGAACCAACCGCGCAC 334
QY 76 Pro***LysGlyLys----- 80
Db 333 CCCGCGCGGGCGCGCCCTGGCGCATGGCGGACTACGGGGGCCCGTCTGCCCCCGTCA 274
QY 81 ---GluLeuGlyLeuArgAla-----ValAlaLeuGlyPheGluAspThrGluVal--- 96
Db 273 GGTAGCCTGGGGCGGAGGTGTGGAGGACCGAGTAGAGGATCGAGAAAAACGCTCGGTGG 214
QY 97 ---ThrThrThrProAlaGlyProLeu 104
Db 213 TAGACCAACCGCGCGGCGCGGATA 187

RESULT 15
US-09-144-759-17/c
; Sequence 17, Application US/09144759
; Patent No. 6117639
; GENERAL INFORMATION:
```

```
; APPLICANT: Hock, Thomas
; APPLICANT: Germann, Ursula
; APPLICANT: Kwong, Ann
; TITLE OF INVENTION: FUSION PROTEINS, DNA MOLECULES, VECTORS, AND HOST CELLS
; FILE REFERENCE: VPI/98-08
; CURRENT APPLICATION NUMBER: US/09/144,759
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 2241
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:man-made
US-09-144-759-17
```

```
Alignment Scores:
Pred. No.: 57.1 Length: 2241
Score: 87.00 Matches: 38
Percent Similarity: 38.46% Conservative: 7
Best Local Similarity: 32.48% Mismatches: 41
Query Match: 15.26% Indels: 32
DB: 3 Gaps: 4
```

US-09-750-240-2 (1-104) x US-09-144-759-17 (1-2241)

```
QY 3 TrpPheSerGlyLeuLeuValProLysValAspGlu----- 14
Db 1575 TGGCGGATGGCATGACGTCCTCCAGATCTCTCGAGGAACCTTGGGCAGTTTCGCGTTTTT 1516
QY 15 -----ArgLysThrAlaTrpGlyGlu 21
Db 1515 GAGCTTTAGTGAGAAACACATCTCGGCGTTCGTGGTTCGCCAGCTACGAGCTCGTGAG 1456
QY 22 ArgAsnGlyGlnLysArgSerArgArgGlyThr-----ArgAlaGlyGly--- 37
Db 1455 GATCGAGAGCAGCT-TTGGGTAGAGACGAGGCTCATTTGAGTCGCCGCGAGTGGCGTTCA 1397
QY 38 -----PheCysThrProArgTyrMetSerCysLeuArgAspAlaGluPro 52
Db 1396 GTATATAAATCGTAGCGTGTGATGTAGTAGCTCTGGATCGCTTCGACTAGCT---GGG 1340
QY 53 ProSerProThrProAlaGlyProProArgCysProTrpGlnAspAlaPheIleArg 72
Db 1339 CCTCTCCAGCGCGCGCGGTCGCCGAGAGATCACAAATGGCAGTGAAGAAGCGGTATTCA 1280
QY 73 ArgGlyGlyPro***LysGlyLysGluLeuGlyLeuArgAlaValAlaLeu 89
Db 1279 CGTTCTCCACCTTCATCGAGAACATTTGGCGGCAGAAATTCGAGCAGAGTCTT 1229
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Search completed: March 1, 2003, 12:17:18  
Job time : 51 secs

GenCore version 5.1.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 1, 2003, 11:05:29 ; Search time 61 Seconds

(without alignments)  
1063.219 Million cell updates/sec

Title: US-09-750-240-2

Perfect score: 570

Sequence: 1 MSWESGLLVKVDKRTAWG.....RAVALGFEDTEVTTTTPAGPL 104

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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 460893 seqs, 311809382 residues

Total number of hits satisfying chosen parameters: 921786

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=200000000 -USBR=US09750240@cgn\_1.1.31 -runat\_25022003\_103943\_25085  
-NCPU=6 -ICPU=3 -NO\_XLPXY -NO\_MAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Model: Applications\_NA:  
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2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:  
3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:  
4: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:  
5: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:  
6: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:  
7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:  
8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:  
9: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:  
10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:  
11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:  
12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:  
13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:  
14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	568	99.6	314	10	US-09-750-240-1
2	545	95.6	3549	10	US-09-750-240-5
3	545	95.6	3552	10	US-09-750-240-10
4	545	95.6	3582	10	US-09-750-240-12

5	545	95.6	4942	9	US-10-201-000-1
6	338.5	59.4	358	9	US-09-933-797-165
7	212.5	37.3	220	10	US-09-728-445-487
8	94	16.5	1533	10	US-09-815-242-7755
9	91.5	16.1	4257	9	US-09-825-288A-1
10	89.5	15.7	1182	9	US-10-071-338-6
11	89.5	15.7	7193	9	US-10-071-338-1
12	87.5	15.4	618	10	US-09-833-381-1050
13	87	15.3	280	9	US-09-796-692-6321
14	87	15.3	16489	9	US-09-764-868-1483
15	86.5	15.2	398	10	US-09-925-299-608
16	86.5	15.2	1038	10	US-09-917-800A-1479
17	86.5	15.2	1078	10	US-09-452-239-41
18	86	15.1	485	9	US-10-004-717-59
19	85	14.9	240	10	US-09-923-876-2469
20	85	14.9	4695	9	US-09-945-901-57
21	85	14.9	4695	9	US-10-007-747-57
22	85	14.9	4695	9	US-10-038-937-57
23	84.5	14.8	2728	9	US-10-152-661-213
24	84	14.7	969	10	US-09-965-703-10
25	84	14.7	1338	10	US-09-965-703-9
26	84	14.7	1850	10	US-09-965-703-8
27	84	14.7	1856	9	US-09-853-450-17
28	84	14.7	1752	10	US-09-965-703-7
29	84	14.7	1878	10	US-09-965-697-1
30	84	14.7	1878	10	US-09-965-703-6
31	84	14.7	2241	9	US-09-042-488B-4
32	84	14.7	2241	9	US-09-042-488B-6
33	84	14.7	3126	9	US-09-042-488B-8
34	84	14.7	13953	9	US-10-096-961-3
35	83	14.6	4682	10	US-09-962-832-243
36	83	14.6	65464	9	US-09-859-888-3
37	82.5	14.5	597	10	US-09-864-761-31718
38	82.5	14.5	1680	10	US-09-815-242-7988
39	82.5	14.5	1372	10	US-09-864-761-15194
40	82.5	14.5	3090	10	US-09-929-315-3
41	82.5	14.5	3090	10	US-09-993-215-3
42	82	14.4	1683	9	US-09-712-363-13
43	81.5	14.3	1026	9	US-09-894-844-113
44	81.5	14.3	1029	9	US-09-712-363-64
45	81.5	14.3	18596	9	US-09-954-531-124

ALIGNMENTS

RESULT 1  
US-09-750-240-1  
; Sequence 1, Application US/09750240  
; Patent No. US20020103147A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammon, H. K.  
; APPLICANT: Insel, P. A.  
; APPLICANT: Ping, P.  
; APPLICANT: Post, S. R.  
; APPLICANT: Gao, M.  
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART FAILURE  
; FILE REFERENCE: 220002056723  
; CURRENT APPLICATION NUMBER: US/09/750,240  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 09/472,667  
; PRIOR FILING DATE: 1999-12-27  
; PRIOR APPLICATION NUMBER: US 09/008,097  
; PRIOR FILING DATE: 1998-01-16  
; PRIOR APPLICATION NUMBER: US 08/924,757  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: US 60/048,933  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: US 08/708,661  
; PRIOR FILING DATE: 1996-09-05  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1

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; LENGTH: 314
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(314)
; OTHER INFORMATION: n = A,T,C or G
US-09-750-240-1
Alignment Scores:
Pred. No.: 2,33e-43 Length: 314
Score: 568.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.65% Indels: 0
DB: 10 Gaps: 0
US-09-750-240-2 (1-104) x US-09-750-240-1 (1-314)
Qy 1 MetSerTrpPheSerGlyLeuValProLysValAspGluArgLysThrAlaTrpGly 20
Db 1 ATGTCATGTTAGTGGCTCTCGTCCCTAAAGTGGATGAACGGAACACGCTGGGGT 60
Qy 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40
Db 61 GAACGCAATGGGCAGAGCGTTCCGGCGCCGCTGCACCTCGGGCAGGTGGCTTCTGCACG 120
Qy 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60
Db 121 CCCCCTATATAGCTGCTCCGGGATGCAGAGCGCCCTCATCCGGAGGGGGCCCAAGGCGCAAG 180
Qy 61 ProArgCysProTrrpGlnAspAlaPheIleArgArgGlyGlyPro**LysGlyLys 80
Db 181 CCTCGTGGCCCTGGCAGATGACGCTTCATCCGGAGGGGGCCCAAGGCGCAAG 240
Qy 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100
Db 241 GAACCTGGGGCTCGGGCAGTGGCCCTGGCTTCGAAGATACCGAAGTGACAACGACACCG 300
Qy 101 AlaGlyProLeu 104
Db 301 GCGGAGCCGCTG 312
RESULT 2
US-09-750-240-5
; Sequence 5, Application US/09750240
; Patent No. US20020103147A1
; GENERAL INFORMATION:
; APPLICANT: Hammon, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; FILE REFERENCE: 220002056723
; CURRENT APPLICATION NUMBER: US/09/750,240
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 3549
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-750-240-1
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; ORGANISM: Homo sapiens
US-09-750-240-5
Alignment Scores:
Pred. No.: 4.03e-40 Length: 3549
Score: 545.00 Matches: 99
Percent Similarity: 97.06% Conservative: 0
Best Local Similarity: 97.06% Mismatches: 3
Query Match: 95.61% Indels: 0
DB: 10 Gaps: 0
US-09-750-240-2 (1-104) x US-09-750-240-5 (1-3549)
Qy 1 MetSerTrpPheSerGlyLeuValProLysValAspGluArgLysThrAlaTrpGly 20
Db 1 ATGTCATGTTAGTGGCTCTCGTCCCTAAAGTGGATGAACGGAACACGCTGGGGT 60
Qy 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40
Db 61 GAACGCAATGGGCAGAGCGTTCCGGCGCCGCTGCACCTCGGGCAGGTGGCTTCTGCACG 120
Qy 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60
Db 121 CCCCCTATATAGCTGCTCCGGGATGCAGAGCGCCACCCACCCCTCGGGGCCCC 180
Qy 61 ProArgCysProTrrpGlnAspAlaPheIleArgArgGlyGlyPro**LysGlyLys 80
Db 181 CCTCGTGGCCCTGGCAGATGACGCTTCATCCGGAGGGGGCCCAAGGCGCAAG 240
Qy 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100
Db 241 GAGCTGGGGCTCGGGCAGTGGCCCTGGCTTCGAGGATACCGAGGTGACAACGACACG 300
Qy 101 AlaGly 102
Db 301 GCGGG 306
RESULT 3
US-09-750-240-10
; Sequence 10, Application US/09750240
; Patent No. US20020103147A1
; GENERAL INFORMATION:
; APPLICANT: Hammon, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; FILE REFERENCE: 220002056723
; CURRENT APPLICATION NUMBER: US/09/750,240
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 3552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-750-240-10
Alignment Scores:
Pred. No.: 4.03e-40 Length: 3552
Score: 545.00 Matches: 99
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Percent Similarity: 97.06% Conservative: 0
Best Local Similarity: 97.06% Mismatches: 3
Query Match: 95.61% Indels: 0
DB: 10 Gaps: 0

US-09-750-240-2 (1-104) x US-09-750-240-10 (1-3552)

QY 1 MetSerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGly 20
Db 1 ATGTCATGGTTTAGTGGCCCTCCTGGTCCCTAAAGTGTGATGAACGGAACAGCCTGGGGT 60

QY 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40
Db 61 GAACGCAATGGCGAAGAGCGTTCCGGCGCGCTGCGCACTCGGCGAGGTGCTTCTGCACG 120

QY 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60
Db 121 CCCGCTATATAGACTCCCTCGGGATGCGAGCCACCCAGCCCTCGCGGGCCCC 180

QY 61 ProArgCysProTrpGlnAspAlaPheIleArgArgGlyGlyPro**LysGlyLys 80
Db 181 CCTCGGTGCCCTGGCAGGATGACGCCCTTCATCCGAGGGCGGCCCCAGGCAAG 240

QY 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100
Db 241 GAGCTGGGGCTGGCGGCGAGTGGCCCTGCGCTTCGAGGATACCGAGGTGACAACGACAGCG 300

QY 101 AlaGly 102
Db 301 GCGGG 306

RESULT 4
US-09-750-240-12
; Sequence 12, Application US/09750240
; Patent No. US20020103147A1
; GENERAL INFORMATION:
; APPLICANT: Hammon, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; TITLE OF INVENTION: FAILURE
; FILE REFERENCE: 22002056723
; CURRENT APPLICATION NUMBER: US/09/750,240
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 3582
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Modified AC-VI
US-09-750-240-12

Alignment Scores:
Pred. No.: 4,07e-40 Length: 3582
Score: 545.00 Matches: 99
Percent Similarity: 97.06% Conservative: 0
Best Local Similarity: 97.06% Mismatches: 3
Query Match: 95.61% Indels: 0
DB: 10 Gaps: 0

US-09-750-240-2 (1-104) x US-09-750-240-1 (1-4942)

QY 1 MetSerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGly 20
Db 145 ATGTCATGGTTTAGTGGCCCTCCTGGTCCCTAAAGTGTGATGAACGGAACAGCCTGGGGT 204

QY 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40
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US-09-750-240-2 (1-104) x US-09-750-240-12 (1-3582)

QY 1 MetSerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGly 20
Db 22 ATGTCATGGTTTAGTGGCCCTCCTGGTCCCTAAAGTGTGATGAACGGAACAGCCTGGGGT 81

QY 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40
Db 82 GAACGCAATGGCGAAGAGCGTTCCGGCGCGCTGCGCACTCGGCGAGGTGCTTCTGCACG 141

QY 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60
Db 142 CCCGCTATATAGACTCCCTCGGGATGCGAGCCACCCAGCCCTCGCGGGCCCC 201

QY 61 ProArgCysProTrpGlnAspAlaPheIleArgArgGlyGlyPro**LysGlyLys 80
Db 202 CCTCGGTGCCCTGGCAGGATGACGCCCTTCATCCGAGGGCGGCCCCAGGCAAG 261

QY 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100
Db 262 GAGCTGGGGCTGGCGGCGAGTGGCCCTGCGCTTCGAGGATACCGAGGTGACAACGACAGCG 321

QY 101 AlaGly 102
Db 322 GCGGG 327

RESULT 5
US-10-201-000-1
; Sequence 1, Application US/10201000
; Publication No. US20020187540A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, James E.
; APPLICANT: COR Therapeutics, Inc.
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
; TITLE OF INVENTION: CYCLASE
; FILE REFERENCE: 44481-5028-01-US
; CURRENT APPLICATION NUMBER: US/10/201,000
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: US/09/474,076
; PRIOR FILING DATE: 1999-12-12
; PRIOR APPLICATION NUMBER: PCT/US98/13694
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/070,904
; PRIOR FILING DATE: 1997-07-01
; PRIOR APPLICATION NUMBER: 08/886,550
; PRIOR FILING DATE: 1997-07-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4942
; TYPE: DNA
; ORGANISM: human type VI adenylyl cyclase
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (145)..(3648)
US-10-201-000-1

Alignment Scores:
Pred. No.: 5.83e-40 Length: 4942
Score: 545.00 Matches: 99
Percent Similarity: 97.06% Conservative: 0
Best Local Similarity: 97.06% Mismatches: 3
Query Match: 95.61% Indels: 0
DB: 9 Gaps: 0
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DB	205	GAACGCAATGGCGAAGCGCTTCGGCGCGCTGGCGACTGGCGCAGGTGGCTTCTGCACG	264
QY	41	ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro	60
Db	265	CCCGCGTATATGAGTGCCTCCCGGATGCAGAGCCACCAGCCACCCTGGGGCCCC	324
QY	61	ProArgCysProTrpGlnAspAspAlaPheIleArgArgGlyGlyPro***LysGlyLys	80
Db	325	CCTCGGTGCCTTCGGCAGGATGACGGCTTCATCCGAGGGCGCGCCAGCGCAGGCAAG	384
QY	81	GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro	100
Db	385	GAGCTGGGGCTGGCGGCGTGGCCCTGGGCTTCAGAGATACCGAGGTGACACGACGCG	444
QY	101	AlaGly 102	
Db	445	GGCGGG 450	
RESULT 6			
US-09-933-797-165			
; Sequence 165, Application US/09933797			
; Patent No. US20020155119A1			
; GENERAL INFORMATION:			
; APPLICANT: Robert A. Sikes et al.			
; TITLE OF INVENTION: Isolation and Use of Fetal Urogenital			
; FILE OF INVENTION: Sinus Expressed Sequences			
; FILE REFERENCE: 9901-007-999			
; CURRENT APPLICATION NUMBER: US/09/933,797			
; CURRENT FILING DATE: 2001-08-22			
; PRIOR APPLICATION NUMBER: US/09/482,933			
; PRIOR FILING DATE: 2000-01-14			
; PRIOR APPLICATION NUMBER: PCT/US99/10746			
; PRIOR FILING DATE: 1999-05/14			
; PRIOR APPLICATION NUMBER: 60/085,383			
; PRIOR FILING DATE: 1998-05-14			
; NUMBER OF SEQ ID NOS: 811			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 165			
; LENGTH: 358			
; TYPE: DNA			
; ORGANISM: Murine			
US-09-933-797-165			
Alignment Scores:			
Pred. No.:		9.81e-23	Length: 358
Score:		338.50	Matches: 62
Percent Similarity:		83.54%	Conservative: 4
Best Local Similarity:		78.48%	Mismatches: 12
Query Match:		59.39%	Indels: 1
DB:		9	Gaps: 1
US-09-750-240-2 (1-104) x US-09-933-797-165 (1-358)			
QY	1	MetSerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGly	20
Db	123	ATGTCATGTTTATGTCCTTCCTGGTTCCTCCAAAGTGGATGAACGAAAAACAGCTTGGGGG	182
QY	21	GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr	40
Db	183	GAACGCAATGGCGAAGCGCCCA---CGCCAGCGCAATCGAGCCAGTGGCTTCTGCVCA	239
QY	41	ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro	60
Db	240	CCTCGGTACATGAGTGCCTTCAGAAATCGGAGCCACCAGGCCCACTCTCGACAGCTCAC	299
QY	61	ProArgCysProTrpGlnAspAspAlaPheIleArgArgGlyGlyPro***LysGly	79
Db	300	ACTCGGTGCCCTTGGCAGGATGAAGCCTTCATCAGGAGGGCGGGCCCGGCAGGGGT	356
RESULT 7			
US-09-728-445-487			
Sequence 487, Application US/09728445			



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Qy 15 ArgLysThrAlaTrpGlyGluArgAsnGlyGlnLysArgSerArgArgGlyThrArg 34
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Db 946 CGGTGAAGCCCATGGGCGGACCAAGTCTCGAAGATGAAGCGCGCGGGGACGCC 887
Qy 35 AlaGlyGlyPheCysThrProArgTyrMetSerCysLeuArgAspAlaGluProProSer 54
   ::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 886 AGTGTGGG-----CCTGCG---CGGAGTCCCGGGAGACCAAGCGCTTCATCA 839
Qy 55 ProThrProAla-----GlyProPro----- 61
   ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 838 CCCCAGCCGCTGCGCGCGCGCAGGGTGCGGTGCGCGCGCGCTCCTCCCGGT 779
Qy 62 ArgCysPro 64
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Db 778 AGATGTCCA 770

RESULT 11
US-10-071-338-1
; Sequence 1, Application US/10071338
; Publication No. US20030022321A1
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham plc et al
; TITLE OF INVENTION: No. US20030022321A1el compounds
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESS: SmithKline Beecham
; STREET: Two, New Horizons Court, Great West Road
; CITY: Brentford
; STATE: <Unknown>
; COUNTRY: UK
; ZIP: TW8 9EP
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: 08-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Valentine, Jill B
; REGISTRATION NUMBER: <Unknown>
; REFERENCE/DOCKET NUMBER: P31731
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 0181-9752000
; TELEFAX: 0181-9756294
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7193 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-071-338-1
Alignment Scores:
Pred. No.: 56.8 Length: 7193
Score: 89.50 Matches: 26
Percent Similarity: 49.21% Conservative: 5
Best Local Similarity: 41.27% Mismatches: 15
Query Match: 15.70% Indels: 17
DB: 9 Gaps: 4

US-09-750-240-2 (1-104) x US-10-071-338-1 (1-7193)
Qy 15 ArgLysThrAlaTrpGlyGluArgAsnGlyGlnLysArgSerArgArgGlyThrArg 34
   ||| ::: ||||| ::: ||||| ||||| ||||| ||||| |||||
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Db 5274 CGGTGAAGCCCATGGGCGGACCAAGTCTCGAAGATGAAGCGCGCGGGGACGCC 5333
Qy 35 AlaGlyGlyPheCysThrProArgTyrMetSerCysLeuArgAspAlaGluProProSer 54
   ::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5334 AGTGTGGG-----CCTGCG---CGGAGTCCCGGGAGACCAAGCGCTTCATCA 5381
Qy 55 ProThrProAla-----GlyProPro----- 61
   ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5382 CCCCAGCCGCTGCGCGCGCGCAGGGTGCGGTGCGCGCGCGCTCCTCCCGGT 5441
Qy 62 ArgCysPro 64
   ||||| |||||
Db 5442 AGATGTCCA 5450

RESULT 12
US-09-833-381-1050/c
; Sequence 1050, Application US/09833381
; Patent No. US20020132090A1
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. US20020132090A1el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833.381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1050
; LENGTH: 618
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(618)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-1050
Alignment Scores:
Pred. No.: 5.53 Length: 618
Score: 87.50 Matches: 30
Percent Similarity: 44.87% Conservative: 5
Best Local Similarity: 38.46% Mismatches: 26
Query Match: 15.35% Indels: 17
DB: 10 Gaps: 4

US-09-750-240-2 (1-104) x US-09-833-381-1050 (1-618)
Qy 18 AlaTrpGlyGluArgAsnGlyGlnLysArgSerArgArg---ArgGlyThrArgAlaGly 36
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 554 CGGTGGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 495
Qy 37 GlyPheCysThrProArgTyrMetSerCysLeuArgAspAlaGlu----- 51
   ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 494 GAC-----GCGGCTGCTGCTGCGGTGTGAGGAGAGAGGTGAGCGCTGCGCGTCCGC 441
Qy 52 -----ProProSerProThrProAlaGly-----ProProArgCysPro 64
   |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 440 GCATCCATTCGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGTGC 381
Qy 65 --TrpGlnAspAlaPheIleArgArgGlyGlyPro**LysGlyLys 80
   ||| ::||| ||||| ||||| ||||| ||||| ||||| |||||
Db 380 GAGGCGCTCGGCTGCGCGGCTGCGGAGCGCGCGCGCGCGCGCGCGCGCGGAAA 331

RESULT 13
US-09-796-692-6321/c
; Sequence 6321, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER
```

```
; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6321
; LENGTH: 280
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-796-692-6321
```

```
Alignment Scores:
Pred. No.: 2.53 Length: 280
Score: 87.00 Matches: 26
Percent Similarity: 40.00% Conservative: 0
Best Local Similarity: 40.00% Mismatches: 23
Query Match: 15.26% Indels: 16
DB: Gaps: 4

US-09-750-240-2 (1-104) x US-09-796-692-6321 (1-280)

QY 19 TtpGlyGluArgAsn-----GlyGlnLysArgSerArgArgGlyThrArgAla 35
Db 236 TGGGGCCCAAGAGCCACAGCTGAGTGGCTTGTGTCTGAGGAGGAGGACCCGCTGT 177
QY 36 Gly---GlyPheCysThrProArgTyrMetSerCysLeuArgAspAlaGluProProSer 54
Db 176 TCCTTGGGGTTCACGCTTCTTCTTGAGGTTGTGT-----CCTCCTTCC 132
QY 55 ProThrProAlaGlyProProArgCysProTtpGlnAspAlaPheIleArgArgGly 74
Db 131 CCACACCTCTGCAGCGCTGCCAGCTCTTCTGTGCGCAA-----AGC 93
QY 75 GlyPro***LysGly 79
Db 92 GGGCCCCCAGATGGGT 78
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```
RESULT 14
US-09-764-868-1483
; Sequence 1483, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT232
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
```

```
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1483
; LENGTH: 16489
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-868-1483

Alignment Scores:
Pred. No.: 240 Length: 16489
Score: 87.00 Matches: 26
Percent Similarity: 40.00% Conservative: 0
Best Local Similarity: 40.00% Mismatches: 23
Query Match: 15.26% Indels: 16
DB: Gaps: 4

US-09-750-240-2 (1-104) x US-09-764-868-1483 (1-16489)

QY 19 TtpGlyGluArgAsn-----GlyGlnLysArgSerArgArgGlyThrArgAla 35
Db 359 TGGGGCCCAAGAGCCACAGCTGAGTGGCTTGTGTCTGAGGAGGAGGACCCGCTGT 418
QY 36 Gly---GlyPheCysThrProArgTyrMetSerCysLeuArgAspAlaGluProProSer 54
Db 419 TCCTTGGGGTTCACGCTTCTTCTTGAGGTTGTGT-----CCTCCTTCC 463
QY 55 ProThrProAlaGlyProProArgCysProTtpGlnAspAlaPheIleArgArgGly 74
Db 464 CCACACCTCTGCAGCGCTGCCAGCTCTTCTGTGCGCAA-----AGC 502
QY 75 GlyPro***LysGly 79
Db 503 GGGCCCCCAGATGGGT 517

RESULT 15
US-09-925-299-608/c
; Sequence 608, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 608
; LENGTH: 398
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (132)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (137)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (138)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (139)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (360)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (373)
; OTHER INFORMATION: n equals a,t,g, or c
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; NAME/KEY: misc_feature
; LOCATION: (377)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (386)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (394)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-608
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Alignment Scores:
Pred. No.:      4.16      Length:      398
Score:          86.50     Matches:      28
Percent Similarity: 42.22%  Conservative: 10
Best Local Similarity: 31.11% Mismatches: 35
Query Match:      15.18%  Indels:      17
DB:               10      Gaps:       4
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US-09-750-240-2 (1-104) x US-09-925-299-608 (1-398)

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QY 13 AspGluArgLysThrAlaTrpGlyGlu-----ArgAsnGlyGlnLysArgSerArg 29
Db 290 GACCGGGAGGAGGCGGCTTCCACCCCACTCGCGCGGTGAT-----CCCGGT 237
QY 30 ArgArgGlyThrArgAlaGlyGlyPheCysThrProArgTyrMetSerCysLeuArgAsp 49
Db 236 CGGCGTGACAGTCGCTCGGTGGCGGGAACGTCCCGAGGGCCCCAGGAGCAGGAATCG 177
QY 50 AlaGlu-----ProProSerProThrProAlaGlyProProArgCysPro 64
Db 176 GGGGACTGTCCCTCACTCTGCGCGCGCAACGAGTGNNNCTTNGCCCGGTGCCCC 117
QY 65 TrpGlnAspAspAlaPheIleArgArg-----GlyGlyPro*** 77
Db 116 CTCGAGCGCGTCTCTGTTTCTCGAAGAACGAAACTTCCTCCAGCGCCCCGAGTCCCTTC 57
QY 78 LysGlyLysGluLeuGlyLeuArgAlaVal 87
Db 56 CGAGCGCGCTCTCTCATCCCGAAGAGTC 27
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Search completed: March 1, 2003, 13:39:42  
Job time : 67 secs

GenCore version 5.1.1.3  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 1, 2003, 09:07:49 ; Search time 263 Seconds

(without alignments)  
673.833 Million cell updates/sec

Title: US-09-750-240-2

Perfect score: 570

Sequence: 1 MSWFGSLLPVKYDKRTAWG.....RAVALGFEDTEVTTTTPAGPL 104

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 3936061 seqs, 852009584 residues

Total number of hits satisfying chosen parameters: 7872122

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MAIRIX=blom62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09750240@cgn2.1.1.86@runat\_25022003.103943.25050 -NCPU=6 -ICPU=3  
-NO\_XLPXY -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Pending\_Patents\_NA\_New.\*

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3: /cgn2.6/ptodata/2/pna/US07\_NEW\_COMB.seq.\*  
4: /cgn2.6/ptodata/2/pna/US08\_NEW\_COMB.seq.\*  
5: /cgn2.6/ptodata/2/pna/US09\_NEW\_COMB.seq.\*  
6: /cgn2.6/ptodata/2/pna/US10\_NEW\_COMB.seq.\*  
7: /cgn2.6/ptodata/2/pna/US60\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	ID	Description
1	545	95.6	1386	1 PCT-US02-36759-83
2	432	75.8	5826	US-10-144-771-5921
3	92.5	16.2	4955	US-60-423-552-78
4	92.5	16.2	4955	US-60-423-552-78
5	90.5	15.9	1173	US-09-398-858-13
6	90.5	15.9	1173	US-10-320-230-13
7	90.5	15.9	1173	US-10-348-110-13
8	90.5	15.9	4884	1 PCT-US02-39133-56
9	90.5	15.9	5079	1 PCT-US02-39133-57
10	89.5	15.7	1182	6 US-10-288-985-6
11	89.5	15.7	1182	6 US-10-289-980-6

12	89.5	15.7	7193	6 US-10-288-985-1
13	89.5	15.7	7193	6 US-10-289-980-1
14	89	15.6	34319	1 PCT-US03-01858-47
15	88.5	15.5	2349	5 US-09-724-676-9445
16	88.5	15.5	2349	5 US-09-724-676-9445
17	88.5	15.5	3394	5 US-09-620-312D-314
18	87	15.3	1622	6 US-10-276-781-61
19	87	15.3	2241	6 US-10-300-757-17
20	87	15.3	2295	6 US-10-300-757-19
21	87	15.3	2301	6 US-10-300-757-21
22	87	15.3	3717	1 PCT-US03-01363-10
23	86.5	15.2	1038	7 US-60-436-643-4032
24	86.5	15.2	1196	6 US-10-144-771-13121
25	86.5	15.2	8495	6 US-10-144-779-234
26	86	15.1	485	5 US-09-585-645A-59
27	86	15.1	18876	6 US-10-329-079-42
28	86	15.1	61944	6 US-10-329-079-34
29	86	15.1	77536	5 US-09-940-316B-1
30	85.5	15.0	1806	6 US-10-329-079-38
31	85.5	15.0	1806	6 US-10-392-027-29
32	85.5	15.0	2605	1 PCT-US02-29264-2809
33	85.5	15.0	2605	1 PCT-US02-29264-2818
34	85.5	15.0	2605	1 PCT-US02-29264-2819
35	85.5	15.0	2605	1 PCT-US02-29264-2820
36	85.5	15.0	14055	1 PCT-US02-37547-1
37	85.5	15.0	61944	6 US-10-329-079-34
38	85.5	15.0	82746	1 PCT-US02-37547-56
39	84.5	14.8	1020	6 US-10-144-771-44214
40	84.5	14.8	2605	1 PCT-US02-29264-2811
41	84	14.7	1656	1 PCT-US02-14719-17
42	84	14.7	2015	6 US-10-144-771-1266
43	84	14.7	57984	5 US-09-949-004-512
44	84	14.7	57985	5 US-09-949-004-589
45	83.5	14.6	6099	6 US-10-144-771-15901

#### ALIGNMENTS

RESULT 1  
PCT-US02-36759-83  
; Sequence 83, Application PC/TUS0236759  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: DUGGAN, Brendan M.  
; APPLICANT: YANG, Junming  
; APPLICANT: GIEYZEN, Kimberly J.  
; APPLICANT: LEE, Soo Yeun  
; APPLICANT: TANG, Y. Tom  
; APPLICANT: AZIMZAI, Yalda  
; APPLICANT: WALIA, Narinder K.  
; APPLICANT: WARREN, Bridget A.  
; APPLICANT: BARROSO, Ines  
; APPLICANT: BECHA, Shanya D.  
; APPLICANT: YUE, Henry  
; APPLICANT: LEHR-MASON, Patricia M.  
; APPLICANT: THANGAVELU, Kavitha  
; APPLICANT: LEE, Sally  
; APPLICANT: EMERLING, Brooke M.  
; APPLICANT: KABLE, Amy E.  
; APPLICANT: KHARE, Reena  
; APPLICANT: BAUGHN, Mariah R.  
; APPLICANT: GANDHI, Ameena R.  
; APPLICANT: TRAN, Uyen K.  
; APPLICANT: RICHARDSON, Thomas W.  
; APPLICANT: MARQUIS, Joseph P.  
; APPLICANT: LAL, Preeti G.  
; APPLICANT: FORSYTHE, Ian J.  
; APPLICANT: LEE, Ernestine A.  
; APPLICANT: SWARNAKAR, Anita.  
; APPLICANT: KALLICK, Deborah A.  
; APPLICANT: GRIFFIN, Jennifer A.  
; APPLICANT: ELLIOTT, Vicki S.  
; APPLICANT: GORVAD, Ann E.

; APPLICANT: HAFALIA, April J.A.  
; APPLICANT: ISON, Craig H.  
; APPLICANT: JIN, Pei  
; APPLICANT: JIANG, Xin  
; APPLICANT: JACKSON, Alan  
; APPLICANT: BHATIA, Umesh  
; APPLICANT: BURRILL, John D.  
; APPLICANT: BLAKE, Julie J.  
; APPLICANT: HO, Ann  
; APPLICANT: ZHENG, Wenjin  
; APPLICANT: GAO, Jing  
; TITLE OF INVENTION: RECEPTORS AND MEMBRANE-ASSOCIATED PROTEINS  
; FILE REFERENCE: PF-1279 PCT  
; CURRENT APPLICATION NUMBER: PCT/US02/36759  
; CURRENT FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: US 60/333,097  
; PRIOR FILING DATE: 2001-11-13  
; PRIOR APPLICATION NUMBER: US 60/335,274  
; PRIOR FILING DATE: 2001-11-15  
; PRIOR APPLICATION NUMBER: US 60/340,542  
; PRIOR FILING DATE: 2001-12-14  
; PRIOR APPLICATION NUMBER: US 60/342,166  
; PRIOR FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: US 60/347,580  
; PRIOR FILING DATE: 2002-01-11  
; PRIOR APPLICATION NUMBER: US 60/348,687  
; PRIOR FILING DATE: 2002-01-14  
; NUMBER OF SEQ ID NOS: 94  
; SOFTWARE: PERL Program  
; SEQ ID NO 83  
; LENGTH: 1386  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID No: 7506194CB1  
PCT-US02-36759-83

Alignment Scores:  
Pred. No.: 1,5e-34 Length: 1386  
Score: 545.00 Matches: 99  
Percent Similarity: 97.06% Conservative: 0  
Best Local Similarity: 97.06% Mismatches: 3  
Query Match: 95.61% Indels: 0  
DB: 1 Gaps: 0

US-09-750-240-2 (1-104) x PCT-US02-36759-83 (1-1386)

Qy 1 MetSerTrpPheSerGlyLeuValProLysValAspGluArgLysThrAlaTrpGly 20  
Db 25 ATGTCATGGTTAGTGGCTCTCTGTCCTAAAGTGGATGAACGGAAACAGCCCTGGGGT 84  
Qy 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40  
Db 85 GAACGCAATGGCAGAACGCTTCGGCGGCCGTGCACTCGGCAGGTGGCTTCTGCACG 144  
Qy 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60  
Db 145 CCCGCTATATGAGCTGCTCCGGGATGCAGAGCCACCCAGCCCTCGGGCCCC 204  
Qy 61 ProArgCysProTrpGlnAspAlaPheLeArgArgGlyGlyPro\*\*\*LysGlyLys 80  
Db 205 CCTCGGTCCCTGGCAGGATGACGCTTCATCCGAGGGGGCGGCCAGGCAAGGCAAG 264  
Qy 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100  
Db 265 GAGCTGGGGCTCGGGCAGTGGCTTGGCTTCGAGGATACCGAGGTGACACGACAGCG 324  
Qy 101 AlaGly 102  
Db 325 GCGGG 330  
RESULT 2

US-10-144-771-5921  
; Sequence 5921, Application US/10144771  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig  
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF  
; FILE REFERENCE: CLO01321  
; CURRENT APPLICATION NUMBER: US/10/144,771  
; CURRENT FILING DATE: 2002-05-15  
; NUMBER OF SEQ ID NOS: 47235  
; SEQ ID NO 5921  
; LENGTH: 5826  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-10-144-771-5921

Alignment Scores:  
Pred. No.: 8.16e-25 Length: 5826  
Score: 432.00 Matches: 81  
Percent Similarity: 85.29% Conservative: 6  
Best Local Similarity: 79.41% Mismatches: 13  
Query Match: 75.79% Indels: 2  
DB: 6 Gaps: 2

US-09-750-240-2 (1-104) x US-10-144-771-5921 (1-5826)

Qy 1 MetSerTrpPheSerGlyLeuValProLysValAspGluArgLysThrAlaTrpGly 20  
Db 96 ATGTCATGGTTAGTGGCTCTCTGTCCTCCAAAGTGGATGAACGGAAACAGCTTGGGG 155  
Qy 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40  
Db 156 GAACGCAATGGCAGAACGCGCCA---CGCCACGCGAATCGAGCCAGTGGCTTCTGCACA 212  
Qy 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60  
Db 213 CTGCTACATGAGCTGCTCAAGAAATCGGAGCCACCCAGCCCTCTGCACTCAC 272  
Qy 61 ProArgCysProTrpGlnAspAlaPheLeArgArgGlyGlyPro\*\*\*LysGlyLys 80  
Db 273 ACTCGTCCCTGGCAGGATGAAGCCTTCATCAGAGGGCGGCCGCGAGGGGTGTG 332  
Qy 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100  
Db 333 GAGCTGGGGCTCGGTCAGTGGCTTGGGGTTTGACGACACTGAGGTG---ACCACACCG 389  
Qy 101 AlaGly 102  
Db 390 ATGGGC 395

RESULT 3

US-60-423-552-78  
; Sequence 78, Application US/60423552  
; GENERAL INFORMATION:  
; APPLICANT: American Home Product Inc.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING MAJOR DEP  
; FILE REFERENCE: AM101250L  
; CURRENT APPLICATION NUMBER: US/60/423,552  
; CURRENT FILING DATE: 2002-11-05  
; NUMBER OF SEQ ID NOS: 256  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 78  
; LENGTH: 4955  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-60-423-552-78

Alignment Scores:  
Pred. No.: 986 Length: 4955  
Score: 92.50 Matches: 25  
Percent Similarity: 48.65% Conservative: 11  
Best Local Similarity: 33.78% Mismatches: 34  
Query Match: 16.23% Indels: 4



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DB: 7 Gaps: 1
US-09-750-240-2 (1-104) x US-60-423-552-78 (1-4955)
QY 2 SerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGlyGlu 21
Db 2972 GCCTGTGGACTATGGCGAGGGTGGCGAGGGTCAGTTCAATGAAGACGGCTCCTTCATCG 3031
QY 22 ArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThrPro 41
Db 3032 GCCAGTACAGGTCAAAGAGCAAGAGGAAACACAGAGGCAAGAGCTCAGAGGCCA 3091
QY 42 ArgTyrMetSerCysLeuArgAspAlaGluPro-ProSerProThrProAlaGlyProPr 61
Db 3092 CGTCACGTGTCAATGTATCTACTCTCTGCGCTAAGCGGCCACCCAGGCACAGCCACC 3151
QY 61 oArgCysProTrpGlnAspAlaPheIleArgArgGly 74
Db 3152 ACTTTCAGTGGGAGGAGGGG-----AGAAGGGGA 3182
RESULT 4
US-60-427-579-78
; Sequence 78, Application US/60427579
; GENERAL INFORMATION:
; APPLICANT: American Home Product Inc.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING MAJOR DEPRES
; FILE REFERENCE: AM101250L
; CURRENT APPLICATION NUMBER: US/60/427,579
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 256
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78
; LENGTH: 4955
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-427-579-78
Alignment Scores:
Pred. No.: 986 Length: 4955
Score: 92.50 Matches: 25
Percent Similarity: 48.65% Conservative: 11
Best Local Similarity: 33.78% Mismatches: 34
Query Match: 16.23% Indels: 4
DB: 7 Gaps: 1
US-09-750-240-2 (1-104) x US-60-427-579-78 (1-4955)
QY 2 SerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGlyGlu 21
Db 2972 GCCTGTGGACTATGGCGAGGGTGGCGAGGGTCAGTTCAATGAAGACGGCTCCTTCATCG 3031
QY 22 ArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThrPro 41
Db 3032 GCCAGTACAGGTCAAAGAGCAAGAGGAAACACAGAGGCAAGAGCTCAGAGGCCA 3091
QY 42 ArgTyrMetSerCysLeuArgAspAlaGluPro-ProSerProThrProAlaGlyProPr 61
Db 3092 CGTCACGTGTCAATGTATCTACTCTCTGCGCTAAGCGGCCACCCAGGCACAGCCACC 3151
QY 61 oArgCysProTrpGlnAspAlaPheIleArgArgGly 74
Db 3152 ACTTTCAGTGGGAGGAGGGG-----AGAAGGGGA 3182
RESULT 5
US-09-398-858-13
; Sequence 13, Application US/09398858
; GENERAL INFORMATION:
; APPLICANT: Lowe, Keith S.
; APPLICANT: Tao, Yumin
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Gregory, Carolyn A.
; APPLICANT: McElver, John A.
```

```
; APPLICANT: Hoerster, George J.
; TITLE OF INVENTION: Cyclin D Polynucleotides, Polypeptides
; FILE REFERENCE: 0926
; CURRENT APPLICATION NUMBER: US/09/398,858
; CURRENT FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 60/101,551
; PRIOR FILING DATE: 1998-09-23
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1173)
US-09-398-858-13
Alignment Scores:
Pred. No.: 285 Length: 1173
Score: 90.50 Matches: 21
Percent Similarity: 57.78% Conservative: 5
Best Local Similarity: 46.67% Mismatches: 12
Query Match: 15.88% Indels: 7
DB: 5 Gaps: 3
US-09-750-240-2 (1-104) x US-09-398-858-13 (1-1173)
QY 28 SerArgArgGlyThrArgAlaGlyGlyPheCysThrProArgTyrMetSerCysLeu 47
Db 635 GCACGCGCGCGAGGA-----GCTGCTGGCTCTTGCAGTCCGCGGAGCTTATCTTGGTG 688
QY 48 ArgAspAlaGluProPro-----SerProThrProAlaGlyProProArgCys--- 63
Db 689 CGGCCAGAGGACCGGCTGCGTGTTCAGGCCGCTCCGAGATCGCGCGCGGTTGCAG 748
QY 64 ---ProTrpGlnAsp 67
Db 749 CCGCCCGTGGCGCGAG 763
RESULT 6
US-10-320-230-13
; Sequence 13, Application US/10320230
; GENERAL INFORMATION:
; APPLICANT: Lowe, Keith S.
; APPLICANT: Tao, Yumin
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Gregory, Carolyn A.
; APPLICANT: McElver, John A.
; APPLICANT: Hoerster, George J.
; TITLE OF INVENTION: Cyclin D Polynucleotides, Polypeptides
; FILE REFERENCE: 0926D
; CURRENT APPLICATION NUMBER: US/10/320,230
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/101,551
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 09/398,858
; PRIOR FILING DATE: 1999-09-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1173)
US-10-320-230-13
Alignment Scores:
Pred. No.: 285 Length: 1173
```

Score: 90.50 Matches: 21  
Percent Similarity: 57.78% Conservative: 5  
Best Local Similarity: 46.67% Mismatches: 12  
Query Match: 15.88% Indels: 7  
DB: 6 Gaps: 3

US-09-750-240-2 (1-104) x US-10-320-230-13 (1-1173)

Qy 28 SerArgArgGlyThrArgAlaGlyPheCysThrProArgTyrMetSerCysLeu 47

Db 635 GCACGGCCGAGGA-----GCTGCTGGCTTTCAGATGCCGGAGCTTATCTTGCCTG 688

Qy 48 ArgAspAlaGluProPro-----SerProThrProAlaGlyProProArgCys--- 63

Db 689 CGGCCAGAGAACCGCTCGCGGTTTCAGGCCCTCCGAGATCGCCCGCGGTTGCAG 748

Qy 64 ---ProTrpGlnAsp 67

Db 749 CGCCCGTGGCCGGAG 763

RESULT 7

US-10-348-110-13

; Sequence 13, Application US/10348110

; GENERAL INFORMATION:

; APPLICANT: Lowe, Keith S.

; APPLICANT: Tao, Yunin

; APPLICANT: Gordon-Kamm, William J.

; APPLICANT: Gregory, Carolyn A.

; APPLICANT: McElver, John A.

; APPLICANT: Hoerster, George J.

; APPLICANT: Maddock, Sheila E.

; TITLE OF INVENTION: Cyclin D Polynucleotides, Polypeptides

; FILE REFERENCE: 0926D2

; CURRENT APPLICATION NUMBER: US/10/348,110

; PRIOR FILING DATE: 2003-01-21

; PRIOR APPLICATION NUMBER: 60/101,551

; PRIOR FILING DATE: 1998-09-23

; PRIOR APPLICATION NUMBER: 09/398,858

; PRIOR FILING DATE: 1999-09-20

; PRIOR APPLICATION NUMBER: 10/320,230

; PRIOR FILING DATE: 2002-12-16

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 13

; LENGTH: 1173

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(1173)

US-10-348-110-13

Alignment Scores:

Pred. No.: 285 Length: 1173

Score: 90.50 Matches: 21

Percent Similarity: 57.78% Conservative: 5

Best Local Similarity: 46.67% Mismatches: 12

Query Match: 15.88% Indels: 7

DB: 6 Gaps: 3

US-09-750-240-2 (1-104) x US-10-348-110-13 (1-1173)

Qy 28 SerArgArgGlyThrArgAlaGlyPheCysThrProArgTyrMetSerCysLeu 47

Db 635 GCACGGCCGAGGA-----GCTGCTGGCTTTCAGATGCCGGAGCTTATCTTGCCTG 688

Qy 48 ArgAspAlaGluProPro-----SerProThrProAlaGlyProProArgCys--- 63

Db 689 CGGCCAGAGAACCGCTCGCGGTTTCAGGCCCTCCGAGATCGCCCGCGGTTGCAG 748

Qy 64 ---ProTrpGlnAsp 67

Db 749 CGCCCGTGGCCGGAG 763

Db 749 CGCCCGTGGCCGGAG 763

RESULT 8

PCT-US02-39133-56

; Sequence 56, Application PC/TUS0239133

; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.

; APPLICANT: GRIFFIN, Jennifer A.

; APPLICANT: RAMKUMAR, Jayalaxmi

; APPLICANT: EMERLING, Brooke W.

; APPLICANT: KABLE, Amy E.

; APPLICANT: ELLIOTT, Vicki S.

; APPLICANT: MARQUIS, Joseph P.

; APPLICANT: BAUGHN, Mariah R.

; APPLICANT: GORVAD, Ann E.

; APPLICANT: YUE, Henry

; APPLICANT: LEE, Ernestine A.

; APPLICANT: BECHA, Shanya D.

; APPLICANT: TANG, Y. Tom

; APPLICANT: TRAN, Uyen K.

; APPLICANT: SWARNAKAR, Anita

; APPLICANT: LEE, Sally

; APPLICANT: ISON, Craig H.

; APPLICANT: HAFALIA, April J.A.

; APPLICANT: TRAN, Bao

; APPLICANT: SPRAGUE, William W.

; APPLICANT: KHARE, Reena

; APPLICANT: GANDHI, Ameena R.

; APPLICANT: GIETZEN, Kimberly J.

; APPLICANT: BHATIA, Umesh G.

; APPLICANT: BURRILL, John D.

; APPLICANT: BLAKE, Julie J.

; APPLICANT: HO, Anne

; APPLICANT: Zheng, Wenjin

; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEA

; FILE REFERENCE: PF-1319 PCT

; CURRENT APPLICATION NUMBER: PCT/US02/39133

; CURRENT FILING DATE: 2002-12-04

; PRIOR APPLICATION NUMBER: US 60/340,747

; PRIOR FILING DATE: 2001-12-07

; PRIOR APPLICATION NUMBER: US 60/342,761

; PRIOR FILING DATE: 2001-12-20

; PRIOR APPLICATION NUMBER: US 60/349,705

; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: US 60/354,764

; PRIOR FILING DATE: 2002-02-06

; PRIOR APPLICATION NUMBER: US 60/356,216

; PRIOR FILING DATE: 2002-02-12

; NUMBER OF SEQ ID NOS: 66

; SOFTWARE: PERL Program

; SEQ ID NO 56

; LENGTH: 4884

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc-feature

; OTHER INFORMATION: Incyte ID No: 7506414CB1

PCT-US02-39133-56

Alignment Scores:

Pred. No.: 1.4e+03 Length: 4884

Score: 90.50 Matches: 39

Percent Similarity: 32.58% Conservative: 4

Best Local Similarity: 29.55% Mismatches: 42

Query Match: 15.88% Indels: 47

DB: 1 Gaps: 8

US-09-750-240-2 (1-104) x PCT-US02-39133-56 (1-4884)

Qy 10 ProLysValAspGluArgLysThrAlaTrpGlyGluArgAsnGlyGlnLysArgSerArg 29

Db 2877 CCGGCCCGCTCGACGCGCCTCGCGGTTGGGCGATCCTGGCAGTGAACGGCAAGA 2936

QY	30	ArqArgGlyThrArgAlaGlyCysThrProArgTyrMetSerCysLeuArgAsp	49
Db	2937	CGTGCGGGATGCCACGCA-----CCAAGAAGCAGTCAGTCGCCTGTCTCCG	2981
QY	50	AlagLupro-----ProSerProThr---	56
Db	2982	GCCCTGCCCTGGAGCTGTGCTGCTGGTGGGAGGACC CGGCACCCCGCGGCTTACGGGA	3041
QY	57	-----ProAlaGly-----ProProArgCysPro	64
Db	3042	ACTGTGCATCCAGAGGCACCTGGGAGAGGCTGGGCATCAGCATCGCGGGGTGCAG	3101
QY	65	-----TrpIasnAspAlaPheIleArgArgGly-----GlyPro	76
Db	3102	GGGCCACGCTGGCAACCCCGCGGACCCACACAGCAGGCGCATCTTCATCTCCAAGGTGAG	3161
QY	77	**LySGlySLeuGlyLeuGlyLeuArgAlaValAlaLeuGlyPhe-----	91
Db	3162	CCCCAGCGGGGCGAGCGCGGCGGCGGCTGGCTGGTTGCGGCTGTGGAGGT	3221
QY	92	GLuaSPThrGLuVaiThrThrProAlaGlyPro	103
Db	3222	GAACCACAGAG-----CCTGCTGGGCT	3245
<b>RESULT 9</b>			
PCT-US02-39133-57			
; Sequence 57, Application PC/TUS0239133			
; GENERAL INFORMATION:			
; APPLICANT: INCYTE GENOMICS, INC.			
; APPLICANT: GRIFFIN, Jennifer A			
; APPLICANT: RAMKUMAR, Jayalaxmi			
; APPLICANT: EMERLING, Brooke M.			
; APPLICANT: KABLE, Amy E.			
; APPLICANT: ELLIOTT, Vicki S.			
; APPLICANT: MARQUIS, Joseph P.			
; APPLICANT: BAUGHN, Mariah R.			
; APPLICANT: GORVAD, Ann E.			
; APPLICANT: YUE, Henry			
; APPLICANT: LEE, Ernestine A.			
; APPLICANT: BECHA, Shanya D.			
; APPLICANT: TANG, Y. Tom			
; APPLICANT: TRAN, Uyen K.			
; APPLICANT: SWARNAKAR, Anita			
; APPLICANT: LEE, Sally			
; APPLICANT: ISON, Craig H.			
; APPLICANT: HAFALIA, April J.A.			
; APPLICANT: TRAN, Bao			
; APPLICANT: SPRAGUE, William W.			
; APPLICANT: LEE, Soo Yeun			
; APPLICANT: KHARE, Reena			
; APPLICANT: GANDHI, Ameena R.			
; APPLICANT: GIETZEN, Kimberly J.			
; APPLICANT: BHATIA, Umesh G.			
; APPLICANT: BURRILL, John D.			
; APPLICANT: BLAKE, Julie J.			
; APPLICANT: HO, Anne			
; APPLICANT: Zheng, Wenjin			
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION			
; FILE REFERENCE: PF-1319 PCT			
; CURRENT APPLICATION NUMBER: PCT/US02/39133			
; CURRENT FILING DATE: 2002-12-04			
; PRIOR APPLICATION NUMBER: US 60/340,747			
; PRIOR FILING DATE: 2001-12-07			
; PRIOR APPLICATION NUMBER: US 60/342,761			
; PRIOR FILING DATE: 2001-12-20			
; PRIOR APPLICATION NUMBER: US 60/349,705			
; PRIOR FILING DATE: 2002-01-15			
; PRIOR APPLICATION NUMBER: US 60/354,764			
; PRIOR FILING DATE: 2002-02-06			
; PRIOR APPLICATION NUMBER: US 60/356,216			
; PRIOR FILING DATE: 2002-02-12			
; NUMBER OF SEQ ID NOS: 66			

```

; SOFTWARE: PERL Program
; SEQ ID NO 57
; LENGTH: 5079
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No.: 7506415CB1
PCT-US02-39133-57

Alignment Scores:
Pred. No.: 1.47e+03 Length: 5079
Score: 90.50 Matches: 39
Percent Similarity: 32.58% Conservative: 4
Best Local Similarity: 29.55% Mismatches: 42
Query Match: 15.88% Indels: 47
DB: 1 Gaps: 8

US-09-750-240-2 (1-104) x PCT-US02-39133-57 (1-5079)
QY 10 ProlysValAspGluArgLysThrAlaThrGlyGluArgAsnGlyGlnLysArgSerArg 29
    ||| :||| ||||| ||| :|||:||||
Db 3072 CTTGGCCGCTCGCAGCGCCTCGGGTTGGGACCGCATCTCTGGCAGTGAACGGGCAAGA 3131
QY 30 ArgArgGlyThrArgAlaGlyGlyPheCysThrProArgTyrMetSerCysLeuArgAsp 49
    ||| ||| ||| ||||| |||||
Db 3132 CGTGGGAGTGCACGCA-----CCAAAGAAGCAGTGCAGTGCCTGCTCCG 3176
QY 50 AlaGluPro-----ProSerProThr--- 56
    ||| ||| ||| ||| |||||
Db 3177 GCCCTGCCTGAGCTCTCGCTCTGCTGGGAGGACCCGCGACCCGGCGCTACGGGA 3236
QY 57 -----ProAlaGly-----ProProArgCysPro 64
    ||| ||| ||| ||| |||||
Db 3237 ACTGTGCATCCAGAAGCGACCTGGGAGGAGGCTGGGCATCAGCATCCCGGGGGTGCAG 3296
QY 65 -----TrpGlnAspAspAlaPheIleArgArgGly-----GlyPro 76
    ||||| ||||| ||||| |||
Db 3297 GGGCCAGCTGGCAACCCCGCGACCCACACAGCAGGGCATCTTCATCTCCAAGGTGAG 3356
QY 77 ***LysGlyLysGluLeuGlyLeuArgAlaValAlaLeuGlyPhe----- 91
    ||| ||| :||| ||| |||||
Db 3357 CCCACGGGGGCACCGCGCGGCGAGCGTGGCTGGGTGCGGTGTTGCGGCTGTTGGAGGT 3416
QY 92 GluAspThrGluValThrThrProAlaGlyPro 103
    ||| ||| ||| ||||| |||||
Db 3417 GAACACGACAG-----CCTGCTGGGCGCT 3440

RESULT 10
US-10-288-985-6/c
; Sequence 6, Application US/10288985
; GENERAL INFORMATION:
; APPLICANT: Barton, Barry
; APPLICANT: Anders, Cecilia
; APPLICANT: Griffin, John Patrick
; APPLICANT: Jensen, Susan
; APPLICANT: Mosher, Roy Henry
; APPLICANT: Paradkar, Ashish Sudhakar
; TITLE OF INVENTION: Novel Process
; FILE REFERENCE: P31733C3
; CURRENT APPLICATION NUMBER: US/10/288,985
; CURRENT FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 09/632,540
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 09/137,737
; PRIOR FILING DATE: 1998-08-21
; PRIOR APPLICATION NUMBER: 08/985,666
; PRIOR FILING DATE: 1997-12-05
; PRIOR APPLICATION NUMBER: GB 9702216.4
; PRIOR FILING DATE: 1997-02-04
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6

```

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; LENGTH: 1182
; TYPE: DNA
; ORGANISM: S. Clavuligerus
; US-10-288-985-6

Alignment Scores:
Pred. No.:      345      Length:      1182
Score:          89.50    Matches:      26
Percent Similarity: 49.21% Conservative: 5
Best Local Similarity: 41.27% Mismatches: 15
Query Match:      15.70% Indels:      17
DB:              6      Gaps:         4

US-09-750-240-2 (1-104) x US-10-288-985-6 (1-1182)

QY 15 ArgLysThrAlaTrpGlyGluArgAsnGlyGlnLysArgSerArgArgGlyThrArg 34
   ||| ::: ||||| : : : : : ||||| ||||| ||||| |||||
Db 946 CGGTGAAGCCATGGGCGCAACCACTTCTCGAAGATGAAGCGCCGCCGGGACGCC 887
   : : : : : ||||| : : : : : ||||| ||||| ||||| |||||

QY 35 AlaGlyGlyPheCysThrProArgTyrMetSerCysLeuArgAspAlaGluProSer 54
   : : : : : ||||| : : : : : ||||| ||||| ||||| |||||
Db 886 AGTGGTGGG-----CCTGC---CGAGTCCCGGGAGACCAGGACGTCTTCATCA 839
   : : : : : ||||| : : : : : ||||| ||||| ||||| |||||

QY 55 ProThrProAla-----GlyProPro----- 61
   ||| : : : ||||| ||||| ||||| ||||| |||||
Db 838 CCCGACGCCGCTCCGCCGCCGAGGTGCGTGGTCCGCCGCCCTCGGCTCTCTCCCGT 779
   ||| : : : ||||| ||||| ||||| ||||| |||||

QY 62 ArgCysPro 64
   ||||| ||||| ||||| ||||| |||||
Db 778 AGATGTCCA 770

RESULT 11
US-10-289-980-6/C
; Sequence 6. Application US/10289980
; GENERAL INFORMATION:
; APPLICANT: Anders, Cecilia
; APPLICANT: Barton, Barry
; APPLICANT: Griffin, John Patrick
; APPLICANT: Jenson, Susan
; APPLICANT: Mosher, Roy Henry
; APPLICANT: Paradkar, Ashish Sudhakar
; TITLE OF INVENTION: Novel Compounds
; FILE REFERENCE: P31731D2C2
; CURRENT APPLICATION NUMBER: US/10/289,980
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 10/214,519
; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 09/350,976
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/018,806
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: GB 9702218.0
; PRIOR FILING DATE: 1997-02-04
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1182
; TYPE: DNA
; ORGANISM: Streptomyces clavuligerus
; US-10-289-980-6

Alignment Scores:
Pred. No.:      345      Length:      1182
Score:          89.50    Matches:      26
Percent Similarity: 49.21% Conservative: 5
Best Local Similarity: 41.27% Mismatches: 15
Query Match:      15.70% Indels:      17
DB:              6      Gaps:         4

US-09-750-240-2 (1-104) x US-10-289-980-6 (1-1182)

QY 15 ArgLysThrAlaTrpGlyGluArgAsnGlyGlnLysArgSerArgArgGlyThrArg 34
   ||| ::: ||||| : : : : : ||||| ||||| ||||| |||||

```

```

; GENERAL INFORMATION:
; APPLICANT: Anders, Cecilia
; APPLICANT: Barton, Barry
; APPLICANT: Griffin, John Patrick
; APPLICANT: Jensen, Susan
; APPLICANT: Mosher, Roy Henry
; APPLICANT: Paradkar, Ashish Sudhakar
; TITLE OF INVENTION: Novel Compounds
; FILE REFERENCE: P31731D2C2
; CURRENT APPLICATION NUMBER: US/10/289,980
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 10/214,519
; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 09/350,976
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/018,806
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: GB 9702218.0
; PRIOR FILING DATE: 1997-02-04
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 7193
; TYPE: DNA
; ORGANISM: Streptomyces clavuligerus
US-10-289-980-1

Alignment Scores:
Pred. No.: 2.6e+03 Length: 7193
Score: 89.50 Matches: 26
Percent Similarity: 49.21% Conservative: 5
Best Local Similarity: 41.27% Mismatches: 15
Query Match: 15.70% Indels: 17
DB: 6 Gaps: 4

US-09-750-240-2 (1-104) x US-10-289-980-1 (1-7193)
QY 15 ArgLysThrAlaTrpGlyGluArgAsnGlyGlnLysArgSerArgArgGlyThrArg 34
||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
Db 5274 CGGTGAAGCCATGGGGCGAACCAGTCTCGAAGATGAAGCGCGCGCGGACGCC 5333

QY 35 AlaGlyGlyPheCysThrProArgTyrMetSerCysLeuArgAspAlaGluProSer 54
::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
Db 5334 AGTGGTGGG-----CCTGCG---CGGAGTCCCGGAGACGAGCGTCTTCATCA 5381

QY 55 ProThrProAla-----GlyProPro----- 61
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5382 CCGCGACCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCCTCCCGGT 5441

QY 62 ArgCysPro 64
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5442 AGATGTCCA 5450

RESULT 14
PCT-US03-01858-47/c
; Sequence 47, Application PC/TUS0301858
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: RRP SEQUENCES AND KNOCKOUT MICE AND USES THEREOF
; FILE REFERENCE: EX02-004C-PC
; CURRENT APPLICATION NUMBER: PCT/US03/01858
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 10/056,790
; PRIOR FILING DATE: 2002-01-23
; PRIOR APPLICATION NUMBER: US 09/908,419
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/219,289
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US 60/277,487
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/304,863
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 60/277,471

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; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US60/305,017
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/328,491
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47
; LENGTH: 34319
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (34274)..(34275)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (34285)..(34285)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (34297)..(34298)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (34301)..(34301)
; OTHER INFORMATION: n is a, c, g, or t
PCT-US03-01858-47

Alignment Scores:
Pred. No.: 1.63e+04 Length: 34319
Score: 89.00 Matches: 35
Percent Similarity: 42.73% Conservative: 12
Best Local Similarity: 31.82% Mismatches: 38
Query Match: 15.61% Indels: 25
DB: 1 Gaps: 5

US-09-750-240-2 (1-104) x PCT-US03-01858-47 (1-34319)
QY 11 LysValAspGluArgLys-ThrAlaTrpGlyGluArgAsnGlyGlnLysArgSerArgAr 30
||| ||| ||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
Db 5343 AAACCGATGAAGCCAGACCTTCTTGGGTGCGGAGTCTCAGACCAAGGTCGTCAG 5284

QY 30 gArgGlyThrArgAlaGlyPheCysThrProArgTyrMetSerCysLeuArgAsp-- 49
| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5283 GGAGGGGGTGGGAGCGGC---TGC-----CTGGGCTTCTGCGAGCATG 5239

QY 50 AlaGluProProSerProThrProAlaGly-----ProProArgCys----- 63
||||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
Db 5238 GTCCCTCCCCCGAACCCTCACCGGTGGAAGGCGCCAGGAGTCCAGTCCCAACC 5179

QY 64 -----ProTrpGlnAspAlaPheIleArgArgGlyGlyPro 76
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5178 ACCACGACCTGCTCTGATGATGAGTCGACGACGAGTCTCTCCATAGACCGGCGC 5119

QY 77 ***LysGlyLysGluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluVal 96
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5118 AGGGCGGGTGGCGCGAGCGGGAGGGGCTGCTGCGGA-----CCGCTC 5071

QY 97 ThrThrThrProAlaGlyProLeu 104
::| ::| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5070 CGCTCGCGCGCGCGCGCGCGCGCTC 5047

RESULT 15
US-09-724-676-9445
; Sequence 9445, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing

```



GenCore version 5.1.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 1, 2003, 07:59:04 ; Search time 1708 seconds  
(without alignments)  
986.142 Million cell updates/sec

Title: US-09-750-240-2

Perfect score: 570

Sequence: 1 MSWFGSLLPVKVDKRTAWG.....RAVALGFEDTEVTTPAGPL 104

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+p2n.model -DEV=xlh  
-Q/cgn2\_1/USPTO.spool/US09750240/runat\_25022003\_103941\_24976/app\_query.fasta\_1.263  
-DB-EST -Qfmt=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS-bits -START=1 -END=-1 -MATRIX=blosom62 -TRANS-human4.0.cdi -LIST=45  
-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09750240@cgn\_1.1.899.0runat\_25022003\_103941\_24976 -NCPU=6 -ICPU=3  
-NO\_XLPXY -NO\_MAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST.\*  
1: em\_estha.\*  
2: em\_esthum.\*  
3: em\_estin.\*  
4: em\_estnu.\*  
5: em\_estov.\*  
6: em\_estpl.\*  
7: em\_estro.\*  
8: em\_hct.\*  
9: gb\_estl.\*  
10: gb\_est2.\*  
11: gb\_hct.\*  
12: gb\_est3.\*  
13: gb\_est4.\*  
14: gb\_est5.\*  
15: em\_estfun.\*  
16: em\_estom.\*  
17: gb\_gss.\*  
18: em\_gss\_hum.\*  
19: em\_gss\_inv.\*  
20: em\_gss\_pln.\*  
21: em\_gss\_vrt.\*  
22: em\_gss\_fun.\*  
23: em\_gss\_nam.\*  
24: em\_gss\_mus.\*  
25: em\_gss\_other.\*  
26: em\_gss\_pro.\*  
27: em\_gss\_rod.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	432	75.8	618	10	B8866520	B8866520 B8866520
2	354	62.1	631	10	B8866451	B8866451 B8866451
3	200.5	35.2	1011	17	CNS02STX	AL212334 Tetraodon
4	127.5	22.4	941	13	BG916212	BG916212 602814927
5	112	19.6	430	10	AW045174	UI-M-BH1-
6	107.5	18.9	697	14	BQ803437	WHE2837_F
7	101.5	17.8	1259	17	AG065197	AG065197 Pan trogl
8	100	17.5	897	12	BG756761	BG756761 602710232
9	99.5	17.5	278	12	BG558370	RH122_66_
10	99.5	17.5	842	12	BF696034	BF696034 601852020
11	99.5	17.5	1048	14	B0716276	B0716276 AGENCOURT
12	97.5	17.1	255	14	BM942641	BM942641 UI-M-CGOp
13	97.5	17.1	272	12	BE981360	BE981360 UI-M-CGOp
14	97.5	17.1	645	12	BE900861	BE900861 601673832
15	96	16.8	366	17	BH625429	BH625429 1007107C0
16	96	16.8	611	10	AV691613	AV691613
17	95.5	16.8	466	13	BJ255561	BJ255561 RJ255561
18	95	16.7	884	17	CNS0283Q	AL185471 Tetraodon
19	94.5	16.6	1044	12	BF585283	BF585283 602101946
20	94.5	16.6	1067	17	AG071547	AG071547 Pan trogl
21	94	16.5	421	17	BH750109	BH750109 SALK_0347
22	93.5	16.4	410	9	AI861296	AI861296 603018F11
23	93.5	16.4	544	13	BI676675	BI676675 1c52b05_x
24	93.5	16.4	559	11	AV107600	AV107600 Zea mays
25	93	16.3	385	10	BE400834	BE400834 AWO008.20
26	93	16.3	514	13	BT431052	BT431052 949064G10
27	93	16.3	514	14	BM706190	BM706190 UI-E-DW0-
28	93	16.3	871	17	AG127460	AG127460 Pan trogl
29	92.5	16.2	301	12	BF924657	BF924657 IL5-NT022
30	92.5	16.2	310	12	BG014040	BG014040 IL5-GN024
31	92.5	16.2	408	12	BG103906	BG103906 RH122_38
32	92.5	16.2	411	12	BG463088	BG463088 EM1_47_D0
33	92.5	16.2	599	12	BF483618	BF483618 WHE2335_H
34	92.5	16.2	615	14	BQ838166	BQ838166 WHE2907_C
35	92.5	16.2	707	9	AL820291	AL820291 AL820291
36	92.5	16.2	891	17	CNS03511	AL228142 Tetraodon
37	92.5	16.2	1033	13	BI152351	BI152351 602917520
38	92.5	16.2	1074	14	BM801345	BM801345 AGENCOURT
39	92	16.1	371	17	BH746357	BH746357 SALK_0400
40	92	16.1	517	14	BQ620765	BQ620765 TaLr1110D
41	92	16.1	574	12	BG649549	BG649549 EM1_80_G0
42	92	16.1	1070	14	BQ226091	BQ226091 AGENCOURT
43	92	16.1	1265	14	BQ922300	BQ922300 AGENCOURT
44	91.5	16.1	368	9	AU173954	AU173954 AU173954
45	91.5	16.1	521	10	BE287548	BE287548 601093167

# ALIGNMENTS

RESULT 1  
BB866520  
LOCUS BB866520 618 bp mRNA linear EST 27-NOV-2001  
DEFINITION BB866520 RIKEN full-length enriched, colon RCB-0549 Cle-H3 CDNA Mus  
musculus cDNA clone G431005N18 5', mRNA sequence.  
ACCESSION BB866520  
VERSION BB866520.1 GI:17112730  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 618)  
AUTHORS Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,  
Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii

Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al. 2001)

# TITLE JOURNAL COMMENT

Unpublished (2001)  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
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1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gsc.riken.go.jp,  
URL: http://genome.gsc.riken.go.jp/  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
wagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.  
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.  
e mouse tissues.  
Location/Qualifiers  
1. .618  
/db\_xref="taxon:10090"  
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## FEATURES source

BASE COUNT 105 a 189 c 196 g 127 t 1 others  
ORIGIN  
Alignment Scores:  
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Score: 432.00 Matches: 81  
Percent Similarity: 85.29% Conservative: 6  
Best Local Similarity: 79.41% Mismatches: 13  
Query Match: 75.79% Indels: 2  
DB: 10 Gaps: 2

US-09-750-240-2 (1-104) x BB866520 (1-618)

Qy 1 MetSerTrpPheSerGlyLeuValProLysValAspGluArgLysThrAlaTrpGly 20  
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Db 37 ATGTGTCATGTTAGTGGGCTCTCTGTTCCAAAGTGGATGAACGGAAACACGCTTGGGGG 96  
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Qy 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40  
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Db 97 GAACCAATGGCAGACGGCCCA---GCCACAGCAATCGAGCCAGTGGCTCTGCGCA 153  
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Qy 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60  
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Qy 61 ProArgCysProTrpGlnAspAlaPheIleArgArgGlyGlyPro\*\*\*LysGlyLys 80  
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Qy 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100  
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Qy 101 AlaGly 102  
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Db 331 ATGGGC 336  
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## RESULT 2

BB866451

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2001)

Contact: Yoshihide Hayashizaki

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Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp,

URL: http://genome.gsc.riken.go.jp/

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh

M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,

Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura

S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and

Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara

Y. and Hayashizaki, Y.



Y. and Hayashizaki, Y.  
Computer-based methods for the mouse full-length cDNA  
encyclopedia: real-time sequence clustering for construction of a  
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
Please visit our web site (<http://genome.gsc.riken.go.jp>) for  
further details.  
e mouse tissues.

## FEATURES

source  
1. .631  
Location/Qualifiers  
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Cle-H3 cDNA"  
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(cell\_type=Nullipotent stem cell, cell\_line=RCB-2070 NE),  
(tissue\_type=bladder, cell\_line=RCB-0544 MBT-2),  
(tissue\_type=bone marrow, cell\_type=stroma cell,  
cell\_line=RCB-2028 SR-4987), (tissue\_type=colon,  
cell\_line=RCB-0549 Cle-H3), (tissue\_type=kidney,  
cell\_line=CCL-142 RAG), (tissue\_type=submandibular gland,  
cell\_line=RCB-1734 SCA-9 clone 15), (strain=BALB/C,  
cell\_type=B cells, cell\_line=RCB-1669 BCL1 Clone 13.20-3B3  
) , (strain=C3H, tissue\_type=brain, cell\_line=RCB-1443  
BC3H1)."   
BASE COUNT 90 a 217 c 174 g 150 t  
ORIGIN

## Alignment Scores:

Pred. No.: 2,26e-21 Length: 631  
Score: 354.00 Matches: 69  
Percent Similarity: 74.51% Conservatve: 7  
Best Local Similarity: 67.65% Mismatches: 24  
Query Match: 62.11% Indels: 2  
DB: 10 Gaps: 2  
US-09-750-240-2 (1-104) x BB866451 (1-631)

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QY 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40  
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Db 97 GAACCTTTGGCAGAGCGCCCA--CGCACGCTAATCGACGCTGCTCTCGCG 153  
QY 41 ProArgTyrMetSerCysLeuArgAspAlaGluProSerProThrProAlaGlyPro 60  
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Db 154 CCTGTGCTACTGAGCTGCTCCGACGTGGAGCCACCCAGCCCACTCTGCTGTAC 213  
QY 61 ProArgCysProTrpGlnAspAlaPheIleArgArgGlyGlyPro\*\*\*LysGlyLys 80  
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Db 214 ACTTGGTGCCTTGGCAGGATGAAGCCTTCATCAAGAGGCGCGCGGGGGTGTG 273  
QY 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100  
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Db 274 GATCTGGGCTGGCGCCAGTGGCCCTCGGGTTGACACACT---GTGGTGAGCACACCT 330  
QY 101 AlaGly 102  
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Db 331 ATCGGC 336

## RESULT 3

CNS02STX/c 1011 bp DNA linear GSS 15-MAY-2000  
LOCUS Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone  
DEFINITION

162F16 of library G from Tetraodon nigroviridis, genomic survey  
sequence.  
AL212334  
AL212334.1 GI:7871153  
GSS: genome survey sequence.  
Tetraodon nigroviridis.  
Tetraodon nigroviridis.  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
Tetraodontidae; Tetraodon.  
1 (bases 1 to 1011)  
Roest-Crollius H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,  
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,  
Saurin, W. and Weissenbach, J.  
Human gene number estimate provided by genome wide analysis using  
Tetraodon nigroviridis DNA sequence  
Unpublished  
2 (bases 1 to 1011)  
Roest-Crollius H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,  
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and  
Weissenbach, J.  
Characterization and repeat analysis of the compact genome of the  
freshwater pufferfish Tetraodon nigroviridis  
Unpublished  
3 (bases 1 to 1011)  
Genoscope.  
Direct Submission  
Submitted (12-APR-2000)  
This sequence is a single read and was generated as part of a large  
scale clone-end sequencing project of the Tetraodon nigroviridis  
genome. For more information, please take a look at  
<http://www.genoscope.cns.fr/Tetraodon>.

## FEATURES

source  
1. .1011  
Location/Qualifiers  
/organism="Tetraodon nigroviridis"  
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ORIGIN

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Score: 200.50 Matches: 46  
Percent Similarity: 61.54% Conservatve: 10  
Best Local Similarity: 50.55% Mismatches: 17  
Query Match: 35.18% Indels: 19  
DB: 17 Gaps: 4

US-09-750-240-2 (1-104) x' CNS02STX (1-1011)

QY 1 MetSerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGly 20  
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QY 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40  
|||||  
Db 223 GAGCGCAATGCAAGAAGCCCAACCGAAGGGAGGCTCG-----TCTCTCTGCAAC 173  
QY 41 ProArgTyrMetSerCysLeuArgAsp-----AlaGluProProSer-----Pro 55  
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Db 172 CCGCGTACATGAGTGCCTGCGGGACCCCGACGCCATGGAGCCCTCGGAGCGGCC 113  
QY 56 ThrProAlaGlyProProArgCysProTrpGlnAspAlaPheIleArgArgGly 75  
|||  
Db 112 CT-CCATCAGCACCCG-----CGGAGGGGTGGC 84  
QY 76 Pro\*\*\*LysGlyLysGluLeuGlyLeuArgAla 86  
|||  
Db 83 GGGGCGCTGGGGGGCGCGCAACTTCGGAGT 51

## RESULT 4

BG916212 941 bp mRNA linear EST 05-JUN-2001  
 LOCUS 602814927F1 NCI\_CGAP\_Mam4 Mus musculus cDNA clone IMAGE:4937095 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BG916212  
 VERSION BG916212.1 GI:14296688  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 941)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth  
 Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone Distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM10870 row: f column: 08  
 High quality sequence stop: 151.

## FEATURES

Source

Location/Qualifiers

1..941  
 /organism="Mus musculus"  
 /strain="NMRI"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:4937095"  
 /clone\_lib="NCI\_CGAP\_Mam4"  
 /tissue\_type="tumor, gross tissue"  
 /dev\_stage="5 months"  
 /lab\_host="DH10B"  
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site.1: SalI;  
 Site.2: NotI; Cloned unidirectionally. Primer: Oligo dr.  
 Library constructed by Life Technologies. Investigators  
 providing samples: Lothar Hennighausen/Priscilla Furth,  
 NIH Reference for transgenic model: Li et al., Cell Growth  
 and Differentiation 7, 3-11 (1996)."  
 206 a 234 c 311 g 189 t 1 others

BASE COUNT

ORIGIN

Alignment Scores:  
 Pred. No.: 0.143 Length: 941  
 Score: 127.50 Matches: 38  
 Percent Similarity: 57.14% Conservative: 6  
 Best Local Similarity: 49.35% Mismatches: 21  
 Query Match: 22.37% Indels: 13  
 DB: 13 Gaps: 4

US-09-750-240-2 (1-104) x BG916212 (1-941)

QY 1 MetSerTrpPheSerGlyLeuLeu-ValProLys-ValAspGluArgLysThrAlaTrpG 20  
 Db 12 ATGTCATGTTGAGAGGGCTCTGGAATCCCAACGTGATGAGCAACAGCTTGGG 71  
 QY 20 lyGluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCys- 39  
 Db 72 GGAAGCGCAATGGCAGAGCGCCCA---CGCCACCGCAATCGAGCCAGTGGTTCAT-G 127  
 QY 40 -----ThrProArgTyrMetSerCys-----LeuArgAspAlaGluProProS 54  
 Db 128 CAGCGACGCTGCTCATCATGAGTGTGCGTCAACAGAAATGTCGAGACACGACCGAGCA 187  
 QY 54 exProThrProAlaGly-----ProProArgCysProTrpGln 66  
 Db 188 CCACGACGTCCTGTCGACGCTGCACAAATCGGAGTGCCTATAGG 234

## RESULT 5

AW045174/c  
 LOCUS 430 bp mRNA linear EST 18-SEP-1999  
 DEFINITION UI-M-BH1-ahh-a-03-0-UI.s1 NIH\_BMAP\_M\_S2 Mus musculus cDNA clone  
 ACCESSION AW045174  
 VERSION AW045174.1 GI:5905703  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 430)  
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 TITLE Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 9704477  
 COMMENT Contact: Chin, H  
 National Institute of Mental Health  
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD  
 20892-9643, USA  
 Tel: 301 443 1706  
 Fax: 301 443 9890  
 Email: mEST@mail.nih.gov  
 Oligo-dr track not found, Not I site shown in beginning of sequence  
 is likely internal to the message. cDNA Library Preparation: M.B.  
 Soares Lab Clone distribution: NIH BMAP cDNA clones will be made  
 available by the means that is soon to be determined. When NIH  
 determines the means for distribution of the BMAP cDNA clones, this  
 record will be updated accordingly when that means is determined.  
 The following repetitive elements were found in this cDNA sequence:  
 94-126, >GC-richLow-complexity  
 Seg primer: M13 Forward  
 POLYA-No.

## FEATURES

source

Location/Qualifiers

1..430  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UI-M-BH1-ahh-a-03-0-UI"  
 /clone\_lib="NIH\_BMAP\_M\_S2"  
 /dev\_stage="27-32 days"  
 /lab\_host="DH10B (Life Technologies)"  
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
 polylinker; Site.1: Not I; Site.2: Eco RI; The  
 NIH\_BMAP\_M\_S2 library is a subtracted library derived from  
 NIH\_BMAP\_M\_S1, which in turn is a subtracted library  
 derived from a mixture of normalized libraries from ten  
 regions of the mouse brain (cerebellum, brain stems,  
 olfactory bulbs, hypothalamus, cortex, amygdala, basal  
 ganglia, pineal gland, striatum, hippocampus). The driver  
 used for subtraction consisted of a pool of 5,000 clones  
 obtained from non-normalized and a pool of 2,000 clones  
 obtained from NIH\_BMAP\_M\_S1 library and a pool of 2,000 clones  
 obtained from non-normalized and normalized mouse brain  
 spinal cord libraries.  
 TAG\_SEQ=None found"

BASE COUNT 76 a 130 c 152 g 72 t

ORIGIN

## Alignment Scores:

Pred. No.: 1.52 Length: 430  
 Score: 112.00 Matches: 34  
 Percent Similarity: 42.27% Conservative: 7  
 Best Local Similarity: 35.05% Mismatches: 38  
 Query Match: 19.65% Indels: 18  
 DB: 10 Gaps: 4

US-09-750-240-2 (1-104) x AW045174 (1-430)

QY 1 MetSerTrpPheSerGlyLeu-----LeuValProLysValAspGluArg 15  
 ::::::::::: |||||  
 Db 1 MetSerTrpPheSerGlyLeu-----LeuValProLysValAspGluArg 15  
 ::::::::::: |||||

```

Db 411 GTTCTTGGCGCTGATGCCCTCGCTGGGCACATGCATGGCAGCCACCGTGGGAAGCGA 352
Qy 16 LysThrAlaTrpGlyGluArgAsnGlyGlnLysArg-----SerArgArgGlyThr 33
Db 351 CTGGAGCGCTGGAGCGCTCCCTGTCACGATAGACACCAAGAGCGGTAGATATCG 292
Qy 34 ArgAlaGlyGlyPheCysThrProArgTyrMetSerCysLeuArgAspAlaGluProPro 53
Db 291 ACTCTGGGGCCCACTCTCGCAGACAAGGTACGTGACGGCACACATGCCACCCCTAGG 232
Qy 54 Ser-----ProThrProAlaGlyProProArgCysProTrpGlnAspAsp 68
Db 231 TCCCGCGCGCTCGGAGAACCAACGCGAGTGGGCGCCAGGTCTCCTCGGGTCCCTCCC 172
Qy 69 AlaPhe-----IleArgArgGlyGlyPro***LysGly 79
Db 171 GGCTTTCCCAACAGTTTGCACGCATCACAGCTCTCGGCCCGTGGCGGC 121

RESULT 6
BQ803437/c 697 bp mRNA linear EST 30-JUL-2002
LOCUS WHE2837_F07_K132S Triticum monococcum vernalized apex cDNA library
DEFINITION Triticum monococcum cDNA clone WHE2837_F07_K13, mRNA sequence.
ACCESSION BQ803437
VERSION BQ803437.1 GI:22018406
KEYWORDS EST.
SOURCE Triticum monococcum.
ORGANISM Triticum monococcum.

REFERENCE
AUTHORS Anderson,O.D., Chao,S., Crossman,C., Dubcovsky,J., Echenique,V.,
Lazo,G.R., Pham,J., Rausch,C.J., Stamova,B., Wilson,C. and Wood,J.
TITLE The structure and function of the expressed portion of the wheat
genomes - Vernalized apex cDNA library from Triticum monococcum
JOURNAL Unpublished (2002)
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 510595973
Fax: 5105959818
Email: oandersn@pw.usda.gov
Sequences have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: SK primer.

FEATURES
source
1. .697
/organism="Triticum monococcum"
/cultivar="G316"
/db_xref="taxon:4568"
/clone="WHE2837_F07_K13"
/clone_lib="Triticum monococcum vernalized apex cDNA
library"
/tissue_type="Vernalized apex"
/dev_stage="One month old plants"
/lab_host="E. coli XL0LR"
/notes="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; One-month old plants were
subjected to vernalization treatment by placing them in
the cold room at 6 C, under 15hr light/9hr dark condition.
Total RNA was prepared from apex tissue extracted from
plants with no cold treatment; and from plants with 2-week
, 4-week and 6-week cold treatment separately. Equal
amount of total RNA was pooled from all four samples, a
cDNA library was made using pooled polyA RNA and cDNA
clones were in vivo excised at the University of
California, Davis (V. Echenique, B. Stamova, J. Dubcovsky
). Plasmid DNA preparations and DNA sequencing were
performed in the OD Anderson lab (all other authors)."
109 a 258 c 217 g 113 t

```

```

Alignment Scores:
Pred. No.: 5.84 Length: 697
Score: 107.50 Matches: 40
Percent Similarity: 33.86% Conservative: 3
Best Local Similarity: 31.50% Mismatches: 43
Query Match: 18.86% Indels: 41
DB: 14 Gaps: 5

US-09-750-240-2 (1-104) x BQ803437 (1-697)
Qy 15 ArgLysThrAlaTrp-GlyGluArg-----AsnGlyGlnLysArgSerArgArgG1 32
Db 696 AGGGCGCGCTCTGGGGCGGTAGCGGGTGGTGAAGGCCACGCACGCCCGGG 637
Qy 32 YThrArgAlaGlyGlyPheCysThrProArgTyrMetSerCys----- 46
Db 636 CACTGCGTCTCCGGGT---TGCCGACCCAGATGTGGGTCTGTCGCGGAGCTCGGAG 580
Qy 47 -----LeuArgAspAlaGluProProSerProThrProAlaG1 59
Db 579 CCGTGCAGACTGCACCGGCCCATGCCGAGCCCTCCACCGCAGCTCCTGTGCGGTGAAG 520
Qy 59 YProProArg----- 62
Db 519 ACCACCGCGAGCGCGCTTTCTTGGGGCTAGCGCGCGGCGGTGATCTGCTCG 460
Qy 63 -----CysProTrpGlnAspAspAlaPheIleArgArgGlyPro***Ly 78
Db 459 AGGTGTAGAGACTTGGCCATGGAGCACTCGCCGT-----CGGAGAGCTGTGTCGCGAGC 406
Qy 78 sGly-LysGluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThr 98
Db 405 AGGACACGGTCTTCGCACCGCGCGCTTGGACTTGGCGTGGGGGAGAGGTACTGC 346
Qy 98 hrThrProAlaGlyPro 103
Db 345 TGGTCGATGTGCTCCA 329

RESULT 7
AG065197 1259 bp DNA linear GSS 03-NOV-2001
LOCUS Pan troglodytes DNA, clone: PTB-054I03.F, genomic survey sequence.
DEFINITION AG065197
ACCESSION AG065197
VERSION AG065197.1 GI:16616999
KEYWORDS GSS.
SOURCE Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-054I03.F.
ORGANISM Pan troglodytes
REFERENCE 1
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE BAC end sequences of Library PTB
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1259)
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chinpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY Vector : pKS145
R.Site 1 : SacI

```

```

FEATURES
  source
    R.Site 2 : SacI.
    Location/Qualifiers
      1..1259
        /organism="Pan troglodytes"
        /db_xref="taxon:9598"
        /clone="PTB-054I03.F"
        /sex="male"
        /cell_type="lymphoblast"
        /clone_lib="PTB Chimpanzee Male BAC Library"
BASE COUNT 173 a 474 c 564 g 26 t 22 others
ORIGIN
Alignment Scores:
Pred. No.: 33.6 Length: 1259
Score: 101.50 Matches: 31
Percent Similarity: 42.55% Conservatve: 9
Best Local Similarity: 32.98% Mismatches: 35
Query Match: 17.81% Indels: 19
DB: 17 Gaps: 3
US-09-750-240-2 (1-104) x AG065197 (1-1259)
QY 5 SerGlyLeuValProLysValAspGluArgLys----- 16
Db 684 AGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGGAATGGACGGGACGCGGG 743
QY 17 -----ThrAlaTrpGlyGluArgAsnGlyGlnLysArgSerArgArgGly 32
Db 744 CGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGAGAGAGCGCGCGCGCGCGCGCG 803
QY 33 ThrArgAlaGlyGlyPheCysThrProArgTyrMetSerCysLeuArgAsp-AlaGluPr 52
Db 804 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 863
QY 52 o-----ProSerProThrProAlaGlyProProArgCys-ProTrpGlnAspAspA 69
Db 864 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 923
QY 69 laPheIleArgArgGlyGlyPro**LysGlyLysGlu 81
Db 924 GT-----CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCAAGAG 955
RESULT 8
BG756761/c 897 bp mRNA linear EST 15-MAY-2001
LOCUS 602710232F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4850910 5',
DEFINITION mRNA sequence.
ACCESSION BG756761
VERSION BG756761.1 GI:14067414
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI692 row: o column: 07
High quality sequence stop: 811.
Location/Qualifiers
1..897
/organism="Homo sapiens"
/db_xref="taxon:9606"
FEATURES
  source
    /clone="IMAGE:4850910"
    /clone_lib="NIH_MGC_48"
    /tissue_type="primary B-cells from tonsils (cell line)"
    /lab_host="DH10B (phage-resistant)"
    /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
    Site_2: EcoRI; cDNA made by oligo-dT priming.
    Directionally cloned into EcoRI/XhoI sites using the
    following 5' adaptor: GGCACGAG(G). Size-selected >500bp
    for average insert size 1.8kb. Library constructed by Ling
    Hong in the laboratory of Gerald M. Rubin (University of
    California, Berkeley) using ZAP-cDNA synthesis kit
    (Stratagene) and Superscript II RT (Life Technologies).
    Note: this is a NIH_MGC library."
BASE COUNT 192 a 255 c 248 g 201 t
ORIGIN
Alignment Scores:
Pred. No.: 33.1 Length: 897
Score: 100.00 Matches: 32
Percent Similarity: 44.33% Conservatve: 11
Best Local Similarity: 32.99% Mismatches: 40
Query Match: 17.54% Indels: 14
DB: 12 Gaps: 5
US-09-750-240-2 (1-104) x BG756761 (1-897)
QY 6 GlyLeuValProLys---ValAspGluArgLysThrAlaTrpGlyGluArgAsnGly 24
Db 811 GGTCTGCTCAGCCCAAGAGGATTCAAAAGATCAAAACAGATTGGGAACCCAGACCCGT 752
QY 25 GlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThrProArgTyrMet 44
Db 751 CAAGGATGGAGAGAGAGAGAAATCCAGGGTGTGGGGTCTCTGT-----TTGCAA 701
QY 45 SerCysLeuArgAspAlaGluProProSerProThrProAlaGlyProProArgCysPro 64
Db 700 CTGGGTTGAAGGATTCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCG 647
QY 65 TrpGlnAspAspAlaPheIleArg-----ArgGlyGly-----Pro 76
Db 646 TGGCAGGAAGGGGGGCGAGCTGCAACCCCAAGGGAGGTGTGGGNTGCCAGATGCTCCA 587
QY 77 ***LysGlyLysGluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAsp 93
Db 586 GCAGGGGGCCAGAGGGGCTCAGAAAGGCTTGCCTCCAGGGAGATGAC 536
RESULT 9
BG558370/c 278 bp mRNA linear EST 10-APR-2001
LOCUS RHIZ2_66_E02.bl_A003 Rhizome2 (RHIZ2) Sorghum propinquum CDNA, mRNA
DEFINITION sequence.
ACCESSION BG558370
VERSION BG558370.1 GI:13587368
KEYWORDS EST.
SOURCE Sorghum propinquum.
ORGANISM Sorghum propinquum
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
TITLE clade; Panicoidae; Andropogoneae; Sorghum.
JOURNAL Cordonnier-Pratt,M.-M., Gingle,A., Paterson,A., Sudman,M. and Pratt
COMMENT An EST database from Sorghum: Sorghum propinquum rhizomes
Unpublished (2000)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Seq primer: JEN REV
High quality sequence start: 4

```





6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD  
20892-9643, USA  
Tel: 301 443 1706  
Fax: 301 443 9890  
Email: nest@mail.nih.gov

Oligo-dt track not found, Not I site shown in beginning of sequence  
is likely internal to the message. cDNA library preparation: M.B.  
Soares Lab Clone distribution: Researchers may obtain BMAP cDNA  
clones from RESEARCH GENETICS. It should be noted that Bento Soares  
is generating a small number of additional specialized  
non-redundant arrays of BMAP cDNAs whose availability will be  
considered under appropriate and limited collaborative arrangements  
The tissue for this library was contributed by Dr. Xin-Yuan Fu,  
Yale University School of Medicine The following repetitive  
elements were found in this cDNA sequence: 1-62,  
>GC-rich#Low complexity  
Seq primer: M13 Forward

POLYA-No. Location/Qualifiers  
1. .272  
source

/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UI-M-CG0p-bdb-c-10-0-UI"  
/clone\_lib="NIH\_BMAP\_Ret4\_S2"  
/lab\_host="DH10B (Life Technologies)"  
/notes="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; Site\_1: Not I; Site\_2: Eco RI; The  
NIH\_BMAP\_Ret4\_S2 library is a substracted library,  
ultimately derived from mouse retina tissue libraries at  
various stages of development. For a detailed description  
of the library from which this clone was derived, please  
visit our web site at brainest.eng.uiowa.edu. The tissue  
for this library was contributed by Dr. Xin-Yuan Fu, Yale  
University School of Medicine  
TAG\_SEQ=None found"

BASE COUNT 45 a 100 c 81 g 46 t  
ORIGIN

Alignment Scores:  
Pred. No.: 17 9 Length: 272  
Score: 97.50 Matches: 24  
Percent Similarity: 38.24% Conservative: 2  
Best Local Similarity: 35.29% Mismatches: 19  
Query Match: 17.11% Indels: 23  
DB: 12 Gaps: 1

US-09-750-240-2 (1-104) x BE981360 (1-272)

QY 20 GlyGluArgAsnGlyGlnLysArgSerArgArgGlyThr----- 33  
||| ||| ||||| ||| ||||| |||||  
Db 47 GGGCGGGCGCGGCGAGTGCAGACAAAGGAGGCTCGGAACATGCTCTACATCTGGC 106  
QY 34 -----ArgAlaGly 36  
||| ||||| ||||| ||||| ||||| |||||  
Db 107 TGGCCTCTCATTCGCCGTCGACCTTGAAGAGCGCTTGAACCTGTCGATGAAGAGCGTCC 166  
QY 37 GlyPheCysThrProArgTyrMetSerCysLeuArgAspAlaGluProSerProThr 56  
::: ||||| ||||| ||||| ||||| ||||| |||||  
Db 167 CACTGGGACACTCCACGACAACTCTTTGACCACCTCCTGCAACTCCGCGACATCCATCT 226  
QY 57 ProAlaGlyProProArgCysPro 64  
||| ||||| ||||| ||||| ||||| |||||  
Db 227 CCCGGCGCGCTCGGCTCTCTCC 250

RESULT 14  
BE900861  
LOCUS 601673832F1 NIH\_MGC\_21 Homo sapiens cDNA clone IMAGE:3956958 5',  
DEFINITION mRNA sequence.  
ACCESSION BE900861  
VERSION BE900861.1 GI:10389459  
KEYWORDS EST.

SOURCE  
ORGANISM

human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 645)  
NIH-MGC http://mhc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
Plate: LLC833 row: o column: 07  
High quality sequence stop: 584.

FEATURES  
Location/Qualifiers  
1. .645  
source

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3956958"  
/clone\_lib="NIH\_MGC\_21"  
/tissue\_type="choriocarcinoma"  
/lab\_host="DH10B (phage-resistant)"  
/notes="Organ: placenta; Vector: pOTB7; Site\_1: XhoI;  
Site\_2: EcoRI; cDNA made by oligo-dt priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCACGAG(G). Size-selected >500bp  
for average insert size 1.8kb. Library constructed by  
Ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 142 a 153 c 207 g 143 t  
ORIGIN

Alignment Scores:  
Pred. No.: 40 Length: 645  
Score: 97.50 Matches: 33  
Percent Similarity: 43.00% Conservative: 10  
Best Local Similarity: 33.00% Mismatches: 42  
Query Match: 17.11% Indels: 15  
DB: 12 Gaps: 5

US-09-750-240-2 (1-104) x BE900861 (1-645)

QY 2 SerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGlyGlu 21  
::||| ||| ::::: ||||| |||||  
Db 142 GCATGGGTAGTGTCTATGTTGGGAGAGTACATTGAAGGCTGGAATTAGCTTGGGGCAG 201  
QY 22 Arg-----AsnGlyGlnLysArgSerArg-----ArgArgGly 32  
|||:::||||| ||| ||||| |||||  
Db 202 GAAGGGACTGGGAGGGGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 261  
QY 33 ThrArgAlaGlyGlyPheCysThrProArgTyrMetSerCysLeuArgAspAlaGluPro 52  
||| ||||| ||||| ||||| |||||  
Db 262 ACAGAGACCTCCCTGTTCAAGGCCCTGACAGCTGTCCTCCGTC-----CCTTCTCC 312  
QY 53 ProSerProThrProAlaGlyProProArgCysProTrpGlnAspAspAlaPheIleArg 72  
||| ||||| ||||| ||||| ||||| |||||  
Db 313 CCTTCCCTGACTCAGGGGTTATGTGGAAGTGTGTGGCAGCAGGAGCG-----GGG 366  
QY 73 ArgGlyGlyPro\*\*\*LysGlyLysGluLeuGlyLeuArgAlaValAlaLeuGlyPheGlu 92  
||| ||||| ||||| ||||| ||||| |||||  
Db 367 AGGGAGGAACAGGAAGGGG---GAGCTGGGAGCTTGGCTGAGGGTCTGGGAATGAG 423  
RESULT 15  
BH625429/c 366 bp DNA linear GSS 30-JAN-2002  
LOCUS BH625429  
DEFINITION .1007107C09.x1 1007 - RescueMu Grid H Zea mays genomic, DNA  
sequence.  
ACCESSION BH625429

Search completed: March 1, 2003, 11:35:39  
Job time : 1713 secs

1  
2  
3  
4



GenCore version 5.1.3 Copyright (c) 1993 - 2003 CompuGen Ltd.	
OM nucleic - nucleic search, using sw model	
Run on:	February 28, 2003, 19:58:51 ; Search time 259.906 Seconds (without alignments) 15700.357 Million cell updates/sec
Title:	US-09-750-240-3
Perfect score:	1812
Sequence:	1 gtttaacgtgtgtctggcat.....gcagcttctcgtggttc 1812
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched:	2185239 seqs, 112599159 residues
Total number of hits satisfying chosen parameters:	4370478
Minimum DB seq length:	0
Maximum DB seq length:	2000000000
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database :	N_Geneseq_101002.* 1: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.* 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.* 3: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.* 4: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.* 5: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.* 6: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.* 7: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.* 8: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.* 9: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.* 10: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.* 11: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.* 12: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.* 13: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.* 14: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.* 15: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.* 16: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.* 17: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.* 18: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.* 19: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.* 20: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.* 21: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.* 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.* 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.* 24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	
SUMMARIES	
Result No.	Score Match Length DB ID Description
1	1812 100.0 1812 22 AAD08562 Human partial card
2	1812 100.0 2127 19 AAV23246 Human adenylycycl
3	1808.4 99.8 3549 22 AAD08563 Human cardiac aden
4	1763.4 97.3 3552 22 AAD08567 Human cardiac aden
5	1763 97.3 4942 20 AAX00461 Human type VI aden
6	1657.8 91.5 3582 22 AAD08568 Human modified car
7	1657.8 84.3 4046 14 AAQ42525 Cardiac adenylyl c
8	1437.2 79.3 4131 21 AAA53923 Type VI adenylyl c
9	1431.8 79.0 5841 24 ABI99680 Mouse ischaemic co

Human type V adeny  
Cardiac adenylyl c  
Cardiac adenylyl c  
Type V adenylyl cy  
Human adenylyl and  
Drosophila melanog  
Adenylyl cyclase t  
Human adenylyl and  
Adenylyl cyclase c  
Drosophila melanog  
Human cDNA sequenc  
Human secreted pro  
Type III adenylyl  
Type VIII adenylyl  
Human pancreatic c  
Type VII adenylyl  
Human adenylyl cy  
Human NS cDNA sequ  
Rat adenylyl cycla  
Adenylyl cyclase t  
Human adenylyl cy  
Human adenylyl cy  
Human polynucleoti  
Drosophila melanog  
Type IV adenylyl c  
Human adenylyl and  
Drosophila melanog  
Human adenylyl cy  
Drosophila melanog  
Human secreted pro  
Murine adenylyl c  
Human type IX aden  
Human nervous syst  
Drosophila melanog  
Human prostate exp

ALIGNMENTS

RESULT 1  
AAD08562  
ID AAD08562 standard; cDNA; 1812 BP.  
XX AC AAD08562;  
XX DT 04-SEP-2001 (first entry)  
XX DE Human partial cardiac adenylylase VI (ACVI) isoform #2 cDNA.  
XX KW Human; cardiant; beta-adrenergic signalling protein; beta-ASP;  
KW myocardiium; gene therapy; beta-adrenergic receptor; beta-AR;  
KW adenylylase; adenylylase; adenylylase; adenylylase;  
KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;  
KW cardiac adenylylase VI; ACVI isoform; beta-ASP transgene; ss.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
XX CDS 1..1812  
XX FT /\*tag= a  
XX FT /product= "Human partial cardiac ACVI isoform #2"  
XX FT /note= "CDS does not include start and stop codon"  
XX FT /EC\_number= "4.6.1.1"  
XX WO200148164-A2.  
XX PN 05-JUL-2001.  
XX PD 26-DEC-2000; 2000WO-US35411.  
XX PF 27-DEC-1999; 99US-0472667.  
XX PR



QY 1681 GCAGCCGGAGCTGAATTTAAACACCTGCTGACATCACTGCTGCCACCTGCAGCAGCTC 1740  
Db 1681 GCAGCCGGAGCTGAATTTAAACACCTGCTGACATCACTGCTGCCACCTGCAGCAGCTC 1740  
QY 1741 AATTACTCTCTGGGCGCTGGAGTCTCCCTCTGTGTGAGGCGACCATGCCACCTGCAGCTTT 1800  
Db 1741 AATTACTCTCTGGGCGCTGGAGTCTCCCTCTGTGTGAGGCGACCATGCCACCTGCAGCTTT 1800  
QY 1801 CCTGAGGTGTTTC 1812  
Db 1801 CCTGAGGTGTTTC 1812

RESULT 2  
AAV23246  
ID AAV23246 standard; cDNA; 2127 BP.  
AC AAV23246;  
XX  
DT 17-JUL-1998 (first entry)  
XX  
DE Human adenylylase isoform VI encoding cDNA.  
XX  
KW Human; adenylylase VI; AC-VI; beta-adrenergic signalling protein;  
KW transgene; gene therapy; congestive heart failure; cardiac function;  
KW adenylylase; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key  
FT CDS  
FT Location/Qualifiers  
FT 1..2127  
FT /product= "adenylylase isoform VI"  
FT /trans\_except= (pos:229..231,aa:Xaa)  
FT /trans\_except= (pos:315..317,aa:Xaa)  
FT /note= "no stop codon given; Xaa = unknown"  
FT misc\_difference 315  
FT /tag= b  
FT /note= "n indicates a gap of about 0.5 kb"  
XX  
XX W09810085-A2.  
XX 12-MAR-1998.  
XX  
XX 05-SEP-1997; 97WO-US15610.  
XX  
XX 16-JUN-1997; 97US-0048933.  
XX 05-SEP-1996; 96US-0708661.  
XX  
XX (COLL-) COLLATERAL THERAPEUTICS.  
XX (REGC) UNIV CALIFORNIA.  
XX  
XX Gao M, Hammond HK, Insel PA, Ping P, Post SR;  
XX  
XX WPI; 1998-193633/17.  
XX P-PSDB; AAW53345.  
XX  
XX Vectors containing transgene(s) encoding beta-adrenergic signalling  
XX proteins - useful for gene therapy of congestive heart failure  
XX  
XX Claim 60; Fig 12A; 114pp; English.  
XX  
XX The present sequence encodes human adenylylase isoform VI (AC-VI)  
XX from the present invention. The present invention describes a  
XX recombinant, replication-defective viral particle (I) comprising a gene  
XX encoding a beta-adrenergic signalling protein (beta-ASP) operably  
XX linked to a promoter. Also described are: (1) a recombinant pro-viral  
XX plasmid (Ia) comprising a gene encoding a beta-ASP, as above, operably  
XX linked to a promoter and further comprising a replication-defective  
XX viral genome; (2) a (mammalian) cell transfected with (1) or (Ia); (3)  
XX an isolated polynucleotide comprising a sequence encoding a human  
XX adenylylase isoform VI (AC-VI), or a variant having AC activity;  
XX (4) a human AC-VI encoded by (3); (5) an isolated polynucleotide

CC sequence which hybridises at high stringency to (3); and (6) a vector  
CC comprising the polynucleotide of (3). (1) can be used to form a  
CC filtered adenovirus particle preparation. (1) is used to enhance  
CC cardiac function in mammals.  
XX  
SQ Sequence 2127 BP; 421 A; 637 C; 615 G; 452 T; 2 other;  
Query Match 100.0%; Score 1812; DB 19; Length 2127;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTTAACGTGGTCTGGGCGCATCTGGCGCAGTGCAGAGTGGGGCGCTTTTCGACGACAG 60  
Db 316 GTTAACGTGGTCTGGGCGCATCTGGCGCAGTGCAGAGTGGGGCGCTTTTCGACGACAG 375  
QY 61 CCGCGCAGCCCTCTGGGGCGCTCTGGTGCCTGTGTCTTTGTATATACATGACATACAG 120  
Db 376 CCGCGCAGCCCTCTGGGGCGCTCTGGTGCCTGTGTCTTTGTATATACATGACATACAG 435  
QY 121 CTCCTCCCATCCGCATCGGGCTGCCGTCTCAGCGGCTTCCACCTTGCAT 180  
Db 436 CTCCTCCCATCCGCATCGGGCTGCCGTCTCAGCGGCTTCCACCTTGCAT 495  
QY 181 TTGATCTTGGCTGGCAACTTAAACCGTGGTGTATGCTTCTCTGGAAGCAGCTCGGTGCC 240  
Db 496 TTGATCTTGGCTGGCAACTTAAACCGTGGTGTATGCTTCTCTGGAAGCAGCTCGGTGCC 555  
QY 241 AATGTGCTGCTGTCTCTGCACCAACGTCAATAGCATCTGCACACATATCCACGACAG 300  
Db 556 AATGTGCTGCTGTCTCTGCACCAACGTCAATAGCATCTGCACACATATCCACGACAG 615  
QY 301 GTGTCTCAGCGCCAGGCTTTTCAGGAGACCCGACGTATACATCCAGGCGGCTCCACCTG 360  
Db 616 GTGTCTCAGCGCCAGGCTTTTCAGGAGACCCGACGTATACATCCAGGCGGCTCCACCTG 675  
QY 361 CAGCATGAGAATCGCGCAGCAGCGGCTGTGTCTCGGTATGCCCGCAGCAGCTTGC 420  
Db 676 CAGCATGAGAATCGCGCAGCAGCGGCTGTGTCTCGGTATGCCCGCAGCAGCTTGC 735  
QY 421 ATGGAGATGAAGAAGACATCAACACAAAAAAGAACATGTTCCCAAGATCTACATA 480  
Db 736 ATGGAGATGAAGAAGACATCAACACAAAAAAGAACATGTTCCCAAGATCTACATA 795  
QY 481 CAGAAGCATGACAATGTGAGCATCTGTTTCAGACATTTAGGGCTTCCACGACCTGGCA 540  
Db 796 CAGAAGCATGACAATGTGAGCATCTGTTTCAGACATTTAGGGCTTCCACGACCTGGCA 855  
QY 541 TCCAGTGCATCGCGCAGGAGTGGTCAATGACCTTGAATGAGCTCTTTGCCGGTTTGC 600  
Db 856 TCCAGTGCATCGCGCAGGAGTGGTCAATGACCTTGAATGAGCTCTTTGCCGGTTTGC 915  
QY 601 AAGCTGGCTGGGAGAAATCACTGCTGAGATCAAGATCTTGGGGGACTGTTACTACTGT 660  
Db 916 AAGCTGGCTGGGAGAAATCACTGCTGAGATCAAGATCTTGGGGGACTGTTACTACTGT 975  
QY 661 GTGTGAGGCTGCCGAGGCGCCGCCACCATGCCCCACTGTGTGTGAGATGGGGTA 720  
Db 976 GTGTGAGGCTGCCGAGGCGCCGCCACCATGCCCCACTGTGTGTGAGATGGGGTA 1035  
QY 721 GACATGATGAGGCCATCTCGCTGTGATGAGGTGACAGGTGTGAATGTGAACATGGCG 780  
Db 1036 GACATGATGAGGCCATCTCGCTGTGATGAGGTGACAGGTGTGAATGTGAACATGGCG 1095  
QY 781 GTGGCATCCACAGGCGGCTGCACATGCGGCGCTTCTGGCTTCCGGAATGGCAGTTC 840  
Db 1096 GTGGCATCCACAGGCGGCTGCACATGCGGCGCTTCTGGCTTCCGGAATGGCAGTTC 1155  
QY 841 GATGTGTGCTCCAAATGATGTGACCTGGCCCAACACATGGAAGCAGGAGCCGGCTGGC 900  
Db 1156 GATGTGTGCTCCAAATGATGTGACCTGGCCCAACACATGGAAGCAGGAGCCGGCTGGC 1215  
QY 901 CGCATCCACATCACTCGGCGCAACACTCGAGTACCTTGAACGGGAGCTACGAATGGAGCCA 960  
|||||

Db	1216	CGATCCACATCACTCGGGCAACACTGCACTACCTTGACGGGGGACTACGAAGTGGAGCCA	1275
Qy	961	GGCCGTGGTGGCAAGCGCAACCGGTACCTCAAGAGCAGCACATTGAGACTTTCTCTCATC	1020
Db	1276	GGCCGTGGTGGCAAGCGCAACCGGTACCTCAAGAGCAGCACATTGAGACTTTCTCTCATC	1335
Qy	1021	CTGGGCCAGCCAGCAAAACGGAAAGAGGAGAAGGCATGCTTGGCCAAGCTGCACGGGACT	1080
Db	1336	CTGGGCCAGCCAGCAAAACGGAAAGAGGAGAAGGCATGCTTGGCCAAGCTGCACGGGACT	1395
Qy	1081	CGGGCCAACTCCATGGAAGGGCTGATGCCCGCATGGTTCCTGATCGTGCCCTTCTCCCGG	1140
Db	1396	CGGGCCAACTCCATGGAAGGGCTGATGCCCGCATGGTTCCTGATCGTGCCCTTCTCCCGG	1455
Qy	1141	ACCAAGACTTCAAGGCCTTCCGCAGATGGGCATTGATGATCCAGCAAAAGACAACCGG	1200
Db	1456	ACCAAGACTTCAAGGCCTTCCGCAGATGGGCATTGATGATCCAGCAAAAGACAACCGG	1515
Qy	1201	GGCAACCACAGATGCCCTGAACCTCAGGATGAGGTGGATGAGTTCCTGAGCCGTGGCCATC	1260
Db	1516	GGCAACCACAGATGCCCTGAACCTCAGGATGAGGTGGATGAGTTCCTGAGCCGTGGCCATC	1575
Qy	1261	GATGCCCGCAGCATTGATCAGCTGCGGAAGCACCATGTGCGCCGCTTTTGTCAACCTTC	1320
Db	1576	GATGCCCGCAGCATTGATCAGCTGCGGAAGCACCATGTGCGCCGCTTTTGTCAACCTTC	1635
Qy	1321	CAGAGAGAGATTTTCAGAAAGATACCTCCCGAAGGTGGATCCCGCTTCGGAGCCCTAC	1380
Db	1636	CAGAGAGAGATTTTCAGAAAGATACCTCCCGAAGGTGGATCCCGCTTCGGAGCCCTAC	1695
Qy	1381	GTTCGCTGTGCCCTGTGTGCTTCTGCTTCATCTGCTTCATCCAGCTTCTAAATTTCCCA	1440
Db	1696	GTTCGCTGTGCCCTGTGTGCTTCTGCTTCATCTGCTTCATCCAGCTTCTAAATTTCCCA	1755
Qy	1441	CACCTCACCTCGATGCTTGGGATTTATGCCAGCATCTTCCTGCTGCTGCTTAATCACCGTG	1500
Db	1756	CACCTCACCTCGATGCTTGGGATTTATGCCAGCATCTTCCTGCTGCTGCTTAATCACCGTG	1815
Qy	1501	CTGATCTGTGCTGTGTACTCTGTGGTTCCTGTGTTCCCTAAGGCCCTGCAACGTCCTGCC	1560
Db	1816	CTGATCTGTGCTGTGTACTCTGTGGTTCCTGTGTTCCCTAAGGCCCTGCAACGTCCTGCC	1875
Qy	1561	CGACGATTTGTCGCTCAGGGGCACATAGCACCGCAGTTGGCATCTTTTCGGTCCCTGCTT	1620
Db	1876	CGACGATTTGTCGCTCAGGGGCACATAGCACCGCAGTTGGCATCTTTTCGGTCCCTGCTT	1935
Qy	1621	GTGTTACTTCTGCCATTGCCAACATGTTCACTGTAAACACACCCCAACGAGCTGT	1680
Db	1936	GTGTTACTTCTGCCATTGCCAACATGTTCACTGTAAACACACCCCAACGAGCTGT	1995
Qy	1681	GCAGCCCGGATGCTGAATTTAACCTCGTGATCATCTGCTGCCACCTGCGACAGCTC	1740
Db	1996	GCAGCCCGGATGCTGAATTTAACCTCGTGATCATCTGCTGCCACCTGCGACAGCTC	2055
Qy	1741	AATTACTTCTCGGCCCTGGATGCTCCCTGTGTGAGGSCACCATGCCCACTGCAAGCTTT	1800
Db	2056	AATTACTTCTCGGCCCTGGATGCTCCCTGTGTGAGGSCACCATGCCCACTGCAAGCTTT	2115
Qy	1801	CTGAGGTGTTTC	1812
Db	2116	CTGAGGTGTTTC	2127

RESULT 3  
AAD08563  
ID AAD08563 standard; DNA; 3549 BP.  
XX  
XX  
XX AAD08563;  
XX  
XX  
DT 04-SEP-2001 (first entry)  
XX  
XX  
DE Human cardiac adenylyclase VI (ACVI) isoform #1 DNA.  
XX

KW	Human; cardiant; beta-adrenergic signalling protein; beta-ASP;
KW	myocardium; gene therapy; beta-adrenergic receptor; beta-AR;
KW	adenylcyclase; adenylate cyclase; cAMP synthetase;
KW	G-protein receptor kinase; GRK; heart disease; congestive heart failure;
KW	cardiac adenylylase VI; ACVI isoform; beta-ASP transgene; ds.
XX	
OS	Homo sapiens.
OS	
XX	
FH	Location/Qualifiers
FT	1..3504
FT	/*tag= a
FT	/product= "human cardiac adenylylase VI isoform #1"
FT	/EC_number= "4.6.1.1"
XX	
XX	WO200148164-A2.
PN	
XX	
PD	05-JUL-2001.
XX	
PF	26-DEC-2000; 2000WO-US35411.
XX	
XX	27-DEC-1999; 99US-0472667.
PR	
XX	(REGC ) UNIV CALIFORNIA.
PA	
XX	
PI	Hammond HK, Gao M;
XX	
XX	WPI; 2001-4118260/44.
DR	P-PSDB; AAE04310.
XX	
DR	
PT	Novel polynucleotide encoding a modified adenylylase polypeptide
PT	useful for enhancing cardiac function in mammalian hearts, and for
PT	treating heart disease, especially congestive heart failure -
XX	
XX	Example 5; Page 122-129; 153pp; English.
XX	
CC	The present invention relates to methods and compositions for enhancing
CC	cardiac function in mammalian hearts by inserting transgenes encoding
CC	beta-adrenergic signalling proteins (beta-ASP) which increase
CC	beta-adrenergic responsiveness within the myocardium using in vivo
CC	gene therapy. The beta-ASPs of the invention include beta-adrenergic
CC	receptors (beta-AR), adenylylases (also referred as adenylylase,
CC	adenylate cyclase and cAMP synthetase) and G-protein receptor kinase
CC	(GRK) inhibitors. The beta-ASP is used for enhancing cardiac function
CC	in mammalian hearts and for treating heart disease, especially
CC	congestive heart failure. The present DNA sequence encodes human
CC	cardiac adenylylase VI (ACVI) isoform which is used for generating
CC	a third beta-ASP transgene, used in the exemplification
CC	of the invention.
CC	

[illegible]

Qy	1383	TGCCGTGGCCCTGTGTGGCTTCTGCTTCATCTGCTTCATCCAGCTCTTAATTTTCCCA	1442
Db	2016	TGCCGTGGCCCTGTGTGGCTTCTGCTTCATCTGCTTCATCCAGCTCTTAATTTTCCCA	2075
Qy	1443	CTCCACCCCTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGCTTAATCACCCTGCT	15020
Db	2076	CTCCACCCCTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGCTTAATCACCCTGCT	21350
Qy	1503	GATCTGTGCTGTGTACTTCCTGTGGTTCTCTGTTCCTTAAGGCCCTGCAACGCTCTGCCG	15626
Db	2136	GATCTGTGCTGTGTACTTCCTGTGGTTCTCTGTTCCTTAAGGCCCTGCAACGCTCTGCCG	21950
Qy	1563	CAGCATTTGTCGGCTCAGGGGCACATAGCACCGCAGTTGGCATCTTTCCGTCCTGCTTGT	16222
Db	2196	CAGCATTTGTCGGCTCAGGGGCACATAGCACCGCAGTTGGCATCTTTCCGTCCTGCTTGT	22550
Qy	1623	GTTTACTTCTGCCATTGCCAACATGTTTACCTGTAAACACACCCCATACGAGCTGTGC	16826
Db	2256	GTTTACTTCTGCCATTGCCAACATGTTTACCTGTAAACACACCCCATACGAGCTGTGC	23150
Qy	1683	AGCCCGGATGCTGAATTTAACACCTGCTGACATCACTGCTGCACCTGCGACCTGCGACGACTCAA	17424
Db	2316	AGCCCGGATGCTGAATTTAACACCTGCTGACATCACTGCTGCACCTGCGACGACTCAA	23750
Qy	1743	TTACTCTCTGGGCTGGATGCTCCCTGCTGTGAGGGCACCATGCCACCTGCAGCTTTCC	18020
Db	2376	TTACTCTCTGGGCTGGATGCTCCCTGCTGTGAGGGCACCATGCCACCTGCAGCTTTCC	24350
Qy	1803	TGAGGTGCTC 1812	
Db	2436	TGAGGTGCTC 2445	
RESULT 4			
ID	AAD08567		
XX	AAD08567 standard; DNA; 3552 BP.		
AC	AAD08567;		
DT	04-SEP-2001 (first entry)		
DE	Human cardiac adenylylase VI (ACVI) isoform #2 DNA.		
KW	Human; cardiac; beta-adrenergic signalling protein; beta-ASP;		
KW	myocardium; gene therapy; beta-adrenergic receptor; beta-AR;		
KW	adenylylase; adenylylase; adenylylase; adenylylase; adenylylase;		
KW	G-protein receptor kinase; GRK; heart disease; congestive heart failure;		
XX	cardiac adenylylase VI; ACVI isoform; beta-ASP transgene; ds.		
OS	Homo sapiens.		
FH	Key	Location/Qualifiers	
CDS		1..3507	
FT	/*tag= a	/product= "Human cardiac adenylylase VI isoform #2"	
FT	/EC_number= "4.6.1.1"		
XX	WO200148164-A2.		
XX	05-JUL-2001.		
XX	26-DEC-2000; 2000WO-US35411.		
XX	27-DEC-1999; 99US-0472667.		
XX	(REGC ) UNIV CALIFORNIA.		
XX	Hammond HK, Gao M;		
XX	WPI; 2001-418260/44.		
XX	P-PSDB; AAE04311.		











Db 1077 GGAGATGAAAGAGACATCAACACAAAAAAGAGACATGATGTTCCACAAGATCTACAT 1136  
QY 480 ACAGAAGCATGACAAATGTACAGATCCTGTTTGCAGACATTTGAGGGCTTCACAGCCCTGGC 539  
Db 1137 ACAGAAGCATGACAAATGTACAGATCCTGTTTGCAGACATTTGAGGGCTTCACAGCCCTGGC 1196  
QY 540 ATCCCAGTGCACCTGCGCAGAGAGCTGGTCATGACCTGAATGAGCTCTTTGCCCGGTTTGA 599  
Db 1197 ATCCCAGTGCACCTGCGCAGAGAGCTGGTCATGACCTGAATGAGCTCTTTGCCCGGTTTGA 1256  
QY 600 CAAGCTGGCTGCGGAGAGATCACTGCCCTGAGGATCAAGATCTTGGGGAGCTTTACTACTG 659  
Db 1257 CAAGCTGGCTGCGGAGAGATCACTGCTGAGGATCAAGATCTTAGGAGAGCTTTACTACTG 1316  
QY 660 TGTGTAGGGCTGCCGAGAGCCCGGCCAGCATGCCCATGCTGTGTGAGATGGGGT 719  
Db 1317 CGTGTAGGGCTGCCGAGAGCCCGGCCAGATCACGCCCATGCTGTGTGAGATGGGGT 1376  
QY 720 AGACATGATTTGAGGCCATCTCGCTGTTACCTGAGGTGACAGGTGTGAATGTGAACATGCG 779  
Db 1377 AGACATGATCGAAGCCATCTCGCTGTTGCTGAGGTGAACAGGTGTGAACGTGAACATGCG 1436  
QY 780 CGTGGGATCCACAGCGGGCGCTGACCTGCGCGCTTGGCTTGGGAAATGGCAGTT 839  
Db 1437 TGTGGGATCCACAGCGGAGCTGTGATTTGCGGCTCTTGGCTTACGGAATGGCAGTT 1496  
QY 840 CGATGTGTGCTCAATGATGTACCTTGACCTGACCTGAACGGGACTACGAAGTGGAGCC 959  
Db 1554 GCGATCCACATCACTCGGCTACACTGCACTGACTTTGAACGGGACTATGAGTGGAGCC 1613  
QY 960 AGCCGCTGGTGGCAAGCGCAACGCTACCTCAAGAGAGCAGCATTTGAGACTTTCTCAT 1019  
Db 1614 AGCCGCTGGTGGTGAACGCAATGCTTACCTCAAGAGAGCAGTGTGAGACTTTCTCAT 1673  
QY 1020 CTTGGGCGCCAGCAGAAACGGAAGAGAGAAAGGATGCTGGCCAGCTGCAGCGGAC 1079  
Db 1674 ACTTGGGCGCCAGCAGAAACGGAAGAGAGAAAGGATGCTGGCCAGCTGCAGCGGAC 1733  
QY 1080 TCGGGCCCACTCCATGGAAGGGTGTATGCGCGATGGTTCCTGATGCTGCTTCTCCCG 1139  
Db 1734 ACGGCCCACTCCATGGAAGGACTGATGCGCGCTGCTGCTGCTTCTCCCG 1793  
QY 1140 GACCAAGGACTCAAGGCCCTTCCGCGAGTGGGATTTGATTCAGCAAGAACACCG 1199  
Db 1794 GACCAAGGACTCAAGGCCATTCGCGCAGATGGGCAATGATGATTCAGCAAGAACACCG 1853  
QY 1200 GGGCACCACAGATGCCCTGAACCTGAGGATGAGGTGATGCTGAGCGGTGCGCAT 1259  
Db 1854 GGTGCCCCAAGATGCTCTGAACCTGGAATGAGGTGATGATGCTGGCGGAGCCAT 1913  
QY 1260 CGATGCCCGCAGCATTTGATGAGTGGGAAGGACCATGTGCGCGGTTTTTGTCTACCTT 1319  
Db 1914 CGATGCCCGCAGCATTTGATGAGTGGGAAGGACCATGTGCGCGGTTTTTGTCTACCTT 1973  
QY 1320 CCAGAGAGAGATTTTGAAGAGATGACTCCCGAAGGTGGATCCCGCTTCGAGGACTA 1379  
Db 1974 CCAGAGAGAGATTTTGAAGAGATGACTCCCGAAGGTGGATCCCGCTTCGAGGACTA 2033  
QY 1380 CGTTGCTGTGCCCTGTGCTTCTGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCC 1439  
Db 2034 CGTTGCTGTGCCCTGTGCTTCTGCTTCATCTGCTTCATCCAGCTTCTCACTTCCC 2093  
QY 1440 ACTTCCACCTGATGCTTGGGATTTATGCGAGCATCTTCTGCTGCTGCTAATCAACGT 1499  
Db 2094 ACTTCCACCTGATGCTTGGATCTATGCGAGCATCTTCTGCTGCTGCTAATCAACGT 2153  
QY 1500 GCTGATCTGTGCTGTACTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1559  
Db 2154 GCTGATCTGTGCTGTACTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2213

QY 1560 CCAGCAGATTGTCGGCTCACGGGCACATAGCACGGCAGTTGGCATCTTTCCGTCCTGCT 1619  
Db 2214 CCAGCAGATTGTCGGCTCACGGGCACATAGCACGGCAGTTGGCATCTTTCCGTCCTGCT 2273  
QY 1620 TGTGTTTACTTCTGCCATTGCCAACATGTTTACACCTGTGTAACACACACCCCATACGAGCTG 1679  
Db 2274 TGTGTTTACTTCTGCCATTGCCAACATGTTTACACCTGTGTAACACACACCCCATACGAGCTG 2333  
QY 1680 TGAGCCCGGATGCTGAATTTAACACCTGCTGACATCAGCTGCGCTGCCACCTGCAGCAGCT 1739  
Db 2334 TGAGCCCGGATGCTGAATTTAACACCTGCTGACATCAGCTGCGCTGCCACCTGCAGCAGCT 2393  
QY 1740 CAATTACTCTCTGGCCTGATGCTCCCTGTGTGAGGCGACCATGCCACCTGCAGCTT 1799  
Db 2394 CAATTACTCTCTGGCCTGATGCTCCCTGTGTGAGGCGACCATGCCACCTGCAGCTT 2453  
QY 1800 TCCTGAGGTGTTT 1812  
Db 2454 TCCTGAGTACTTC 2466  
RESULT 7  
AAQ42525  
ID AAQ42525 standard; DNA; 4046 BP.  
XX  
AC AAQ42525;  
XX  
DT 14-SEP-1993 (first entry)  
XX  
DE Cardiac adenylyl cyclase gene.  
XX  
KW Regulation; cardiac function; heart; heart failure; ss.  
XX  
OS Canis familiaris.  
XX  
FH Key Location/Qualifiers  
FT CDS 131..3627  
FT /\*tag= a  
XX  
PN EP543137-A.  
XX  
PD 26-MAY-1993.  
XX  
PF 12-OCT-1992; 92BP-0117374.  
XX  
PR 18-NOV-1991; 910S-0793961.  
XX  
PA (AMCY ) AMERICAN CYANAMID CO.  
XX  
PI Ishikawa Y;  
XX  
XX WPI; 1993-168873/21.  
DR P-PSDB; AAR37309.  
XX  
PT Purified DNA encoding cardiac adenylyl cyclase - useful to screen  
for cpds. which stimulate activity of the cyclase  
XX  
PS Claim 1; Fig 2; 34pp; English.  
XX  
CC A canine heart cDNA library was constructed in lambda gt10 and was  
screened with a 970 bp AatI-HincII fragment from type I adenylyl  
cyclase cDNA probe (encodes the first cytoplasmic domain of adenylyl  
cyclase, which has significant homology to other previously known  
types of adenylyl cyclase). One positive clone, of 5.4 kb was obd.  
CC  
CC Positive colonies were subcloned into pUC18 and further subcloned  
and sequenced bidirectionally. The 5.4 kb clone was used to  
rescreen the library and on overlapping clone contg. the 5' end of  
the gene was isolated. Together the two clones cover the complete  
canine cardiac adenylyl cyclase gene. The gene is suspected of  
being involved in the regulation of cardiac function and it is thought  
that decreased activity of adenylyl cyclase in the heart may be a  
major factor in the development of heart failure. Thus the adenylyl

CC cyclase gene is useful to screen cpds. which stimulate the activity  
CC of the cyclase.

SQ Sequence 4046 BP; 743 A; 1206 C; 1254 G; 843 T; 0 other:

Query Match	84.3%	Score	1527.8;	DB	14;	Length	4046;	
Best Local Similarity	91.0%	Pred. No.	0;					
Matches 1648;	Conservative	0;	Mismatches	157;	Indels	6;	Gaps	2;

Qy	5	ACGTGGTCTGGGCATCTCGCGGCAGTGCAGGTGCGGGGGCGCTTTCGACGACAGACCCGC	64
Db	762	ACGTGGTCTGGGCATCTCGCGGCAGTGCAGGTGCGGGGGCGCTTTCGACGACAGACCCGC	821
Qy	65	GCAGCCCTCTGCGGGCCTCTGGTGCCTGTGTCTTTGTATACATCGATACAGCTCC	124
Db	822	GCAGCCCTCTGTGGCCCTCTGGTGCCTGTGTCTTTGTATACATCACTACAGCTCC	881
Qy	125	TCCCATCCGATCGGGCTCCGCTCCCTCAGCGGCTGGGCTCTCCACCTTGCATTTGA	184
Db	882	TACCATCCGATCGGGCAGCTGTCTCAGTGGCTGGGCTGTCCACCTGCATTTGA	941
Qy	195	TCTTGGCCTGGCACTTAACCGTGGTATGCCCTCTCGAAGCAGCTCGTGCCAATG	244
Db	942	TCTTGGCCTGGCACTCAACCGCTGACGCTTCTCTGGAAGCAGCTCGTGCCAACA	1001
Qy	245	TGCTGCTGCTCTCGACCAACGCTATTAGCATCTGCACACTATCCAGCAGAGTGT	304
Db	1002	TGCTGCTGCTCTCTGCACCAACGCTATTGGCATCTGCACACTATCCACGCTGAGGTCT	1061
Qy	305	CTCAGCGCCAGGCGCTTTCAGGAGACCCGAGTATACATCCAGCGCCGGCTCCACCTGCAGC	364
Db	1062	CTCAGCGCCAGGCGCTTTCAGGAGACCCGCGGTACATTCAGCGCCGGCTGCACCTGCCAG	1121
Qy	365	ATGAATTCGCAGCAGGAGCGGTGCTGTCTCGGTATGCCAGACGCTTGCATGG	424
Db	1122	ATGAACCGGCAGCAGGAAGCGGTGCTGTCTCGGTGTCGCTGCCAGCATGTTCGCATGG	1181
Qy	425	AGATGAAGAAGACATCAACCAAAAAGAGAC---ATGTTCCCAAGATCTACATAC	481
Db	1182	AGATGAAGAAGATCAACCAAAAAGAGACATGATGTTCCCAAGATCTACATCC	1241
Qy	482	AGAAAGCATGACAATGTCAGCATCTCTGTTGCAGACATTCAGGGGCTCACAGCCTGGCAT	541
Db	1242	AGAAAGCATGACAATGTCAGCATCTCTGTTGCAGACATTCAGGGCTCACAGCCTGGCGT	1301
Qy	542	CCCAGTGCATGCGCAGGAGCTGTGTCATGACCCGAAATGAGCTCTTTGCCCGTTTGACA	601
Db	1302	CCCAGTGCATGCGCAGGAGCTGTGTCATGACCCGAAATGAGCTCTTTGCCCGTTTGACA	1361
Qy	602	AGCTGGCTGCGGAAATCACTGCTCAGGATCAAGATCTTGGGGAGCTGTTACTACTGTG	661
Db	1362	AGCTGGCTGCGGAAATCACTGCTCAGGATCAAGATCTTGGGGAGCTGTTACTACTGTG	1421
Qy	662	TGTCAGGCTGCCGAGGCGCCGGCCAGCATGCCACTGCTGTGTGGAGATGGGGTAG	721
Db	1422	TGTCAGGCTGCCGAGGCGCCGGCCAGCATGCCACTGCTGTGTGGAGATGGGGTAG	1481
Qy	722	ACATGATTGAGGCATCTCGCTGTTAGCTGAGGTGACAGGTGTGAATGTGAACATGCGCG	781
Db	1482	ACATGATCGAGGCATCTCGCTGTTGCTGAGGTGACAGGTGTGAACATGAGCGC	1541
Qy	782	TGGGCATCCACAGGGGCGGTGACATCGCGCGCTTGGCTTCGGGAATGGCAGTTCG	841
Db	1542	TGGGCATCCACAGGGGCGGTGACATCGCTGTTGCTGTTGGCTTCGGGAATGGCAGTTCG	1601
Qy	842	ATGTGTGGTCCAATGATGTGACCTTGGCCCAACCATGGAAGCAGGAAGCGGCTGGCC	901
Db	1602	ACGTGTGGTCCAATGATGTGACCTTGGCCCAACCATGGAAGCAGGAAGCGGCTGGCC	1658
Qy	902	GCATCCACATCACTGCGGCAACACTGCAGTACCTTGAACGGGGACTAGAACTGAGCGAG	961
Db	1659	GCATCCACATCACTGCGGCAACACTGCAGTACCTTGAACGGGGACTAGAACTGAGCGAG	1718

RESULT 8  
AAA53923

AAA53923  
ID AAA53923 standard; cDNA; 4131 BP.

AA  
AC

XX  
DT 03-JAN-2001 (first entry)

XX Type VI adenyl cyclase coding sequence.

Adenylyl cyclase; type I; type II; recombinant; enzyme; cAMP;  
KW  
cyclic AMP; adenosine monophosphate; screening; stimulation;  
KW

KW inhibition; treatment; cholera; pituitary tumour; heart failure;  
 KW ischaemia; endocrine disorder; cell necrosis;  
 KW pseudohypoparathyroidism; endocrine deficiency; human; ss.  
 XX

OS Homo sapiens.

XX Key Location/Qualifiers  
 FH 14..3556  
 FT CDS

FT /\*tag= a  
 FT /product= type VI adenylyl cyclase

XX US6107076-A.

XX 22-AUG-2000.

XX 04-OCT-1996; 96US-0726214.

XX 04-OCT-1995; 95US-0005498.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX Gilman AG, Tang W;

XX WPI; 2000-578539/54.

DR P-PSDB; AAB02010.

XX Novel soluble mammalian polypeptide composition comprising adenylyl  
 PT cyclase activity for screening stimulators and inhibitors of adenylyl  
 PT cyclase, is activated by Gsalpha

PS Disclosure; Columns 75-78; 73pp; English.

XX A recombinant Adenylyl cyclase is described which lacks membrane  
 CC bound domains. Separation and purification of the recombinant  
 CC enzyme is much easier compared with wild type enzymes and the  
 CC recombinant enzyme is more stable than the wild type enzyme which  
 CC allows easier screening of compounds that stimulate and inhibit  
 CC Adenylyl cyclase activity. The recombinant adenylyl cyclase comprises  
 CC a chimera of adenylyl cyclase C.1 and C.2 domains linked covalently.  
 CC The domains may be linked by a linker peptide. The recombinant  
 CC adenylyl cyclase is useful for screening inhibitors and stimulators  
 CC of adenylyl cyclase activity. Inhibitors of the enzyme are useful for  
 CC treating cholera, pituitary tumors, heart failure, ischaemia,  
 CC endocrine disorders and cell necrosis. Stimulators of adenylyl  
 CC cyclase are useful for treating pseudohypoparathyroidism and other  
 CC endocrine deficiencies.

XX Sequence 4131 BP; 835 A; 1190 C; 1182 G; 924 T; 0 other;

SQ Query Match 79.3%; Score 1437.2; DB 21; Length 4131;  
 Best Local Similarity 87.5%; Pred. No. 0;  
 Matches 1584; Conservative 0; Mismatches 223; Indels 3; Gaps 1;

QY 5 ACGTGGTCTGGGCATCTGGGGCAGTCGAGGTCGGGGGGCTTCGACGACAGCCGC 64  
 DB 687 ATGTGGTCTGGGCATCTAGCAGCCGTGCAAGTCGGGGGGTGGCCGCAACCCAC 746

QY 65 GCAGCCCTCTCGGGGCTCTGGTGGCCCTGTGTCTTGTATACATCGCATACAGCTCC 124  
 DB 747 GCAGCCCTCTAGCAGGCTTTGGTGGCCCGGTGTCTTCGTATACCTACACATTC 806

QY 125 TCCCATCCGATCGGGCTGCCCTCTCAGCGGCTTGGGCTCTCCACCTTGCATTGA 184  
 DB 807 TTCCCATTCGATCGAGCGCGGTGCTCAGTGGCTGGGTCTTCCACCTGCATTGA 866

QY 185 TCTTGGCCTGGCACTTAACCGTGGTATGCCCTTCTTGAAGAGCTCGGTGCCAATG 244  
 DB 867 TTTTGGCCTGGCATCTCAACAATGGTGACCCCTTCTTTGGAAGCAGCTCGGTCTAACG 926

QY 245 TGCTGCTGTTCCCTCTGCACCAACGCTATTAGCATCTGCACACACTATCCAGCAGGTGT 304  
 DB 927 TGGTGCTCTTCTGTGCACCAATGCCATCGGTGTCTGCACGCACTACCCCGCTGAAGTGT 986

QY 305 CTACGCCAGCGCTTTTCAGGAGACCGCAGTTACATCCAGGCCGCTCCACCTGCAGC 364  
 DB 987 CTACGCCCAAGCCTTTTCAGGAGACCGCCTGTGTTACATCCAGGCCGCTGCATTGCAGC 1046  
 QY 365 ATGAGAATCGGCAGCAGGAGCGGCTGCTGCTGGTATTGCCCCAGCAGCTTGCCATGG 424  
 DB 1047 ATGAGAATCGACAGCAGGAACGCTGCTGCTGGTGTGCCCCAGCATGTTGCCATGG 1106  
 QY 425 AGATGAAGAAGACATCAACACAAAAAAGAAC---ATGTTCCCAAGATCTACATAC 481  
 DB 1107 AAATGAAGAAGATATCAACAAAAAAGAACATGATGTTCCACAAGATTTTACATCC 1166  
 QY 482 AGAAGCATGACAATGTCAGCATCTGTTGCAGACATGAGGGCTTCACACGCTTGCAT 541  
 DB 1167 AGAAGCATGACATGTCAGCATCTGTTGCCGACATCGAGGGCTTCACACGCTTGCCT 1226  
 QY 542 CCCAGTGCATGCGCAGGAGCTGGTCAATGACCTGAAATGAGCTCTTTGCCCGGTTGACA 601  
 DB 1227 CCCAGTGCATGCGCAGGAACTGGTCAATGACCTGAAATGAGCTCTTTGCCCGGTTGACA 1286  
 QY 602 AGCTGGCTGGGAGATCACTGCTGAGGATCAAGATCTTGGGGAGCTGTACTACTGTG 661  
 DB 1287 AGCTGGCTGGGAGATCACTGCTGAGGATCAAGATCTTAGGAGACTGTACTACTGTG 1346  
 QY 662 TGTGAGGCTGGCGGAGGCGGCCGCCACCATGCCACTGCTGTGTGGAGATGGGGTAG 721  
 DB 1347 TGTGCGGCTGGCGGAGGCGGCCGACACCATGCCACTGCTGTGTGGAGATGGGGTAG 1406  
 QY 722 ACATGATTGAGGCAATCTGCTGCTGAGTGTGAGGTGACAGGTGGAATGTGAACATGCGG 781  
 DB 1407 ACATGATGAGGCAATCTGCTGCTGAGTGTGAGGTGGAACATGTGAACATGCGG 1466  
 QY 782 TGGSCATCCACAGCGGCGGTGCTGCTGCGCGTCCCTGCTGCGAAATGGCAGTTCG 841  
 DB 1467 TGGSCATCCACAGCGGCGGTGCTGCTGCGCGTCCCTGCTGCGAAATGGCAGTTCG 1526  
 QY 842 ATGTGTGTCCTCAATGATGTGACCTGGCCAAACACATCGAAGAGAGAGCGGCTGGCC 901  
 DB 1527 ATGTGTGTCCTCAACGATGTGACCTGGCCAAACACATCGAAGAGAGAGCGGCGGCC 1586  
 QY 902 GCATCCACATCACTCGGGCAACACTGCAGTACCTGACGGGGAGCTAGAAATGAGCCAG 961  
 DB 1587 GCATCCACATCACTCGGGCCACACTGCAGTACCTGAAACGGGGAGCTATGAGTGGAGCCAG 1646  
 QY 962 GCGTGTGTGCAAGCAACGCTGCTCAAGGAGCAGCAGCATTTGAGACTTTCCTCATCC 1021  
 DB 1647 GCGTGTGTGCGGCAACGCTGCTCAAGGAGCAGTGCATTGACACCTTCTCATAC 1706  
 QY 1022 TGGGCGCCAGCAAAACGGAAGAGAGAAAGCATCTGTCGCAAGCTGCAGCGGACTC 1081  
 DB 1707 TAGGAGCCAGCAAAACGGAAGAGAGAAAGGCAATGCTGTTCAAGCTGCAGCGGAGC 1766  
 QY 1082 GGGCCAACTCCATGAAGGCTGATGCGCGGATGGGTTCTCTGATGCTGCTTCTCCCGGA 1141  
 DB 1767 GGGCCAACTCCATGAAGGACTGATGCGCGGCTGGGTTCTGACCTGCTTCTCCCGGA 1826  
 QY 1142 CCAAGGACTCCAAGGCTTCCGCCAGATGGCATTTGATTTCCAGCAAAAGACAAACCGG 1201  
 DB 1827 CCAAGGACTTAAGGCATTCGACAGATGGCATCGATGACTCTAGCAAGAGAACCGG 1886  
 QY 1202 GCACCCAAAGTGGCTGAACCTCGAGGATGAGTGGATGAGTTCCTGAGCGCTGCCATCG 1261  
 DB 1887 GTGCCCCAAGATGCTCTGAACCTCGAGGATGAGGTGGAGAGTTCTGGGCGAGCCATCG 1946  
 QY 1262 ATGCCCCAGCATTTGATCAGCTGCGGAAGACCATGTCGCGCGGTTTTTGTCTACCTTCC 1321  
 DB 1947 ATGCCCCAAGCATCGACAGCTGCGTAAGGACCATGTCGCGCGGTTCTCTGCTACCTTCC 2006  
 QY 1322 AGAGAGAGGATTTTGAAGAAGTACTCCCGAAGGTGGATCCCGGCTTCGAGGAGCTTACG 1381  
 DB 2007 AGAGGAGGATCTCGAAGAAGATTTACGGAAGTAGACCTCTCGTTTGGAGAGCTTACG 2066  
 QY 1382 TTGCTGTGCGCTGTTGGTCTTCTGCTTCTATCTGCTTCACTCCAGCTTCTTAATTTCCAC 1441

Db 2067 TCGCCTGTGCCCTCTCGGTTTCTGCTTCATCTGTTTTCATCCAGTTCTCTCGTATTCACCAC 2126  
QY 1442 ACTCCACCTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGCTGCTTAATCACCCTGC 1501  
Db 2127 ACTCCGCTGATCTCGGGATTTATGCCGGATCTTCTTTTGGCTGCTGCTGCTGCTGCTG 2186  
QY 1502 TGATCTGCTGTGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1561  
Db 2187 TCATCTGTCTGTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2246  
QY 1562 GGAGCATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1621  
Db 2247 GCAGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2306  
QY 1622 TGTCTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1681  
Db 2307 TGTCTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2366  
QY 1682 CAGCCCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1741  
Db 2367 CGGCCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2426  
QY 1742 ATTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1801  
Db 2427 ATTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2486  
QY 1802 CTGAGGTGTT 1811  
Db 2487 CTGAGTACTT 2496

## RESULT 9

ID ABI99680  
XX ABI99680 standard; cDNA; 5841 BP.  
AC ABI99680;  
DT 07-MAR-2002 (first entry)  
XX Mouse ischaemic condition related cDNA sequence SEQ ID NO:716.  
DE Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;  
XX vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.  
KW Mus musculus.  
XX WO200188188-A2.  
PN 22-NOV-2001.  
PD 18-MAY-2001; 2001WO-JP04192.  
XX 18-MAY-2000; 2000JP-0145977.  
PR (UYUNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.  
XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;  
PI WPI; 2002-034733/04.  
XX P-PSDB; ABB57257.  
DR Examining the ischemic condition (e.g. occlusive ischemia) by measuring  
XX expression levels of particular genes defined in the specification or  
PT by determining the expression profile of a gene group comprising these  
XX genes -  
XX Claim 2; Page 1771-1780; 2690pp; English.  
PS The present invention describes a method for examining ischaemic  
XX conditions, comprising measuring the expression levels of particular  
CC genes (I) in a test sample or determining the expression profile of a  
CC gene group in the sample comprising genes selected from (I). The method

CC is useful for examining the ischaemic condition (e.g. compressive  
CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring  
CC expression levels of particular genes (ABI99202 to ABI99912, encoding  
CC the protein sequences in ABB57020 to ABB57374) or by determining the  
CC expression profile of a gene group comprising these genes. The  
CC expression levels or expression profiles produced by these genes are  
CC used as an indicator when screening for ischaemic condition-improving  
CC drugs or therapeutics for ischaemic diseases. ABI99913 and ABI99914  
CC represent PCR primers for a mouse ischaemic condition related sequence,  
CC which are used in the exemplification of the present invention.

XX SQ Sequence 5841 BP; 1214 A; 1558 C; 1673 G; 1396 T; 0 other;

Query Match 79.0%; Score 1431.8; DB 24; Length 5841;  
Best Local Similarity 87.7%; Pred No. 0;  
Matches 1588; Conservative 0; Mismatches 217; Indels 6; Gaps 2;

QY 5 AGCTGTGCTGGGCATCCTGGCGCAGTGCAGTGGGGCGCTTTCGCAGCAGACCCCGC 64  
Db 727 ATGTGTCTCTGGGCATCCTAGCAGCCGTGCAAGTGGGGGTGCCCTGGCAGCAATCCAC 786  
QY 65 GCAGCCCTCTCGGGCCTCTGGTGGCCCTGTTCTTTGTATACATCGCATACACGCTCC 124  
Db 787 ACAGCCCTCTCGGGCCTCTGGTGGCCCTGTTCTTCTGTACATCCTACCTCTCTTC 846  
QY 125 TCCCATCGCATCGCGCTGCCCTCCTCAGCGGCTGGCCCTCTCCACCTTGCATTTGA 184  
Db 847 TTCCCATCGCATCGCGCAGCCGAGTACTCAGCGGCTGGCCCTCTCTACTCTGCATTTGA 906  
QY 185 TCTTGCCCTGGCAACTTAACCGTGTGTATGCTTCTCTGSAAGCAGCTCGGTGCCAATG 244  
Db 907 TTTTGCCCTGGCAGCTCAACAGCAGCGCCCTCTCTTTGGAAGCAGCTCGGTGCTAAGC 966  
QY 245 TGCTGCTTCTCTGTCACCAACGTCATAGCATCTGCACACACTATCCAGCAGGTGT 304  
Db 967 TGGTCTCTCTCTGTCACCAATGCCATGCCGTGTCTGCACACACTACCTGTGAGTGT 1026  
QY 305 CTCAGCGCCAGGCTTTTCAGGAGACCGCGAGTTACATCCAGCGCGGCTCCACCTGCAGC 364  
Db 1027 CTCAGCGCCAGCTTTTCAGGAGACCGCGAGTTACATCCAGCGCGGCTGCACCTGCAGC 1086  
QY 365 ATGAGAACTGGCAGCAGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 424  
Db 1087 ATGAGAACTGGCAGCAGGAAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1146  
QY 425 AGATGAAGAGACATCAACACAAAAGAGAGAC-ATGTTCCACAGATCTACATAC 481  
Db 1147 AGATGAAGAGACATCAACACAAAAGAGAGACATGATGTTCCATAGATCTACATCC 1206  
QY 482 AGAAGCATGACAATGTCAGCATCCTGTTTTCAGACATTTGAGGGCTTCACCGCTGGCAT 541  
Db 1207 AGAAGCATGATAATGTCAGCATCCTGTTTTCAGACATTTGAGGGCTTCACCGCTGGCAT 1266  
QY 542 CCCAGTGCATCGCGCAGGAGCTGTCATGACCTGAATGAGCTCTTTGCCCGGTTTGACA 601  
Db 1267 CCCAGTGCATCGCGCAGGAACTGGTTCATGACCTTTGAATGAGCTCTTTGCCCGGTTTGACA 1326  
QY 602 AGCTGGCTGGGAGAACTCACTGCTGAGGATCAAGATCTTTGGGAGCTCTTACTACTGTG 661  
Db 1327 AGCTGGCTGGGAGAACTCACTGCTGAGGATCAAGATCTTTAGGAGCTCTTACTACTGTG 1386  
QY 662 TGTGAGGCTGGGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 721  
Db 1387 TGTGAGGCTGGGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1446  
QY 722 ACATGATTGAGGCCATCTCGCTGGTACGTGAGGTGACAGGTGTGAATGTGACATGCGCG 781  
Db 1447 ACATGATTGAGGCCATCTCGCTGGTACGTGAGGTGACAGGTGTGAATGTGACATGCGCG 1506  
QY 782 TGGGATCCACAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 841  
Db 1507 TGGGATCCACAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1566

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QY 842 ATGTGTGGTCCAAATGATGTGAACCTGGCCAAACACATGSAAGCAGGAGGCGGCTGGCC 901
Db 1567 ATGTCTGGTCAAACGATGTGACCTTGCTAACACATGAGGGCGGGGC---GGCCGGC 1623
QY 902 GCATCCACATCACTCGGGCAACACTGCAGTACCTGACGAGCGGGACTAGAGTGGAGCCAG 961
Db 1624 GCATCCACATCACTCGGGCTACACTGCAGTACTTGAACGGGGACTATGAGTGGAGCCAG 1683
QY 962 GCGTGTGGTGAAGCGCAACGCGTACCTCAAGGAGCAGCAGCATTTGAGACTTTCCTCATCC 1021
Db 1684 GCGTGTGGTGAAGCGCAATGCGTACCTCAAGGAGCAGTGCATTTGAGACCTTCTCTATAC 1743
QY 1022 TGGCGCCAGCCAGAAACGAAAGAGGAGAGAGCATGCTGGCCAACTGCAGCGGACTC 1081
Db 1744 TTGGCGCAGCCAAACGAAAGAGGAGAGAGCATGCTGGCCAACTTTCAGCGGACAC 1803
QY 1082 GGGCCAACTCCATGGAAGGCTGATGCCGCGATGGGTTCCTGATCGCTTCTCCCGGA 1141
Db 1804 GGGCCAACTCCATGGAAGGACTGATGCCCGCTGGGTTCCTGACCGTCTTCTCCCGGA 1863
QY 1142 CCAGGACTCCAGGCGCTTCCGCCAGATGGGCATTTGATGATTTCCAGCAAAAGACAACCGG 1201
Db 1864 CCAGGACTCCAGGCAATTCGCCAGATGGGCATTTGATGATTTAGCAAAAGACAACCGG 1923
QY 1202 GCACCCAAAGATGCCCTGAACCTGAGGATGAGGTGGATGAGTTCCTGAGCCGTGCCATCG 1261
Db 1924 GTGCCAAAGATGCTCTGAACCTGAAGATGAGGTGGATGAGTTCCTGGCGGAGCCATCG 1983
QY 1262 ATGCCCCAGCATTTGATCACTGCGGAGGAGCAGCATGTCGCCGGTTTTTGTCTACCTTCC 1321
Db 1984 ATGCCCCAGCATTTGATCACTGCGGTAAGGAGCAGCATGTCGCCGGTTTTTGTCTACCTTCC 2043
QY 1322 AGAGAGGAGTATTTGAGAAAGTACTCCCGAAGTGGATCCCGCTTCGGAGCCCTACG 1381
Db 2044 AGAGAGGAGTATTTGAGAAAGTATTTACGGAAGTAGATCTCGCTTCGGAGCCCTACG 2103
QY 1382 TTGCGCTGTGCCCTGTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTCTAATTTCCAC 1441
Db 2104 TCGCTGTGCCCTGTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTCTGTTGCCAT 2163
QY 1442 ACTCACCCGTGATCTTGGGATTTATCCAGCATCTTCTGCTGCTGCTGCTAATCACCTGC 1501
Db 2164 ACTCACCCGTGATCTGCGGATTTATCCGCTATCTTCTGCTGCTGCTGCTGCTGCTGCTG 2223
QY 1502 TGATCTGTGCTGTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1561
Db 2224 TGATCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2283
QY 1562 GCAGCATTTGCGGCTACGGGCAACATAGCAGCCGAGTTGGCATCTTTTCCGTCCTGCTTG 1621
Db 2284 GCAATATTTGCGGCTACGGGTCACAGCACCGCGGTTGGAATCTTCTCGGTTCTGCTTG 2343
QY 1622 TGTTTACTTCTGCCATTTGCCAATGTTTACCTGTATACCCACACCCCATACGGAGCTGTG 1681
Db 2344 TGTTCATCTCTGCCATCGCCAAACATGTTTACCTGTATACACACCCCAATAGGACCTTGG 2403
QY 1682 CAGCCCGGATGCTGAATTTAAACCTGCTGACATCACTGCTGCTGCTGCTGCTGCTGCTGCTG 1741
Db 2404 CAGCCCGGATGCTGAATTTAAACCTGCTGACATCACTGCTGCTGCTGCTGCTGCTGCTGCTG 2463
QY 1742 ATTACTCTGTGGGCTGGATGCTCCCTGTGTGAGGAGCAGCATGCCCCACCTGCAGCTTTC 1801
Db 2464 ATTACTCTGTGGGACTGGATGCTCCCTGTGTGAGGAGCAGCATGCCCCACCTGCAGCTTTC 2523
QY 1802 CTGAGGTGTTTC 1812
Db 2524 CTGAGTACTTC 2534
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RESULT 10  
AA00462  
ID AAX00462 standard; DNA; 4523 BP.  
XX

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AC AAX00462:
XX 25-MAY-1999 (first entry)
XX Human type V adenylyl cyclase coding sequence.
XX Type V adenylyl cyclase; human; hac5; heart disease; brain;
KW therapy; diagnosis; ds.
XX Homo sapiens.
XX WO9901546-A1.
XX 14-JAN-1999.
XX 01-JUL-1998; 98WO-US13540.
XX 01-JUL-1997; 97US-0886362.
XX 01-JUL-1997; 97US-0070901.
XX (CORT-) COR THERAPEUTICS INC.
XX Tomlinson JA;
XX WPI; 1999-106048/09.
XX P-PSDB; AAW30600.
XX Newly isolated and purified human type V adenylyl cyclase (hac5)
PT polypeptide - useful for identifying potential therapeutic agents
PT that modulate hac5 activity, and for the diagnosis of
PT hac5-associated diseases and disorders
XX
XX Claim 3; Fig 1a-h; 40pp; English.
XX
XX This sequence encodes the human type V adenylyl cyclase (hac5) of the
CC invention. hac5 has a similar putative structure to other adenylyl
CC cyclase isoforms but, like type VI, is distinguishable in that it has a
CC larger N-terminus and a relatively shorter C-terminus as it lacks the
CC C2b region. The hac5 polypeptides are useful in assays that screen for
CC potential therapeutic agents, which modulate hac5 activity. These
CC polypeptides are also useful in assays for the diagnosis of diseases and
CC disorders. Agonists of hac5 are useful control agents in such assays, and
CC they may have useful effects in vivo for treating disease. Antibodies
CC acting as (antagonists have diagnostic and therapeutic effects, and are
CC useful in immunoassays for hac5. (Antagonists are particularly useful in
CC treating diseases caused by abnormal hac5 activity (e.g. in the heart and
CC brain), and in diseases, which are alleviated by modulating hac5
CC activity. The oligonucleotides are useful in methods that inhibit or
CC regulate hac5 expression in vivo and in vitro. The cloning of the human
CC isotype of AC5 enables the development of tissue-specific and selective
CC pharmacological agents for use in treating particular human diseases
CC associated with hac5.
XX
SQ Sequence 4523 BP; 840 A; 1419 C; 1428 G; 836 T; 0 other;
Query Match 49.4%; Score 895; DB 20; Length 4523;
Best Local Similarity 69.8%; Pred. No. 5.7e-229;
Matches 1277; Conservative 0; Mismatches 525; Indels 27; Gaps 4;
QY 5 ACGTGTGCTGTGGGCATCCTTGGCGGCAGTGCAGGTGCGGGGCGCTTTCGACAGACAGCCGC 64
Db 1046 ATGCGCTCATCGCGTGGTGTGCTGGCCGCTCCAGGTGGTGGCGCTGCTGCGCGAGCAC 1105
QY 65 GCAGCCCTCTCGGGGCTCTGGTGGCCCTGTGTTCTTTGTATACATGCATACAGCTCC 124
Db 1106 GCAGCGCTCTGAGGGCATCTGTTGGACCGCTGTTCTTCTATCTACACCATCTACAGCTGC 1165
QY 125 TCCCATCCGATCGGGGCTGCGTCTCAGCGGCTGGGCTCTCCACCTTGCAATTGA 184
Db 1166 TGCCCGTGGCAGTCGCGGCGCAGTGTCTCAGCGGGGTGCTCTCGCCCTCCACCTGG 1225
QY 185 TCTTGGCTGGCAACTTAACCGTGGTGTGATGCCTTCTCTGGAAGCAGCTCGGTGCCAATG 244
```

12826	DB	CCATCGCCCTCGCCGACCAACGCCGACCGACAGTTCCTGCTGAAGCAGCTTGTCTCCAAATG	12825
245	QY	TGCTGCTGTTCTCTGTCACCAACGGTCATTAGCATCTGCACACACTATCCAGCAGAGTGT	304
1286	DB	TTCTCATTTTCTCTGTCACCAACATCGTGGTGTCTGCACCCACTATCCGGCTGAGTCT	1345
305	QY	CTCAGCGCGAGCCCTTTCAGGAGACCCGCGAGTTACATCCAGGCCGGGTCCACCTGCGAGC	364
1346	DB	CCGACAGCAGGCTTTCAGGAGACCCGAGAGTGCATCCAGCGCGGCTCCACTCGCAGC	1405
365	QY	ATGAGATCGGCAGCAGGAGCGCTGCTGCTGTGCGTATTGCCCCCAGCAGCTTGCCATGG	424
1406	DB	GGGAGACCGAGCAGGAGAACGGCTCCTGCTGTCTGTCTCCCGCTCATGTGTGCCATGG	1465
425	QY	AGATGAAGAGACATCAACACAAAAAAGAAGA---CATGTTCCACAAGATCTACATAC	481
1466	DB	AGATGAAGCAGACATCAACGCCACGACGAGGATATGATGTTCCATAAATTTACATCC	1525
482	QY	AGAAGCATGACATGTTCAGCATCCTGTTTGCAGACATGAGGGCTTCACCGCCTGGCAT	541
1526	DB	AGAAACATGACACGTGAGCATCCTGTTTGCTGACATCGAGGCTTCACCGCCTGGCGT	1585
542	QY	CCCAGTGCAGTCGCGAGGAGCTGGTCATGACCCCTGNAATGAGCTCTTTCGCCGTTTGACA	601
1586	DB	CCCAGTGCATGCAAGAGAACTGGTCATGACCCCTCAAGAGAGCTTTCGCCGCTTGTGACA	1645
602	QY	AGCTGGCTGGCGAGAACTCACTGCTCAGGATCAAGATCTTGGGGAGCTGTTACTACTGTG	661
1646	DB	AGCTGGCGCAGAGAACTACTGTTTACGTATTAAAGATCCTTGGGGATTGTTATTACTGCG	1705
662	QY	TGTCAGGGCTGCGGAGGCCCGGGCCGACCATGCCACCTGCTGTGTGGAGATGGGGTAG	721
1706	DB	TCTCGGGCTCGCCTGAAGCAAGGSCGTGACCGGCCACTGCTGTGTGGAGATGGGCATGG	1765
722	QY	ACATGATTGAGGCATCTGCTGCTGATGAGTGCACAGGTGTGAATGTGAACATGCGCG	781
1766	DB	ACATGATCGAGGCCATCTGTTGGTCCGGAGGTGACAGGGGTGAACGTGAACATGCGGTG	1825
782	QY	TGGGCATCCACAGCGGGCGGTGCACCTGGCGGGTCTTGGCTTGGCGAAATGGCAGTTCCG	841
1826	DB	TGGCAATTACAGCGGCGAGTACACTGCGGTGCTCTGGTCTCAGGAAGTGGCAGTTCCG	1885
842	QY	ATGTGTGTCATGATGTGACCCCTGGCCCAACCATGGAAGCAGGAAGCCGGCTGGCC	901
1886	DB	ACGTCTGCTTAACGATGTCAACGCTAGCCCAACCATGAGGCTGGCGCAAGGCAGGAC	1945
902	QY	GCATCCACATCACTCGGGCAACACTGCACTACCTGNAACGGGGACTACCAAGTGGAGCCAG	961
1946	DB	GCATCCACATCAACAAAGTTACATCAACTGAAATGGGGACTACGAGGTGGAGCCAG	2005
962	QY	GCCGTGTGGCAAGCGCAACGGCTACCTCAAGGACGACATTCAGACTTTCCTCATCC	1021
2006	DB	GCTGTGGGGCGAGCGACAGCCTACCTCAAGAGCAGATATCGAGACCTTCTCTCATCC	2065
1022	QY	TGGCGCCACCGCAAAACGGAAAGAGGAGGATGCTGGCCAAAGTGCAGCGGACTC	1081
2066	DB	TGCGCTGCACCCAGAAGCGGAAAGAGAGAGGCGCCATGATCGCAAGATGAACGCCAGA	2125
1082	QY	GGGCAACTCCATGGAAGGCTGATGCCCGATGGTTCTCTGATGCTGCTTCTTC---	1137
2126	DB	GAACCAACTCCATCGGGCAACACCCACACACTGGGGGGCTGAGCGCCCTTCTACAAAC	2185
1138	QY	-----CGGACCAAGGACTCCAAGGCCTTCGCCAGATGGCATTTGATGATTCACAGA	1189
2186	DB	ACCTGGGTGCACACAGGTGTCCAGGAGATGAACGGATGGCTTTGAAGACCCCA---	2242
1190	QY	AAGACAACCGGGCACCCCAAGATGCCCTGAAACCCCTGAGGATGAGTGGATGAGTTCCTGA	1249
2243	DB	---AGGACAAGAAGCCCGAGGAGTGCGAACCCCTGAGSATGAATGATGATGAGTTCTCG	2299
1250	QY	GCGGTGCCATCGATCCCGCAGATTTGATCAGCTCGGAAGGACCATGTGCGCCGGTTTT	1309
2300	DB	GCGGTGCCATTTAGCCGAGGACATGTATGAGCTTCGGTCTGAGCAGCTCGCAAGTTC	2359

Qy	1310	TGCTACCTTCCAGAGAGAGGATTTTGAGAAGAAGTACTCCGGGAAGGTGGATCCCGCT	1369
Db	2360	TCCTGACCTTCCAGGAGCCTCGACTTAGAGAAGAAGTACTCCAGCAGGTAGACACCGAT	2419
Qy	1370	TCGGAGCCTACGTTGGCTGGCCCTCTTGCTCTGCTTTCATCTGCTTCATCCAGCTTC	1429
Db	2420	TTGGTGGCTATGGGGGTGGCCCTCGCTCTTCTCTTCACTGCTTTGTCAGATCA	2479
Qy	1430	TAAATTTTCCACACACTCCACCCTGATGCTTGGGATTTATGCCAGCATCTCTGCTGTGC	1489
Db	2480	CCATCGTGCCCCACTCCATATTCATGCTCAGCTTCTACTGACCTGTGTTCCCTGCTGTGA	2539
Qy	1490	TAATCACCGTGATCTGCTGCTGTACTCTCTGCTGCTCTGTTCTCTTAAAGCCCTGC	1549
Db	2540	CCTTGGTGGTGTGCTGTGATCTACTCTCTGGTAAAGCTCTTCCCTCCCACTGC	2599
Qy	1550	AACGTCTGTCCCCAGCATTTGCCGTACGGGCACATAGCACCCGACGTTGGCATCTTTT	1609
Db	2600	AGACCTTCTCCAGGAAGATCGTGGGTCCCAAGATGAACAGACCCCTGTTGGGGTGTCA	2659
Qy	1610	CGTCCCTGCTGTGTTTACTTCTGCATTGCCAATGTTCACTGTAACCCACACACCCCA	1669
Db	2660	CCATCACCTTGTGTTCTTGGCGGCTTTGTCAATGTTTACGTGCAACTTCCAGGACC	2719
Qy	1670	TACGAGCTGTGACGCCGGATGCTGAATTTAACACCTGCTGACATCACTGCCTGCCACC	1729
Db	2720	TGCTGGGCTGCTTGGCACAGGAGCAACATCAGGCGCAGCAGGTCAACCGTGTCAAG	2779
Qy	1730	TGCAGAG-----CCTCAATTACTCTCTGGGCTTGATGCTCCCTCTGCTGAGGGCACCA	1783
Db	2780	TGGCGAGTCGGCGCTCACTACAGCCTGGGCGATGACAGGGGCTCTGTGGCAGCCCT	2839
Qy	1784	TGCCACCTGCAGCTTTCTCTGAGGTGTC	1812
Db	2840	GGCCAACTGCAACTTCCCGAGTACTTC	2868

RESULT 11	
AAQ95540	
ID	AAQ95540 standard; DNA; 4356 BP.
XX	
AC	
AC	AAQ95540;
XX	
XX	
DT	31-JAN-1996 (first entry)
XX	
DE	Cardiac adenyllyl cyclase gene.
XX	
KW	Cardiac adenyllyl cyclase; effector enzyme; ss.
XX	
OS	Homo sapiens.
XX	
PH	Key
FT	Location/Qualifiers
FT	148..3702
XX	/*tag= a
XX	
PN	TW243453-A.
XX	
PD	21-MAR-1995.
XX	
PF	02-JUL-1992; 92TW-0105242.
XX	
PR	12-JUN-1992; 92US-0899068.
XX	
PA	(AMCY ) AMERICAN CYANAMID CO.
XX	
WPI	1995-214006/28.
DR	P-PSDB; AAR78519.
XX	
PT	Cardiac adenyllyl cyclase and corresp. DNA - having specified
PS	sequences
XX	
PS	Claim 1; Fig 2; 45pp; Chinese.



xx AAQ9540 encodes AAR78519, the novel effector enzyme cardiac adenylyl  
CC cyclase.  
xx  
SQ Sequence 4356 BP; 836 A; 1372 C; 1373 G; 775 T; 0 other;  
  
Query Match 48.98; Score 884.6; DB 16; Length 4356;  
Best Local Similarity 69.1%; Pred. No. 3.4e-226;  
Matches 1259; Conservative 0; Mismatches 549; Indels 15; Gaps 3;  
  
QY 5 ACGTGGTCTGGGCATCCTGGCGCAGTCGAGGTGCGGGGGCGCTTTCGACGACACCCGC 64  
DB 821 ACGGCTCATCGCGTGGTCTGGCGCTGAGGTGGGGCTGCTCTGCCCGACGCGC 880  
  
QY 65 GCAGCCCTCTGCGGGCTCTGGTGCCTGTGTCTTGTATACATCGCATACGCTCC 124  
DB 881 GCAGCGCTCGAGGGCATCTGGTGACCGGTGTTCTATCTACACCATCTACACGCTGC 940  
  
QY 125 TCCCATCCGCATGCGGGCTGCGGTCTCTCAGCGCGCTGGGCCCTTCCACCTTGCATTGA 184  
DB 941 TGCCGTGCGCATGCGGGCGCGCTCTCAGCGAGTGTCTTGTGCGGCCCTGCACCTGG 1000  
  
QY 185 TCTGGCTTGGCACTTAACCGTGGTGTATGCTTCTCTGAGGACGCTCGTGCCCAATG 244  
DB 1001 CCATGCGCTTGGCGCGCAACGCCAGACCGGTTCCTGCTCAAGCAGCTGCTTCCAATG 1060  
  
QY 245 TGCTGCTGTTCCTGTCACCAACGTCAATTAGCATCTGCACACACTATCCAGCAGAGTGT 304  
DB 1061 TCCTCATTTTCTCTGACCAACATCTGTGGTGTCTGTACCCACTACCGCGTGCAGTCT 1120  
  
QY 305 CTCAGCCCGAGGCTTTAGAGAGCCGCGAGTTACATCCAGGCGCGCTCCACCTGCAGC 364  
DB 1121 CCCAGACAGAGGCTTCCAAGAGACCGCGAGTGCATCCAGGACGCGCTCCACTCGCAAC 1180  
  
QY 365 ATGAGATCGGCAGCAGCGGTGCTGTCTGCGGTATTTGCCACGACGTTGCCATGG 424  
DB 1181 GGGAGACCAACAGACAGAGCGGCTCTGCTGTCTGCTGCGCCCGAGGTTGCCATGG 1240  
  
QY 425 AGATGAAGAGAGCATCAACACAAAAAAGAAGA- --CATGTTCCACAAGATCTACATAC 481  
DB 1241 AGATGAAGCAGACATCAATGCCAGCAGGAGGATGATGTTCATTAAGATTTCATACC 1300  
  
QY 482 AGAAGCATACAATGTGACGATCCTGTGTTGACAGACATGAGGGCTTCCACGAGCTGGCAT 541  
DB 1301 AGAAACATGACAAGTGAAGTCTGTTGCTGACATCGAGGGCTTCAACGAGCTTGCAT 1360  
  
QY 542 CCAGTGCATGCGCAGGAGCTGGTCAATGACCCCTGATGAGCTCTTTGCCCGGTTGACA 601  
DB 1361 CCCAGTGCATGCCAGGAGCTGGTCAATGACGCTCAATGAGCTCTTGCGCCGCTTCGACA 1420  
  
QY 602 AGCTGGCTGGGAGATTCATCTGAGGATCAAGATCAAGATCTTGGGGAGCTGTACTACTGTG 661  
DB 1421 AGCTGGCTGGGAGATTCATCTGTTAGGTATTAAGATCTTGGGGAGTGTATTACTGTG 1480  
  
QY 662 TGTACGGCTGCGGAGGCGCGGACCATGCCACTGCTGTGTGAGATGGGGTAG 721  
DB 1481 TCTCTGGCTGCTGAAAGCAGGCGCGACACGCCACTGCTGCTGAGATGGGCATGG 1540  
  
QY 722 ACATGATTGAGGCCATCTCCCTGGTAGCTGAGGTGACAGGTGGAATGTGAATGGCGG 781  
DB 1541 ACATGATTGAGGCCATCTCCCTGGTAGGAGGTGACAGGGGTGAACGTGAACATGGCGG 1600  
  
QY 782 TGGGCATCCACAGCGGGCGGTGCATCTGCGCGCTCTCTTGGCTTGGGAAATGGCAGTTCG 841  
DB 1601 TGGGAATTCACGCGGGGAGTACATCTGCGGTGTCTCTGTCTCAGGAAGTGGCAGTTCG 1660  
  
QY 842 ATGTGTGTCATATGATGTGACCTTGCCCAACCATGGAAGCAGGAAGCGGGCTGGCC 901  
DB 1661 ACCTCTGGTCTAATGACGTCACTGCGCCCAACCATATGGAAGCTGGAGGCAAGGCTGGGC 1720  
  
QY 902 GCATCCACATCTCGGGCAACACTGCAGTACCTGACGGGGACTACGAAAGTGGAGCCAG 961  
DB 1721 GCATCCACATCACAAAGGCCACACTCAGCTACCTGAACTGAACTGACTAGAGTGGAGCCAG 1780

QY 962 GCGTGTGGCAAGCGCAACGCGTACCTCAAGGAGCAGACATTCAGAGCTTTCCTCATCC 1021  
DB 1781 GCTCGGGGGGAGCGCAACGCTACCTCAAGGAGCAGATTCAGAGCTTTCCTCATCC 1840  
  
QY 1022 TGGGCGCCAGCCAGAAACGAAAGAGAGAGCATGCTGGCCAAAGCTGACGAGGACTC 1081  
DB 1841 TGGCTCACCCAGAGCGGAAAGAAAGAGGCGCATGTCGCCAAGATGAATGCCAGA 1900  
  
QY 1082 GGGCCAACTCCATGGAAGGCGTGTATGCGCGCATGGGTTCCTGATCGTGCCCTTCCCGGA 1141  
DB 1901 GAACCAACTCCATTTGGGCACAACGCCCTGCTGGGGGGCGGAACGCTTCTTACAAAC 1960  
  
QY 1142 CCAAGGACTCCCAAGGCCCTTCGCCAGATGGGCATTTGATTTCCAGCAAAAGACAACCGG 1201  
DB 1961 ACCTAGAGGCAACCAAGGTGTCCAAAGGAGATGAAGCCATGGGCTTCAAGAGCCCCAAG 2020  
  
QY 1202 GCA-----CCCAGATGCCCTGAAACCTGAGGATGAGGTGGATTCCTGAGCCGTG 1255  
DB 2021 ACAAGAAACGCCAGGAAAGTGCGAACCTGAGGATGAAGTGGATGAATTTCTGGGCGCG 2080  
  
QY 1256 CCATCGATGCCCCGACGATTTGATCAGCTGCGGAAGGACCATGTGCGCGGTTTTTGTCTCA 1315  
DB 2081 CCATTGACGCCAGGAGCATCGACAGGCTGCGGTGCGSAGCAGCTCCGCAAGTTCTCTCTGA 2140  
  
QY 1316 CTTTCCAGAGAGAGGATTTTGAGAAAGTACTCCCGAAAGGTGGATCCCGCTTCGGAG 1375  
DB 2141 CTTTCCAGGAGGCTGACTTAGAAAAGAGTACTCCAAAGAGGTGGATACCGATTCGGTG 2200  
  
QY 1376 CTTACGTTGGCTGCGCTGTTGCTTCTGCTTCATCTGCTTCATCCAGAGCTTCTAATTT 1435  
DB 2201 CTTACGTTGGCTGCGCTGCTGCTTCTCTCTTCATCTGCTTGTCCAGATCACCATCG 2260  
  
QY 1436 TCCACACATCCACCTGATGTTGGGATTTATGCCAGCATCTTCCCTGCTGCTGCTAATCA 1495  
DB 2261 TACCCCACTCCGTTTCATGTTGAGTTTCTACTTTGACCTGTTTCTGCTGCTGACGTGG 2320  
  
QY 1496 CCGTGTGATCTGTGCTGTGTACTTCTGTTTCTGTTTCCCTTAAGGCCCTGCAACGTC 1555  
DB 2321 TGGTATTTGTGCTGCTGATCTATTCCTTCGCTGGAAGCTCTTCCCGGGCGCGTCCAGAGCC 2380  
  
QY 1556 TGTCCCGCAGCATTTGCTCCGCTCAGGGCAGACATAGCAGCCGAGTTGGCATCTTTTCCGTCC 1615  
DB 2381 TCTCGAGAAAGATCGTGCCTCCAAAGACCAACAGCAGCCCTGGTGGGGGTGTTCACCATCA 2440  
  
QY 1616 TGCTTGTGTTTACTTCTGCCATTTGCCAACAATGTTTCACTGTAAACCACACCCCATACGA 1675  
DB 2441 CCCTGTTGTTTCTGCTGCGCTTTCGTCACCAATGTTTCACTGTGTAACTCCGAGGACCTGTTGG 2500  
  
QY 1676 GCTGTGACGCCCGGATCTGAATTTTAACACTGCTGACATCACTGCTGCCACCT----- 1730  
DB 2501 GCTGCTGGCGGAGGACACACATCAGCAGCCCGGGTCAACGCGTGCACGTTGGCGG 2560  
  
QY 1731 -GCAGCAGCTCAATTACTCTCTGGGCTGGATGCTCCCTGTTGTGTGAGGGCACCATTGCCCA 1789  
DB 2561 CGTCGGGCGCAACCTCAGCCTGGGCGACGAGCAGGSGCTTCTGCGGCACGCCCTTGGGCCA 2620  
  
QY 1790 CTTGACGCTTTCCTGAGGTGTTTC 1812  
DB 2621 CTTGCAACTTCCCGAGTACTTC 2643

RESULT 12  
AAQ37543  
ID AAQ37543 standard; cdna; 4356 BP.  
XX  
AC AAQ37543;  
XX  
DT 17-JUN-1993 (first entry)  
XX  
DE Cardiac adenylyl cyclase type V gene.  
XX  
KW CACV; therapy; diagnostic; cardiac function; cyclic AMP; cAMP; heart;

failure; ss.  
Canis familiaris.  
Key Location/Qualifiers  
CDS 148..3702  
/\*tag= a  
BP529622-A.  
03-MAR-1993.  
27-AUG-1992; 92EP-0114637.  
29-AUG-1991; 91US-0751460.  
(AMCY ) AMERICAN CYANAMID CO.  
Ishikawa Y, Konaki AF;  
WPI; 1993-068688/09.  
P-PSDB; AAR32882.  
Isolated nucleic acid mol. encoding Cardiac adenylyl cyclase type  
v - useful for determining and modifying cardiac function  
Claim 1; Page 15-27; 38pp; English.  
Left ventricular tissue of canine heart was used as a source of mRNA.  
A cDNA library was prepd. in lambda gt10 phage. A 970 bp Aat-HincII  
fragment from type I adenylyl cyclase cDNA was used as probe. The  
clones isolated were used to obtain cDNA encoding CACV. This probe  
may also be used to screen a human cardiac cDNA library to obtain  
the cDNA encoding human CACV. CACV, its analogues and antibodies  
are useful in therapy or diagnostic assays, e.g. in modifying and  
determining cardiac function. A decrease in CACV content of the  
heart contributes to impaired cAMP prodn. and in heart failure. The  
CACV can also be used to screen for cpds. which stimulate or inhibit  
the activity of the cyclase.  
SQ Sequence 4356 BP; 837 A; 1367 C; 1377 G; 775 T; 0 other;  
Query Match 48.8%; Score 883.4; DB 14; Length 4356;  
Best Local Similarity 68.9%; Pred. No. 7.2e-226;  
Matches 1243; Conservative 0; Mismatches 551; Indels 9; Gaps 2;  
QY 5 ACGTGTGCTGGGCATCCTGGCGGAGTCAGGTGCGGGGCGCTTCGCGAGACCCCG 64  
DB 821 ACGCGCTCATCGCGGTGGTGGCGGTGCAGGTGGTGGGCGCTGCTGCGCCCGAGCCGC 880  
QY 65 GCAGCCCTCTGCGGGCCTCTGCTGCGCTGCTGCTTCTATATACATCGCATACACGCTCC 124  
DB 881 GCAGCGCTCCGAGGCGATCTGGTGACCGTGTCTCTATCTACACCATCTACAGCTGC 940  
QY 125 TCCCCATPCGATGCGGGTGGCGTCTCAGCGGCGTGGCGCTCTCCACCTTGCATTGGA 184  
DB 941 TGCCTGTGCGCATGCGGGCGCGCTCCTCAGCGGAGTGTCTCTGTCGGCCCTGCACCTGG 1000  
QY 185 TCTTGCGCTGGCAACTTACCGTGGTGTATGCTCTCTCTGGAAGCAGCTCGGTGCCAATG 244  
DB 1001 CCATCGCCTTGGCGCGCACGCCCGACCGCGTTCCTGCTCAAGAGCTCGCTCCCAATG 1060  
QY 245 TGTGTGCTGTCTCTGCACCAACGCTATAGCATCTGCACACATATCCAGCAGAGGTGT 304  
DB 1061 TCCCTATTTCTCTGCACCAACATCGTGGGTGTCTGTACCCACTACCCGGCTGAGGTCT 1120  
QY 305 CTCAGCGCGCCCTTTCAGGAGCCCGCAGTTATACATCCAGGCGCGGTCTCCACCTGCAGC 364  
DB 1121 CCAGAGACAGCCCTTCCAAGAGACCGGGAGTGCATCCAGGCGGCTCCACTCGCAC 1180  
QY 365 ATGAGNAATCGGACGAGGCGGCTGCTGCTGCTGGTATTTGCCGACGACGTTGGCATGG 424  
DB 1181 GGGAGAACCAACGAGGAGCGGCTCCTGCTGTCTGCTCTGCTGCGCCGACACGTTGGCATGG 1240

QY 425 AGATGAAGAAGACATCAACACAAAAAAGAGAC---ATGTTCCACAAGATCTACATAC 481  
DB 1241 AGATGAAGACAGACATCAATGCAAGCAGAGAGATATGATGTTCCATAGATTTATCATCC 1300  
QY 482 AGAAGCATGACAATGTTCAGCATCTCTGTTTGCAGACATTTAGGGGCTTTCACCAGCCTGGCAT 541  
DB 1301 AGAAACATGACAACGTGAGCATCTCTGTTGCTGACATCGAGGGCTTCACCAGCTGGCAT 1360  
QY 542 CCCAGTGCAGTGGCAGGAGCTGGTCATGACCTGNAATGAGCTCTTTGGCCCGGTTTGACA 601  
DB 1361 CCCAGTGCAGTGGCAGGAGCTGGTCATGACCTCAATGAGCTCTTCGCCCGCTTCGCACA 1420  
QY 602 AGCTGGCTCGGAGAAATCACTGCTGAGGATCAAGATCTTTGGGGACTCTTACTACTGTG 661  
DB 1421 AGCTGGCTCGGAGAAATCACTGTTTACGTATTAAAGATCTCGGGGATGTTTATTACTGTG 1480  
QY 662 TGTGAGGGCTGCCGAGGCGCGGCGACCATGCCCACTGCTGTGTGGAGATGGGGGTAG 721  
DB 1481 TCTCTGGGCTGCTGAAGCGAGGCGGACACGCCCACTGCTGCGGTGAGATGGGCATGG 1540  
QY 722 ACATGATTGAGGCCATCTGCTGGTACGTGAGGTGACAGGTGTGATGTGAACATGCGCG 781  
DB 1541 ACATGATTGAGGCCATCTGCTGGTCCGGGAGGTGACAGGGGTGAACGTGAACATGCGCG 1600  
QY 782 TGGGCATCCACAGCGGCGCTGCACTGCGGCGCTCTTGGCTTGGGAAATGCGAGTTCCG 841  
DB 1601 TGGGAATTCACAGCGGCGGAGTACACTGCGGTGCTCTGCTCAGGAAGTGGCAGTTCCG 1660  
QY 842 ATGTGTGTGTCATGATGTGACCTGGCGCAACACATGGAAGCAGGAAGCCGGGTGGCC 901  
DB 1661 AGGTCTGTGTTTATGACGTACGCTGCGGCAACCATATGGAAGCTGGAGCAAGGCTGGGC 1720  
QY 902 GCATCCACATCACTCGGCAACACACTGCAGTACTGACCGGGGACTACGAAGTGGAGCCAG 961  
DB 1721 GCATCCCAATCAACAGGCCACACTGAGTACTGAAACGGTACTACGAGGTGGAGCCAG 1780  
QY 962 GCGGTGTGGCAAGCGCAACGCGTACTCAAGGAGCAGCAGCATTTGAGACTTTCCCTCATCC 1021  
DB 1781 GCTGCGGGGCGAGCGCAACGCTACCTCAAGGAGCAGCATATCGAGACCTTCTTCATCC 1840  
QY 1022 TGGGCGCCAGCAGAAACGGAAGAGGAAAGGATGCTGGCCAAGTGCAGCGGACTC 1081  
DB 1841 TCGCGTGCACCCAGAGCGAAAGAAAGAGGACCATGATCGCCAGATGAATTCGCGAGA 1900  
QY 1082 GGGCAACTCCATGGAAGGCTGATGCGCGGATGGTTCCTGATCGTCTCTCCCGGA 1141  
DB 1901 GAACCAACTCCATTTGGGCACAACCCGCCCACTGGGGGGCCGAACGCTCCCTCTACAACC 1960  
QY 1142 CCAAGGACTTCCAAAGGCTTCCCGCCAGATGGGCAATTGATTTCCAGCAAGACAACCGGG 1201  
DB 1961 ACCTAGGAGGCAACCAAGGTGTCCAAGGAGATGAAGCGCATGGCTTCGAAGACCCCAAG 2020  
QY 1202 GCA-----CCCAAGATGCCCTGAACCCCTGAGAGATGAGTGGATGATTCCTGAGCGGTG 1255  
DB 2021 ACAAGAACCCCAAGAAAGTGCAGAACCCCTGAGGATGAAGTGGATGAATTTCTTGGCGCG 2080  
QY 1256 CCATGATGCCCGCAGCATTGATCAGTTCGCGAAGGACCATGTCGCCCGGTTTTTCTCA 1315  
DB 2081 CCATTGACCCAGGAGCATATCGACAGCTGCGGTGCGAGCAGCTGCGCAAGTTCTCCCTGA 2140  
QY 1316 CTTTCAGAGAGAGGATTTTGAGAAAGTACTCTCCGGAAGTGGATCCCGCTCCGGAG 1375  
DB 2141 CTTTCAGGAGGCTGACTTAGAAAGAGTACTTCAAGCAGGTGGATGACCATTCGGTG 2200  
QY 1376 CTTACGTTGCGCTGCGCTGTTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTCTAAATTT 1435  
DB 2201 CTTACGTSAGTGTGCTGCGTGTCTTCTCTCTTCTATCTGCTTTGTCAGATCACCATCG 2260  
QY 1436 TCCACACTCCACCTGATGCTTGGGATTTATGCCAGCATCTTCTCTGCTGCTGCTTAATCA 1495  
DB 2261 TACCACCTCCGTTGTCATGTTGAGTTTCTACTTGACCTGTTTCTCTGCTGCTGACGTTGG 2320





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QY 842 ATGTGTGGTCCAAATGATGTGACCCCTGGCCAAACACACATGGAAGACGAGCCGGGCTGGCC 901
Db 1261 AGTGTGGTCTAACGATGTACACTGGCCAAACACACATGGAAGCTGGCGCAAGGCGCC 1320
QY 902 GCATCCACATCACTCGGCAACACTGCGAGTACCTGAACGGGACTACGAAGTGGAGCCAG 961
Db 1321 GCATCCACATCACTCAAGGCCACACTCAACTACTGAACGGGACTATGAGTGGAGCCAG 1380
QY 962 GCGGTGGTGGCAAGGCAACGGGTACCTCAAGGAGCAGCACATTCAGACTTTCCTCATCC 1021
Db 1381 GCTGTGGTGGTGGCGCATGCTCACTCAAGGAGCAGACATCGAGACCTTCCTCATCC 1440
QY 1022 TGGGGCCCAAGCAGAAACGGAAGAGGAGAAAGGATGCTGCGCCAGCTGCGAGCGAGCTC 1081
Db 1441 TCGCGTGTACCCAGAGCGGAAGAAGAGAGAGGCGCATGATCGCCAAAGATGAACCGCCAGA 1500
QY 1082 GGGCCAACTCCATGGAAGGCTGATGCGCGGATGGTTCCTGATCGTGGCTTCTCC --- 1137
Db 1501 GAACCAACTCCATTTGGACACAATCGCCCTCACTGGGGAGCTGAGCGCCCTTCTTACAACC 1560
QY 1138 -----CGGACCAAGGACTCCAAGGCCCTTCGGCCAGATGGGCATTTGATGATTCAGCA 1189
Db 1561 ACTTGGTGGCAACACAGGTGTCCAGGAATGAAGAGATGGGCTTGAGGACCCCA --- 1617
QY 1190 AAGACAACCGGGGACCCCAAGATGCCCTGAACCCCTGAGGATGAGTGGATGCTCTGA 1249
Db 1618 ---AGGACAAGAATGCCAGGAAGTGCACACCTTGAGGATGAAGTGGACGAGTTCTGG 1674
QY 1250 GCGGTGCCATCAGTCCCGCCAGCATGATCAGCTGCGGAGGAGCAACATGTGCGCCGGTTT 1309
Db 1675 GTCGAGCCATCAGTCCAGGAGTATTTGACAGACTGCGATCCGAACACGCTCCGAAAGTTCC 1734
QY 1310 TGTCTACCTTCCAGAGAGAGATTTTGAGAAGATFACCTCCGGAAGTGGATCCCGCT 1369
Db 1735 TCTTGACCTTTAGGAGCCCGACTTAGAGAGAAGATCTCCAGCAGGTGGATGACCGAT 1794
QY 1370 TCGGAGCCPACGTTGCGCTGCGCTGTTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTC 1429
Db 1795 TTGGTGCCTATGTGGCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1854
QY 1430 TAATTTCCACACATCCACCTTGATGCTGGGATTTATGCCAGCATCTCTCTGCTGCTGCT 1489
Db 1855 CCATTTGCGCCACATCCCTGTTTCATGCTGAGCTTCTACCTGCTGCTGCTGCTGCTGCTGCT 1914
QY 1490 TAATCACCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1549
Db 1915 CCTTGGTGGTGTATATCTGTGATCTAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1974
QY 1550 AAGCTGTCTCCGAGCATTTCCGCTCAGGGCAGATAGCAGCCAGTTGGCATCTTTT 1609
Db 1975 AGACACTCTCCAGGAAGATGTGCGATCCAGGAAGAACACACCCCTGGTGGGTTTCA 2034
QY 1610 CGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1669
Db 2035 CCATCACCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2094
QY 1670 TACGGAGCTGTGCAAGCCCGGATGCTGAATTTAACACCTGCTGACATCACTGCTGCTGCTGCT 1729
Db 2095 TGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 2154
QY 1730 TGCAGCAG-----CTCAATTAATCTCTGGGCTGGATGCTCCCTGTGTGAGGCGACCA 1783
Db 2155 TGATGAGTTCGGGCTTCAACTACAGCCTGGGCGAGCAGGAGGCTTCTGTGGCAGCGCCC 2214
QY 1784 TGGCCACCTGCACTTCTCTGAGGTGTC 1812
Db 2215 AGTCCAATGCACTTCCAGAGTACTTC 2243
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RESULT 14  
AAD28058  
ID AAD28058 standard; cDNA; 3137 BP.  
XX

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AC AAD28058;  
XX  
DT 22-APR-2002 (first entry)  
XX  
DE Human adenylyl and guanylyl cyclase (ADGUC)-2 cDNA.  
XX  
KW Human; adenylyl and guanylyl cyclase; ADGUC-2; cardiovascular disorder;  
KW angina pectoris; myocardial infarction; vision disorder; keratitis;  
KW iritis; cataract; neurological disorder; epilepsy; Alzheimer's disease;  
KW Pick's disease; stroke; mental disorder; mood and anxiety disorder;  
KW reproductive disorder; infertility; endometriosis; impotence; asthma;  
KW smooth muscle disorder; migraine; bacterial infection; gene therapy;  
KW transgenic animal; vaccine; enzyme; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..2514  
FT /tag= a  
FT /product= "Human ADGUC-2 protein"  
FT  
XX WO200202757-A2.  
XX  
PD 10-JAN-2002.  
XX  
XX 26-JUN-2001; 2001WO-US20491.  
XX  
PR 29-JUN-2000; 2000US-215476P.  
PR 04-AUG-2000; 2000US-223545P.  
PR 31-AUG-2000; 2000US-229876P.  
PR 22-SEP-2000; 2000US-234838P.  
PR 29-SEP-2000; 2000US-236483P.  
XX  
XX (INCY-) INCYTE GENOMICS INC.  
XX  
PI Gandhi AR, Tribouley C, Ding L, Lu DAM, Lee EA, Yue H, Yang J;  
PI Baughn MR, Thornton M, Yao MG, Walla NK, Tang YT, Elliott VS;  
PI Lu Y;  
XX  
XX WPI; 2002-154740/20.  
XX P-PSDB; AAE17130.  
XX  
XX Novel human adenylyl and guanylyl cyclases and polynucleotides encoding  
XX the cyclases, useful for treating, diagnosing or preventing  
XX cardiovascular, neurological, vision, reproduction and smooth muscle  
XX disorders  
XX  
XX Claim 5; Page 112-113; 116pp; English.  
XX  
XX The invention relates to human adenylyl and guanylyl cyclases (ADGUC)  
XX preferably ADGUC1-ADGUC5 and nucleic acid molecules encoding such  
XX polypeptides. ADGUC sequences are useful in the diagnosis, prevention  
XX and treatment of cardiovascular disorders (e.g. angina pectoris,  
XX myocardial infarction, ischaemic heart disease, hypertension and  
XX atherosclerosis), vision disorders (e.g. keratoconjunctivitis sicca,  
XX keratitis, iritis, cataract), neurological disorders (e.g. epilepsy,  
XX Alzheimer's disease, Pick's disease, Huntington's disease, dementia,  
XX Parkinson's disease, Creutzfeldt-Jakob disease, stroke, schizophrenia,  
XX mental disorders including mood and anxiety and prion diseases including  
XX kuru), reproductive disorders (e.g. infertility, endometriosis,  
XX impotence, uterine fibroid and gynaecomastia), smooth muscle disorders  
XX (e.g. arrhythmias, asthma and migraine) and bacterial infections.  
XX ADGUC polynucleotides are useful for creating knock-in humanised animals  
XX or transgenic animals to model human diseases. They are useful in  
XX somatic or germline gene therapy. ADGUC polynucleotides are also useful  
XX for detecting differences in the chromosomal location due to  
XX translocation, inversion, etc. among normal, carrier or affected  
XX individuals. ADGUC polypeptides are useful in a number of drug screening  
XX techniques and in vaccines. The present sequence is human ADGUC-2 cDNA.  
XX  
SQ Sequence 3137 BP; 553 A; 973 C; 1044 G; 567 T; 0 other;
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Query Match

44.1%; Score 799; DB 24; Length 3137;

Best Local Similarity 73.5%; Pred. No. 2.4e-203;			Matches 1069; Conservative 0; Mismatches 365; Indels 21; Gaps 3;		
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QY	722	ACATGATTGAGGCATCTCGCTAGCTGAGGTGACAGGTGCAATGTGAACATGCGC	781		
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QY	842	ATGTGTGTCATATGATGTACCTTGCCCAACCATCTGGAAGCAGGAAGCGGCTGGCC	901		
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QY	1310	TGCTCACCTTCCAGAGAGAGGATTTTGAAGAAGTACTCCCGGAAGTGGATCCCGCT	1369		
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XX	DT 26-MAR-2002 (first entry)				
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XX	Drosophila; developmental biology; cell signalling; insecticide;				
XX	pharmaceutical; gene; ss.				
XX	Drosophila melanogaster.				
XX	W0200171042-A2.				
XX	27-SEP-2001.				
XX	23-MAR-2001; 2001WO-US09231.				
XX	23-MAR-2000; 2000US-191637P.				
XX	11-JUL-2000; 2000US-0614150.				
XX	(PEKE ) PE CORP NY.				
XX	Venter JC, Adams M, Li PWD, Myers EW;				
XX	WPI; 2001-656860/75.				
XX	P-PSDB; ABB63398.				
XX	New isolated nucleic acid detection reagent for detecting 1000 or more				
XX	genes from Drosophila and for elucidating cell signalling and cell-cell				
XX	interactions -				
XX	Claim 1; SEQ ID NO 16985; 21pp + Sequence Listing; English.				
XX	The invention relates to an isolated nucleic acid detection reagent				
XX	capable of detecting 1000 or more genes from Drosophila. The invention is				
XX	useful in developmental biology and in elucidating cell signalling and				
XX	cell-cell interactions in higher eukaryotes for the development of				
XX	insecticides, therapeutics and pharmaceutical drugs. The invention				

CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
CC sequences (ABL01840-ABL16175) and the encoded proteins  
CC (ABB57737-ABB27072).  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences).

SQ Sequence 4827 BP; 1115 A; 1377 C; 1340 G; 995 T; 0 other;

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Best Local Similarity 24.6%; Score 445.8; DB 23; Length 4827;									
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QY	707	TGAGATGGGGTGTAGACATGATTGAGGCCATCTCGCTGCTACGTGAGTGACAGTCTGA	766						
DB	1907	TCGAATGGGACTCGATATGTTGACCCATCGCACTGTTTCGGGAAGTGTGCGCGTGA	1966						
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GenCore version 5.1.3  
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14: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
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## SUMMARIES

Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	1812	100.0	1812	10	US-09-750-240-3		Sequence 3, Appli
2	1808.4	99.8	3549	10	US-09-750-240-5		Sequence 5, Appli
3	1763.4	97.3	3552	10	US-09-750-240-10		Sequence 10, Appli
4	1763	97.3	4942	9	US-10-201-000-1		Sequence 1, Appli
5	1657.8	91.5	3582	10	US-09-750-240-12		Sequence 12, Appli
6	895	49.4	4523	9	US-10-175-158-1		Sequence 1, Appli
7	319.4	17.6	2601	10	US-09-925-297-352		Sequence 352, App
8	284	15.7	3518	9	US-10-131-911-2		Sequence 2, Appli
9	216.8	12.0	4473	10	US-09-751-100B-1		Sequence 1, Appli
10	209.4	11.6	4985	12	US-10-071-223-1		Sequence 1, Appli
11	207.8	11.5	5515	10	US-09-751-100B-98		Sequence 98, Appli
12	124.4	6.9	330	9	US-09-764-868-182		Sequence 182, App
13	124.4	6.9	330	9	US-09-989-442-71		Sequence 71, Appli
14	124.4	6.9	330	10	US-09-764-869-445		Sequence 445, App
15	79.2	4.4	11881	9	US-09-764-868-1351		Sequence 1351, Ap
16	79.2	4.4	11881	9	US-09-764-868-1353		Sequence 1353, Ap
17	79.2	4.4	11881	10	US-09-764-869-2124		Sequence 2124, Ap
18	64.4	3.6	1259	9	US-10-051-643-123		Sequence 123, App
19	64.4	3.6	1259	9	US-09-880-505-123		Sequence 123, App

## ALIGNMENTS

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RESULT 1
US-09-750-240-3
; Sequence 3, Application US/09750240
; Patent No. US20020103147A1
; GENERAL INFORMATION:
; APPLICANT: Hammon, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; FILE OF INVENTION: FAILURE
; FILE REFERENCE: 220002036723
; CURRENT APPLICATION NUMBER: US/09/750,240
; CURRENT FILING DATE: 2001-10-12
; PRIORITY APPLICATION NUMBER: US 09/472,667
; PRIORITY FILING DATE: 1999-12-27
; PRIORITY APPLICATION NUMBER: US 09/008,097
; PRIORITY FILING DATE: 1998-01-16
; PRIORITY APPLICATION NUMBER: US 08/924,757
; PRIORITY FILING DATE: 1997-09-05
; PRIORITY APPLICATION NUMBER: US 60/048,933
; PRIORITY FILING DATE: 1997-06-16
; PRIORITY APPLICATION NUMBER: US 08/708,661
; PRIORITY FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
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; LENGTH: 1812
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-750-240-3

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; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
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; ORGANISM: Homo sapiens  
US-09-750-240-5

Query Match 99.8%; Score 1808.4; DB 10; Length 3549;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1809; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY	63	GCCAGCGCCCTCTGCGGGCTCTGGTCCCTGTGTTCTTGTATACATCCATACAGCT	122
DB	696	GCCAGCGCCCTCTGCGGGCTCTGGTCCCTGTGTTCTTGTATACATCCATACAGCT	755
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DB	756	CTCTCCCATCCGATCGGGCTCCGCTCTCTCAGCGGCTGGGCTCTCTCCACCTTGCATT	815
QY	183	GATCTTGGCTGGCACTTAACCGTGGTGATGCTTCTCTGGAAGCAGCTCGGTGCCAA	242
DB	816	GATCTTGGCTGGCACTTAACCGTGGTGATGCTTCTCTGGAAGCAGCTCGGTGCCAA	875
QY	243	TGTGCTGCTTCTCTCTGCAACCACTGATAGCATCTGCACACATATCCACAGAGT	302
DB	876	TGTGCTGCTTCTCTCTGCAACCACTGATAGCATCTGCACACATATCCACAGAGT	935
QY	303	GTCTCAGCGCAGGCTTTTCAGAGAGCCGAGTTACATCCAGCGCGGCTCCACCTGCA	362
DB	936	GTCTCAGCGCAGGCTTTTCAGAGAGCCGAGTTACATCCAGCGCGGCTCCACCTGCA	995
QY	363	GCATGAGATCGCAGAGCGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	422
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QY	1263	TGCGCGCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1322
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QY	1383	TGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1442
DB	2016	TGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2075
QY	1443	CTCCACCCCTGATGCTGGGATTTATGCCAGCATCTTCTGCTGCTGCTGCTGCTGCTGCTG	1502
DB	2076	CTCCACCCCTGATGCTGGGATTTATGCCAGCATCTTCTGCTGCTGCTGCTGCTGCTGCTG	2135
QY	1503	GATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1562
DB	2136	GATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2195
QY	1563	CAGCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1622
DB	2196	CAGCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2255
QY	1623	GTTTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1682
DB	2256	GTTTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2315
QY	1683	AGCCCGGATGCTCAATTTAAACCTGCTGACATCACTGCTGCTGCTGCTGCTGCTGCTGCTG	1742
DB	2316	AGCCCGGATGCTCAATTTAAACCTGCTGACATCACTGCTGCTGCTGCTGCTGCTGCTGCTG	2375
QY	1743	TTACTCTCTGCGGCTGGATGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1802
DB	2376	TTACTCTCTGCGGCTGGATGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2435
QY	1803	TGAGGTGTTT 1812	
DB	2436	TGAGGTGTTT 2445	

RESULT 3  
US-09-750-240-10  
; Sequence 10, Application US/09750240  
; Patent No. US20020103147A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammon, H. K.  
; APPLICANT: Insel, P. A.  
; APPLICANT: Ping, P.  
; APPLICANT: Post, S. R.  
; APPLICANT: Gao, M.









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Db 2342 GCAGCATGTCGCTCACGGGCACATAGACCGCAGTTGGCATCTTTTCGCTCCTGTTG 2401
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QY 1622 TGTGTTACTTCTGCAATGCAACATGTTACCTGTAAACACACCCCCATACGAGCTGTG 1681
      |||
Db 2402 TGTGTTACTTCTGCAATGCAACATGTTACCTGTAAACACACCCCCATACGAGCTGTG 2461
      |||
QY 1682 CAGCCCGGATGCTGAATTTAAACACCTGCTGACATCACTGCTGCCACCTGCAGCAGCTCA 1741
      |||
Db 2462 CAGCCCGGATGCTGAATTTAAACACCTGCTGACATCACTGCTGCCACCTGCAGCAGCTCA 2521
      |||
QY 1742 ATTACTCTCTGGCCTGGATGCTCCCTGTGTGAGGGCAGCATGCCACCTGCGAGCTTTC 1801
      |||
Db 2522 ATTACTCTCTGGCCTGGATGCTCCCTGTGTGAGGGCAGCATGCCACCTGCGAGCTTTC 2581
      |||
QY 1802 CTGAGGTGTTCT 1812
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Db 2582 CTGAGTACTTCT 2592
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RESULT 5
US-09-750-240-12
: Sequence 12, Application US/09750240
: Patent No. US20020103147A1
: GENERAL INFORMATION:
: APPLICANT: Hammon, H. K.
: APPLICANT: Insel, P. A.
: APPLICANT: Ping, P.
: APPLICANT: Post, S. R.
: APPLICANT: Gao, M.
: TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
: TITLE OF INVENTION: FAILURE
: FILE REFERENCE: 220002056723
: CURRENT APPLICATION NUMBER: US/09/750,240
: CURRENT FILING DATE: 2001-10-12
: PRIOR APPLICATION NUMBER: US 09/472,667
: PRIOR FILING DATE: 1999-12-27
: PRIOR APPLICATION NUMBER: US 09/008,097
: PRIOR FILING DATE: 1998-01-16
: PRIOR APPLICATION NUMBER: US 08/924,757
: PRIOR FILING DATE: 1997-09-05
: PRIOR APPLICATION NUMBER: US 06/048,933
: PRIOR FILING DATE: 1997-06-16
: PRIOR APPLICATION NUMBER: US 08/708,661
: PRIOR FILING DATE: 1996-09-05
: NUMBER OF SEQ ID NOS: 13
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 12
: LENGTH: 3582
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Modified AC-VI
US-09-750-240-12

Query Match 91.5%; Score 1657.8; DB 10; Length 3582;
Best Local Similarity 95.4%; Pred. No. 0;
Matches 1730; Conservative 0; Mismatches 77; Indels 6; Gaps 2;

QY 3 TAACTGTGTGCTGGGATCCTGGCGGAGTCAGGTGCGGGGCGCTTCGCGAGCAGACC 62
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Db 657 TTACGTGTGTGCTGGGATCCTGGCGGAGTCAGGTGCGGGGCGCTTCGCGAGCAGACC 716
      |||
QY 63 GCGCAGCCCTCTGCGGGCTCTGTGTCCTGTGTTCTTTGTATACATCGCATACACGCT 122
      |||
Db 717 GCGCAGCCCTCTGCGGGCTCTGTGTCCTGTGTTCTTTGTATACATCGCATACACGCT 776
      |||
QY 123 CTTCCCATCCGATCGGGCTGCCCTCTCAGCGGCTTGGGCTCTCCACCTTGCATTT 182
      |||
Db 777 CTTCCCATCCGATCGGGCTGCCCTCTCAGCGGCTTGGGCTCTCCACCTTGCATTT 836
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QY 183 GATCTGGCTGGCACTTAACTGGGTGATGCTTCTCTGGAAGCAGCTCGGTGCCAA 242
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Db 837 GATCTGGCCTGGCACTTAAACCGTGGTGATGCTTCTCTGGAAGCAGCTCGGTGCCAA 896
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QY 243 TGTGCTGCTGTTCTCTGCAACACGTCTATTAGCATCTGCACACATATATCCAGCAGAGT 302
      |||
Db 897 TGTGCTGCTGTTCTCTGCAACACGTCTATTAGCATCTGCACACATATATCCAGCAGAGT 956
      |||
QY 303 GTCTCAGCCCGAGGCTTTTTCAGGAGACCGCAGTTACATCCAGGCGCGCTCCACCTGCA 362
      |||
Db 957 GTCTCAGCCCGAGGCTTTTTCAGGAGACCGCAGTTACATCCAGGCGCGCTCCACCTGCA 1016
      |||
QY 363 GCATGAGAAATCCGACAGGAGGCGCTGCTGTCGGTATTGCCCCACAGCTTCCCAT 422
      |||
Db 1017 GCATGAGAAATCCGACAGGAGGCGCTGCTGTCGGTATTGCCCCACAGCTTCCCAT 1076
      |||
QY 423 GGAGATGAAGAAGACATCAACACAAAAAAGAAAGAC --- ATGTTCCACAAGATCTACAT 479
      |||
Db 1077 GGAGATGAAGAAGACATCAACACAAAAAAGAAAGACATGATGTTCCACAAGATCTACAT 1136
      |||
QY 480 ACAGAAGCATGACAATGTGAGCATCTCTGTTTGCAGACATTTGAGGGCTTCCACAGCTGCG 539
      |||
Db 1137 ACAGAAGCATGACAATGTGAGCATCTCTGTTTGCAGACATTTGAGGGCTTCCACAGCTGCG 1196
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QY 540 ATCCAGTGCCTGCGCAGGAGCTGTCATGACCCCTGAATGAGCTCTTTGCCCGGTTTGA 599
      |||
Db 1197 ATCCAGTGCCTGCGCAGGAGCTGTCATGACCTTGAATGAGCTCTTTGCCCGGTTTGA 1256
      |||
QY 600 CAAGCTGGCTCGGAGAAATCACTGCTGAGGATCAAGATCTTTGGGGAGCTGTTACTACTG 659
      |||
Db 1257 CAAGCTGGCTCGGAGAAATCACTGCTGAGGATCAAGATCTTTAGGAGACTGTTACTACTG 1316
      |||
QY 660 TGTGTCAGGGCTGCGGAGGCGCCGCGCCACCATGCCCCACTGCTGTGTGGAGATGGGGT 719
      |||
Db 1317 CGTGTGAGGGCTGCGGAGGCGCCGCGCCACCATGCCCCACTGCTGTGTGGAGATGGGGT 1376
      |||
QY 720 AGACATGATGAGGGCTGCTGCTGAGTGTGAGGTGACAGTGTGAATGTGAACATGCG 779
      |||
Db 1377 AGACATGATGAGGGCTGCTGCTGAGTGTGAGGTGACAGTGTGAATGTGAACATGCG 1436
      |||
QY 780 CGTGGGCATCCACAGCGGCGCTGACCTGCGGCGCTTCTGCTTCCGAAATGCGAGTT 839
      |||
Db 1437 TGTGGCATCCACAGCGGCGCTGACCTGCGGCGCTTCTGCTTCCGAAATGCGAGTT 1496
      |||
QY 840 CGATGTGTGCTCAATGATGTGACCTTGGCCCAACACATGGAAGCAGGAGCGCGGCTGCG 899
      |||
Db 1497 TGATGTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1553
      |||
QY 900 CCGCATCCACATCACTGCGGCGCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 959
      |||
Db 1554 GCGCATCCACATCACTGCGGCGCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 1613
      |||
QY 960 AGGCGTGTGTCGCAAGCGCAACGCTGACCTCAAGGAGCAGCAGCTTACAGCTTCTCTCAT 1019
      |||
Db 1614 AGGCGTGTGTCGCAAGCGCAACGCTGACCTCAAGGAGCAGCAGCTTACAGCTTCTCTCAT 1673
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QY 1020 CTTGGCGCCAGCCAGAAACGGAAGAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1079
      |||
Db 1674 ACTTGGCGCCAGCCAGAAACGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1733
      |||
QY 1080 TCGGGCAACTCCATGGAAGGCTGATGCCGCGATGGGTTCCTGATGCTGCTTCTCCCG 1139
      |||
Db 1734 ACGGGCAACTCCATGGAAGGCTGATGCCGCGCTGGGTTCCTGATGCTGCTTCTCCCG 1793
      |||
QY 1140 GACCAAGGACTCCAAGGCTTCCGCGAGATGGCAGATTTGATGATTTCCAGCAAGAACACCG 1199
      |||
Db 1794 GACCAAGGACTCCAAGGCTTCCGCGAGATGGCAGATTTGATGATTTCCAGCAAGAACACCG 1853
      |||
QY 1200 GGGCAGCCCAAGATGCCCTGAACCTTGAAGATGAGTGTGATGATGATGATGATGATGATG 1259
      |||
Db 1854 GGGTGCACCAAGATGCTCTGAACCTTGAAGATGAGTGTGATGATGATGATGATGATGATG 1913
      |||
QY 1260 CGATGCGCGCAGCATGATGACCTGCGGGAAGGAGCAGCTGTCGCGCGGCTTTTCTCACCTT 1319
      |||
Db 1914 CGATGCGCGCAGCATGATGACCTGCGGGAAGGAGCAGCTGTCGCGCGGCTTTTCTCACCTT 1973
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Db 2126 GAACCAACTCCATCGGCGCAACCAACCACTGGGGGCTGAGCGCCCTTCTACAACC 2185  
QY 1138 -----CGACCAAGGACTCCAAAGCCCTTCGCCAGATGGGCATTGATGATTCAGCA 1189  
Db 2186 ACCTGGGTGCAACACAGGTCTCCAGAGATGAAGCGGATGGGCTTTGAAGACCCCA--- 2242  
QY 1190 AAGACAACCGGGACCCACAGATGCCCTGAACCCCTGAGGATGAGTGGATGCTCTGA 1249  
Db 2243 ---AGGACAAGAAGCCCGAGGAGTGCGAACCCCTGAGGATGAAGTGGATGCTTCTGG 2299  
QY 1250 GCCGTGCCATCGATGCCCGCAGCAATTCATCAGCTGCGGGAAGGACCATGTGCGCGGTTT 1309  
Db 2300 GCCGTGCCATTCAGCGCAGAGCAATTCATGAGCTTCGGTCTGAGCAGCTCCGCAAGTTC 2359  
QY 1310 TGCTCACTTCCAGAGAGAGGATTTTGAAGAAGTACTCCCGAAGGTGGATCCCGCT 1369  
Db 2360 TCGTGACCTTCAGGGAGCTTGACTTAGAGAAGAGTACTCCAAGCAGGTAGAGACCGAT 2419  
QY 1370 TCGGAGCTACGTTGCTGTGCCCTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1429  
Db 2420 TTGGTGCTATGTGGCTGTGCTCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2479  
QY 1430 TAATTTTCCCACTACACCTGATGCTTGGGATTTATGCCAGCATCTTCTCTGCTGCTGC 1489  
Db 2480 CCATCGTCCCACTCCATATTCATGCTCAGCTTCTACCTGACCTGTTCCTGCTGCTGA 2539  
QY 1490 TAATCACCGTGTGATCTGTGCTGTGCTACTCTCTGCTGCTCTCTCTCTCTCTCTCT 1549  
Db 2540 CTTGGTGGTGTGTGCTGTGATCTACTCTCTGCTGCTCTCTCTCTCTCTCTCTCTCT 2599  
QY 1550 AACGCTGTGCCGAGCATGTCCGCTCAGCGGCACATAGCAGCCGAGTTGGCATCTTT 1609  
Db 2600 AGACCTCTCCAGGAAGCTGCGGTCCCAAGATGAACAGCACCTGGTGGGTGTCTCA 2659  
QY 1610 CCCTCTCTGCTGTGTTTACTTTCGCAATTCGCAACATGTTACCTGATTAACCAACCCCA 1669  
Db 2660 CCATACCTCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2719  
QY 1670 TAGCGAGCTGTGCGACCGGATGCTGAATTTAACAATGCTGATGATGCTGCTGCTGCT 1729  
Db 2720 TGTGTGGCTGTGGCACAGGACACACATACAGCCGAGCCAGGTCAAGCGTGTACG 2779  
QY 1730 TGACGAG-----CTCAATTAATCTCTGGGCTGGATGCTCCCTGTGTGAGGGCACCA 1783  
Db 2780 TGGCGAGTGGCGGCTCAACTACAGCTGGGCGATGAGCAGGGCTTCTGTGGCAGCCCT 2839  
QY 1784 TGCCCACTGCGAGCTTCTCTGAGGTCTC 1812  
Db 2840 GGCCCAACTGCAACTTCCCGGAGTACTTC 2868

RESULT 7  
US-09-925-297-352  
; Sequence 352, Application US/09925297  
; Patent No. US200081659A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA105  
; CURRENT APPLICATION NUMBER: US/09/925,297  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05989  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 928  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 352  
; LENGTH: 2601  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:

; NAME/KEY: misc feature  
; LOCATION: (2520)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (2572)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-925-297-352  
  
Query Match 17.6%; Score 319.4; DB 10; Length 2601;  
Best Local Similarity 64.5%; Pred. No. 3.2e-76;  
Matches 515; Conservative 0; Mismatches 271; Indels 13; Gaps 2;  
  
QY 294 AGCAGAGGTGTCTCAGCGCCAGGCTTTTCAGGAGACCCGAGTTATCATCCAGGCCCGCT 353  
Db 34 AACAGCCGCAAGCAGCCGAAGCCCTTCCTGGAGGCCGCCAGCTCGCTGGAGGTGAAGT 93  
QY 354 CCACCTGCGAGCATGAGAATCGGCGAGGAGCGGCTGTGCTGTGCTGTGCTGTGCTGTGCT 413  
Db 94 GAACCTTGGAGAGAGCAGCGCAGCAGCAGGAGAACCTTCATGCTTTCCATCTCTGCCCAAGCA 153  
QY 414 CGTTGCCATGGAGATGAAGAAGACATCAACACA-----AAAAAAGAACACAT 461  
Db 154 CGTGGCTGAGGATGCTGAAGACATGAAGAAGAGAGAGCCAGAGCCAGCAGCA 213  
QY 462 GTTCCACAAGATCTACATACAGAAGCATGACAAATGTGACGATCCTGTTTGCAGACATTGA 521  
Db 214 GTTCAACACCATGATACATGTACCGTCAAGAGAACGTGACGATCCTCTTTGCCGACATCGT 273  
QY 522 GGGCTTCACGAGCTGGGATCCAGTGCAGTGCAGTGCAGGAGGAGTGGTGCATGACCTGATGA 581  
Db 274 GGGCTTTACCCAGCTGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 333  
QY 582 GCTCTTTGCCCGTGTGACAAGCTGCTGCGGAGAACTCACTGCTCAGGATCAAGATCTT 641  
Db 334 GCTCTTTGCCCGTGTGACAAGCTGCGAGCTGAATACCCAGCTGCGGATTAAGATCCT 393  
QY 642 GGGGAGCTGTTACTACTGTGTGTCAGGGGTGCGGAGGCCCGGCGCAGCACCACCTGCTG 701  
Db 394 GGGCGAGTGTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 453  
QY 702 CTGTGTGAGATGGGGGTAGACATGATTGAGGCCATCTGCTGTGCTGCTGCTGCTGCTGCTG 761  
Db 454 CTCCATCTCTCATGGGCTGGCCATGTGTGAGGCCATCTGCTGTGCTGCTGCTGCTGCTGCTG 513  
QY 762 TGTGAATGTGAACATCGCGTGGGCATCCACAGCGCGCGCTGCATCTGCGGCGCTCTTGG 821  
Db 514 GACTGGGTGGACATCGCTGTGGGGTGCACACGCGGACCGCTGCTGGGGGCTGCTGCTGG 573  
QY 822 CTTGCGGAAATGGCAGTTTCGATGTGTGTCCTCAATGATGTGACCTTGGCCAAACACATGGA 881  
Db 574 CCAGAAAGCGCTGGCAGTAGACGCTGTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 633  
QY 882 AGCAGAAAGCGGCTGGCGGCATCCACATCACTCCGGGCAACACTGCAGTACTGACCG 941  
Db 634 GCGCGGCGCATCCCTTGGGCGGTGCACATCTCCAGAGACCATGGATGCTGCTGAAAGG 693  
QY 942 GGACTACGAAGTGGAGCCAGGCGGTGGCAAGCCCAACCGCTCACTCAAGGAGCAGCA 1001  
Db 694 GGAGTTGATGTGGAGCCAGGCGATGGGCGCAGCCCTGTGATTAACCTAGAGAGAAGG 753  
QY 1002 CATTGAGACTTTCCTCATCTCTGGGCGCC-AGCCAGAAAGGAAAGAGAGAAAGGATGC 1060  
Db 754 TATTGAACCTTACCTCATCTATTGCTTCCAAAGCCAGAGGTGAGAAACAGCCACCCAGAA 813  
QY 1061 TGCCCAAGCTGCAGCGGAC 1079  
Db 814 TGCCCTCAATGCTCGGCC 832

RESULT 8  
US-10-121-911-2  
; Sequence 2, Application US/10121911  
; Patent No. US20020164632A1

```

: GENERAL INFORMATION:
: APPLICANT: Kapeller-Libermann, Rosana
: TITLE OF INVENTION: 21529, A NOVEL ADENYLATE CYCLASE
: FILE REFERENCE: 5800-47
: CURRENT APPLICATION NUMBER: US/10/121.911
: PRIOR FILING DATE: 2002-04-12
: PRIOR APPLICATION NUMBER: US/09/412,210
: PRIOR FILING DATE: 1999-10-05
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 3518
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (0)...(0)
: OTHER INFORMATION: 21529 adenylate cyclase
: NAME/KEY: CDS
: LOCATION: (247)...(3480)
: US-10-121-911-2

Query Match      15.7%; Score 284; DB 9; Length 3518;
Best Local Similarity 56.4%; Pred. No. 1.4e-66;
Matches 617; Conservative 0; Mismatches 435; Indels 42; Gaps 3;

Qy 6 CGTGGTGTGGGCATCTCTGGGGCAGTGCAGGTGGGGGGCGCTTTTCGACGAGACCCGCG 65
Db 528 CTTGTGTGGCTCGGCTGTAGCGTAGGCCAGCGCTTCTGTTCACCGGGGGCGTGGT 587

Qy 66 CAGCCCTCTCGGGCCTCTGGTGCCTCTGTTCTTTGTATACATCGATACACGCTCT 125
Db 588 GAGCGCCTGGACACAGGTGCTCTATTTCTCTGTCATCTTCACGGCGTATGCCATGCT 647

Qy 126 CCCCATCGCATCGGGCTGCGCTCCTCAGCGGCTGGCGCTCTCCACCTTGCATTTGCAT 185
Db 648 GCCCTTGGCATCGGGAGCGCGCGCTCGCGGGCTCGCCCTCCACTCTCGCATCTGCT 707

Qy 186 CTTGGCCTGGCAACTT-----AACCGTGTGTAGTCCCTTCCTCTG--GAAGCAGCT 233
Db 708 GGTCTCGGGCTGTATCTTTGGGCCACACGCCGACTCACGGCTGCACTGCTGCCGAGTT 767

Qy 234 CGGTGCCAATGTGCTGTTCTCTGACCAACGTCAATAGCATCTGCACACACTATCC 293
Db 768 GGCACAAACGACGTGCTGTTCTCTGTGGGGAACGTGGCAGGAGTGTACCACAGCGCT 827

Qy 294 AGCAGAGTGTCTCAGCGCCAGGCTTTTCAGAGACCCGAGTTCATCCAGGCCCGCT 353
Db 828 GATGGCGCGCCCTGCGGGGCACGTTCCGGGAGGCACTCAGCTCCCTGCACTCAGCGG 887

Qy 354 CCACCTGCAGCATGAGAAATCGGCAGCAGGCGGCTGCTGCTGTCGGTATTTGCCCCAGCA 413
Db 888 CGGCTGCACACCGAGAGAGACCAAGACACCTTCTCTGTCCATCTTCTCTGCTTA 947

Qy 414 CGTTGCCATGGAGTGAAGAAGACATCAACACAAAAAAGAG----- 457
Db 948 CTTGCCCGAGAGATGAAGGCAGAGATCATGSCACGGCTGCAGGCAGGACGAGGGTCA 1007

Qy 458 -----ACATGTTCCAAAGATCTACATACAGAGCATGACAATGTCAAGAT 503
Db 1008 GCCAGAGAGCACTAACAATTTCCACAGCTCTATGTCAAGAGGCCACAGGGAGTCA 1067

Qy 504 CTTGTTTCAGACATTTAGGGCTTCAACAGCCTGGCATCCGAGTGCATCGCGCAGGAGCT 563
Db 1068 GCTGTATGCTGACATCTGTGGGCTTACCGGCTGTGCCACGAGTGTCCCTTAAGAGCT 1127

Qy 564 GGTGATGACCTGAATGAGCTTTTTCGCCGCTTTTGACAAGCTGGCTGGGGAATCACTG 623
Db 1128 GGTGCTCATGCTCAATGAGCTCTTTGGCAAGTTCGACCAGATTGCCAAGGACGATG 1187

Qy 624 CTTGAGGATCAAGATCTTTGGGGGACTGTTTACTCTGTGTGTACGGGCTGCGGAGCCG 683
Db 1188 CATCGGATCAAGATCTTTGGGGGACTGTTTACTCTGTGTGTCTGGGCTGCCACTCTCA 1247

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Db 1426 TGCATTCAATGGCTTAGGCATGATAAAAGCCATCGAGCAGTCTTGCAGGAGAA 1485  
QY 763 GTCAATGTGAACATGCGGTGGGCATCCACAGCGCGGTGCACCTGCGCGTCTTGGC 822  
Db 1486 GAGATGTTGAACATGCGGTGGGTTCACACGGGCACTGCTGCTGTGGCATCTGGGC 1545  
QY 823 TTCCGGAATGGCAGTTCGATGTGTGTCATGATGTGACCTGCGCCCAACACATGGAA 882  
Db 1546 ATCAGGAGGTTTAAATTTGATGTGTGTCATGATGTGACCTGCGCTTATCTCATGGAG 1605  
QY 883 GCAGGAAGCGCGGTGGCGCATCCACATCACTCGGGCAACACTGCAGTACCTGAACGGG 942  
Db 1606 CAGCTGGGAGTGGCTGGCAAGTTTACATATCTAGGCGCACTGCAAAATACTTAGACGAC 1665  
QY 943 GACTAGCAAGTGGAGCGGCGGTGGTGGCAAGCGC 978  
Db 1665 AGGTATGAATGGAAGATGGGAGATTATGAGCGC 1701

RESULT 10  
US-10-071-223-1  
; Sequence 1, Application US/10071223  
; Patent No. US20020137174A1  
; GENERAL INFORMATION:  
; APPLICANT: Storm, Daniel R.  
; APPLICANT: Hacker, Beth  
; APPLICANT: Tomlinson, James E.  
; APPLICANT: COR Therapeutics, Inc.  
; APPLICANT: University of Washington  
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL  
; TITLE OF INVENTION: CYCLASE  
; FILE REFERENCE: 44481-5029-02-US  
; CURRENT APPLICATION NUMBER: US/10/071,223  
; CURRENT FILING DATE: 2002-02-11  
; PRIOR APPLICATION NUMBER: 09/473,717  
; PRIOR FILING DATE: 1999-12-29  
; PRIOR APPLICATION NUMBER: PC/US98/13541  
; PRIOR FILING DATE: 1998-07-01  
; PRIOR APPLICATION NUMBER: 60/098,559  
; PRIOR FILING DATE: 1997-07-01  
; PRIOR APPLICATION NUMBER: 08/886,440  
; PRIOR FILING DATE: 1997-07-01  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 4985  
; TYPE: DNA  
; ORGANISM: human type IX adenylyl cyclase  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (17)...(3898)  
US-10-071-223-1

Query Match 11.6%; Score 209.4; DB 12; Length 4985;  
Best Local Similarity 62.1%; Pred. No. 2.3e-46;  
Matches 330; Conservative 0; Mismatches 201; Indels 0; Gaps 0;  
QY 426 GATGAAGAAGACATCAACACAAAAAAGACACATGTTCCACAAAGATCTACATACAGAA 485  
Db 1123 GAAGAAAAAGTCTCCATCAACAAAAGCTTATACCTTCGCCCTTTTAAGATGCACGA 1182  
QY 486 GCATGACATGTCAGCATCTGTTTGCAGACATTTAGGGGCTTACACGCTGGCATCCCA 545  
Db 1183 GATCGAAGAAGTACGATATTTTATGACAGATATCGGGCTTACCAAGATGAGTGCCAA 1242  
QY 546 GTGCACTGCGCAGGAGTGGTCATGACCTGAATGAGCTCTTGCCTGGGTTTGACAACT 605  
Db 1243 CAACTGCTCCCGACGCCCTTGGTGGGTCTCTTGAACATCTGTTCGGTCTCGACCGCT 1302  
QY 606 GCGTCGGGAGATCACTGCCTGAGGATCAAGATCTTGGGGGACATGTTTACTACTGTGTGTC 665  
Db 1303 GTGTGAGGAGACCAAGTGTGAGAAAAATCAGCACCTTGGGACATCTTACTACTCGGTGGC 1362

QY 666 AGGCTGCGGAGCGCGCGGAGCATCCACCTGCTGTGTGGAGATGGGGGTAGACAT 725  
Db 1363 GGGCTGTCCGAGCGCGCGGCGGACCATCTGCTGATCGAGATGGGCTGGGCAT 1422  
QY 726 GATTGAGGCCATCTCGCTGGTACGTGACAGGTGTGAATGTGAACATCGCGTGGG 785  
Db 1423 GATCAAGCCATCGAGCAGTCTTCCAGAGAGAAGAGATGGTGAACATGAGAGTCGG 1482  
QY 786 CATCCACAGCGCGCGGTGCACTGCGGGGTCTTGGCTTGGGAAATGCGATTCGATGT 845  
Db 1483 GGTGCACACGGGCGCGCTCTTTCGGGCATCTGGGCATGAGGAGGTTTAAATTTCACT 1542  
QY 846 GTGGTCCAATGATGACCTGCGCAACACATGAAGCAAGCAAGCGGTGGCGGCAT 905  
Db 1543 GTGGTCCAACGATGTAACCTGGCCATCTCATGAGCAGCTGGGAGTGGCGGCAAGT 1602  
QY 906 CCACATCACTCGGCAACACTGCACTGCACTGAACGGGACTACGAAGTGA 956  
Db 1603 TCACATTTCTGAGGCGCGGCAAAATACTTAGATGACCGGTACGAATGGA 1653

RESULT 11  
US-09-751-100B-98  
; Sequence 98, Application US/09751100B  
; Patent No. US20020142436A1  
; GENERAL INFORMATION:  
; APPLICANT: Medical Research Council  
; TITLE OF INVENTION: Human Adenylyl Cyclase and Use Therefor  
; FILE REFERENCE: P27948A  
; CURRENT APPLICATION NUMBER: US/09/751,100B  
; CURRENT FILING DATE: 2000-12-28  
; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 98  
; LENGTH: 5515  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (539)...(4600)  
; OTHER INFORMATION:  
US-09-751-100B-98

Query Match 11.5%; Score 207.8; DB 10; Length 5515;  
Best Local Similarity 62.0%; Pred. No. 6.5e-46;  
Matches 329; Conservative 0; Mismatches 202; Indels 0; Gaps 0;  
QY 426 GATGAAGAAGACATCAACACAAAAAAGACACATGTTCCACAAAGATCTACATACAGAA 485  
Db 1645 GAAGAAAAAGTCTTCCATCCAAAAAGCTCTATAGCCTTCGGCCTTTTAAGATGCACGA 1704  
QY 486 GCATGACATCTCAGCATCTGTTTGCAGACATTTAGGGCTTACCAGCCTGGCATCCCA 545  
Db 1705 GATCGAAGAAGTACGATATTTTATGACAGATATCGTGGGCTTACCAAGATGAGTGCCAA 1764  
QY 546 GTGCACTGCGCAGGAGTGGTCATGACCTGAATGAGCTCTTTCGCCGCTTTCACAACT 605  
Db 1765 CAAGTCTGCCACGCCCTGGTGGGTCTCTGACAGATCTGTTCGCTCGCTTCGACCGCT 1824  
QY 606 GCGTCGGGAGAAATCACTGCCTGAGAGTCAAGATCTTGGGGGACATGTTTACTACTGTGTGTC 665  
Db 1825 GTGTGAGGAGACCAAGTGTGAGAAAAATCAGCACCTTGGGACATGTTTACTACTCGGTGGC 1884  
QY 666 AGGCTGCGGAGCGCGCGGCGGACCATGCCACTGCTGTGTGGAGATGGGGGTAGACAT 725  
Db 1885 GGGTGTCCCGAGCGCGCGGCGGACCATGCTCTGCTGATCGAGATGGGCGCTGGGCAT 1944  
QY 726 GATTGAGGCCATCTCGCTGGTGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGG 785  
Db 1945 GATCAAGGCCATCGAGCAGTCTTCCAGGAGAGAAGAGATGCTGAACATGAGAGTCGG 2004  
QY 786 CATCCACAGCGCGCGGTGCACTCGCGGCTCTTGGCTTGGGAAATGGGCAATGCGATGT 845

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Db 2005 GGTCACACGGCCACCGCTCTTGGCGCATCTTGGCGCATGAGGAGTTTAAATTTGACGT 2064
Qy 846 GTGTCCAAATGATGTACCTGCGCCACACATGGAAGCAGGAGCCGCGCTGGCCCAT 905
Db 2065 GTGTCCAAATGATGTACCTGCGCCACATCTCATGAGCAGCTGGGAGTGGCCGGAAGT 2124
Qy 906 CCACATCACATCGGCGCAACACTGCGTAGTACCTGAACGGGGGACTACCAAGTGA 956
Db 2125 TCACATTTCTGAGGCCACCGCAAAATFACTTAGATGACCGGTACGAAATGGA 2175

RESULT 12
US-09-764-868-182
; Sequence 182, Application US/09764868
; Patent No. US2002016811A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ32
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 182
; LENGTH: 330
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (272)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (285)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (289)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-868-182

Query Match 6.9%; Score 124.4; DB 9; Length 330;
Best Local Similarity 64.2%; Pred. No. 5.3e-24;
Matches 185; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

Qy 669 GCTGGCGAGCGCGGCGGACCATGCCACTGCTGTGTGAGATGGGGTAGACATGAT 728
Db 1 GCTGCCACTCTCACTGCCAGACCATGCCATCAACTGCGTGGCGCATGGGCGCTGGACATGTG 60
Qy 729 TGAGGCCATCTCGTGTGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGCGAT 788
Db 61 CKGGCCATCAGAAACTGCGGGCAGCCACTGGCGTGGACATCAACATGCGTGTGGCGGT 120
Qy 789 CCACAGCGGCGCGTGCATCGGCGTCTTTGGCTTGGGAAATGGCAGTTTCGATGTG 848
Db 121 GCACCTACGGCAGCGTACTGTGGAGTCACTCGGCTGCAGAAGTGGCAGTACGACGTTG 180
Qy 849 GTCCATCATGTGACCTTGGCCACACCATGGAAGCAGGAGCGGGCTGCGCCCATCCA 908
Db 181 GTCACATGATGCATCACTGGCTGAAACCATGAGGAGCGGCTGTACCGGGCGAGTGCA 240
Qy 909 CATCACTCGGCAACACTGAGTACTCAACGGGCACTACCAAGTGA 956
Db 241 CATCACAGGGGTACCCCTGGCCCTGCTGGCANGGGCTTATCTGCTGNGGA 288

RESULT 13
US-09-989-442-71
; Sequence 71, Application US/0989442
; Publication No. US20030013649A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJZ08
; CURRENT APPLICATION NUMBER: US/09/989,442
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,757
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/226,868
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/216,647
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,267
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/216,880
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,270
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/251,869
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/235,834
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/234,274
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/234,223
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/228,924
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/224,518
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,369
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/224,519
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,964
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/241,809
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/249,299
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/236,327
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/241,785
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/244,617
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 60/225,268
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,368
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/251,856
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/251,868
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/229,344
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/234,997
; PRIOR FILING DATE: 2000-09-25
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1	PRIOR FILING DATE: 2000-11-17	
2	PRIOR APPLICATION NUMBER: 60/249,217	
3	PRIOR FILING DATE: 2000-11-17	
4	PRIOR APPLICATION NUMBER: 60/249,217	
5	PRIOR FILING DATE: 2000-11-17	
6	PRIOR APPLICATION NUMBER: 60/249,211	
7	PRIOR FILING DATE: 2000-11-17	
8	PRIOR APPLICATION NUMBER: 60/249,215	
9	PRIOR FILING DATE: 2000-11-17	
10	PRIOR APPLICATION NUMBER: 60/249,264	
11	PRIOR FILING DATE: 2000-11-17	
12	PRIOR APPLICATION NUMBER: 60/249,214	
13	PRIOR FILING DATE: 2000-11-17	
14	PRIOR APPLICATION NUMBER: 60/249,297	
15	PRIOR FILING DATE: 2000-11-17	
16	PRIOR APPLICATION NUMBER: 60/232,400	
17	PRIOR FILING DATE: 2000-09-14	
18	PRIOR APPLICATION NUMBER: 60/231,242	
19	PRIOR FILING DATE: 2000-09-08	
20	PRIOR APPLICATION NUMBER: 60/232,081	
21	PRIOR FILING DATE: 2000-09-08	
22	PRIOR APPLICATION NUMBER: 60/232,080	
23	PRIOR FILING DATE: 2000-09-08	
24	PRIOR APPLICATION NUMBER: 60/231,414	
25	PRIOR FILING DATE: 2000-09-08	
26	PRIOR APPLICATION NUMBER: 60/231,244	
27	PRIOR FILING DATE: 2000-09-08	
28	PRIOR APPLICATION NUMBER: 60/233,064	
29	PRIOR FILING DATE: 2000-09-14	
30	PRIOR APPLICATION NUMBER: 60/233,063	
31	PRIOR FILING DATE: 2000-09-14	
32	PRIOR APPLICATION NUMBER: 60/232,397	
33	PRIOR FILING DATE: 2000-09-14	
34	PRIOR APPLICATION NUMBER: 60/232,399	
35	PRIOR FILING DATE: 2000-09-14	
36	PRIOR APPLICATION NUMBER: 60/232,401	
37	PRIOR FILING DATE: 2000-09-14	
38	PRIOR APPLICATION NUMBER: 60/241,808	
39	PRIOR FILING DATE: 2000-10-20	
40	PRIOR APPLICATION NUMBER: 60/241,826	
41	PRIOR FILING DATE: 2000-10-20	
42	PRIOR APPLICATION NUMBER: 60/246,475	
43	PRIOR FILING DATE: 2000-11-08	
44	PRIOR APPLICATION NUMBER: 60/231,243	
45	PRIOR FILING DATE: 2000-09-08	
46	PRIOR APPLICATION NUMBER: 60/233,065	
47	PRIOR FILING DATE: 2000-09-14	

Best Local Similarity 54.2%; pred. NO. 5.3e-24;  
Matches 185; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

Qy	669	GCTCGGAGCCCGGGCCGACACATGCCCACTGCTGTGTGGAGATGGGGGTAGACATGAT	728
Db	1	GGTCTTCTCACTGCGAGCACATGCCATCAACTCGTGCCTGGCTGGACATGTG	60
Qy	729	TGAGGCATCTCGCTGTGCTGAGGTGACAGTGTGAATGTGAACATCGCGTGGGCAT	788
Db	61	CKKGCATCAGNAACTGGCGACCACTGCGGTGGACATCACTCGTGTGGCGCT	120
Qy	789	CCACAGCGCGCGGTGCACATGCGCGCTTCCTTGGCTTCGCGAAATGCACTTCGATGTGTG	848
Db	121	GCACCTCAGGCAAGGCTACTGTGTGGAGTCACTCGGGCTGCAGAGTGCAGTACGACCTTG	180
Qy	849	GTCCAATGATGTGACCTGCGCCAAACACATGGAAGCAGAAACCGGCTGCGCGCATCCA	908
Db	181	GTACATGATGTACACTGCTTACCACATGAGGACGCGGGTGTACCAAGGCGAGTGCA	240
Qy	909	CATCACTCGGCAACACTGCAGTACCTGAACGGGGACTACGAAGTGA	956
Db	241	CATCACAGGGCTACCTCGGCCCTGCTGGCANGGGCTTATGCTNGGA	288



US-09-764-868-1351

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RESULT 14
US-09-764-869-445
; Sequence 445, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764,869
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 445
; LENGTH: 330
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (272)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (285)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (289)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-764-869-445

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	Query Match	6.98;	Score 124.4;	DB 10;	Length 330;
	Best Local Similarity	64.29;	Pred. No. 5.3e-24;		
	Matches 185;	Conservative 0;	Mismatches 103;	Indels 0;	Gaps 0;
Qy	669	GCTCCGGAGCCCGGGCCGACCATGCCCACCTGTGTGTGGAGATGGGGGTAGACATGAT	728		
Db	1	GCTGCCACTCTCAGTGCACAGACCATGCCATCAACTGCGTGCAGCATGGGCCCTGGACATGTG	60		
Qy	729	TGAGGCCATCTCGTGTACGTGTAGGTGACAGGTGTGAATGTGACATGCGCGTGGGCAT	788		
Db	61	CKKGGCCATCAGGAAACTGCGGGGAGCCACCTGGCGGTGGACATCAACATGCGGTGGGGCGT	120		
Qy	789	CCACAGCGGGGCGGTGCACCTCGCGCGTCTCTTGGCTTGGCGAAATGGCAGTTTCGATGTGTG	848		
Db	121	GCACTCAGGCAGCGTACTGTGTGGAGTCATCGGGCTGCAGAAGTGGCAGTACGACGTTTG	180		
Qy	849	GTCCAATGATGTACCTTGGCCCAACCATCGAAGCAGACCCGGGTGCCCGCATCCA	908		
Db	181	GTCCATGATGTACACTGGCTTACCATGTGGAGGACGGCGGTGTACCAGGGCGAGTGCA	240		
Qy	909	CATCACTCGGGCACACTGCAGTACTCTGAAACGGGGACTACGAAGTSGA	956		
Db	241	CATCACAGGGGCTACCTTGGCCCTGCTGGCANGGGCTTATGCTGNGA	288		

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RESULT 15
US-09-764-868-1351
; Sequence 1351, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ32
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to palm or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1351
; LENGTH: 11881
; TYPE: DNA
; ORGANISM: Homo sapiens

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Query Match	4.4%	Score 79.2	DB 9	Length 11881
Best Local Similarity	63.4%	Prod. No. 5.2e-11		
Matches 137	Conservative	0	Mismatches 78	Indels 1
Gaps				
QY	746	TACGTGAGGTGACACAGTGTGAATGTGAACATCGCGGTGGCATCCACAGCGGCGCGTGC	805	
DB	227	TCCGGCAGCCACTGCGGTGGACATCAACATCGTGGTGGCGTGCACTCAGCAGCGTAC	286	
QY	806	ACTGCGGCGTCTTGGCTTGGGAAATGGCAGTTGCATGTGTGTGTCCTCAATGATGTACCC	865	
DB	287	TGTGTGGAGTCATCGGGTGCAGAAAGTGGCAGTACGACGTTTGGTCACATGATGTACAC	346	
QY	866	TGGCCAAACCATGGAAGCAGGCGGTGGCG -CATCCATCATCATCGGCAACA	924	
DB	347	TGGCTAACCATATGAGGAGCGCGGTGTACAGAGGTGAGACCTAGGGCCCTAGGCAGCTA	406	
QY	925	CTGCAGTACCTGAACGGGACTTACGAAGTGGAGCCA	960	
DB	407	CAGCAGAGGCCAACGAGGCTTACCACAGGCTGCCA	442	

Search completed: March 1, 2003, 09:04:11  
Job time : 106.396 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 28, 2003, 22:03:11 ; Search time 44.382 seconds  
(without alignments)  
12520.796 Million cell updates/sec

Title: US-09-750-240-3  
Perfect score: 1812  
Sequence: 1 gttacgtggtctggcgcatt.....gcagctttctgaggtgttc 1812

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
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2: /cgn2.6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2.6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2.6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2.6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgn2.6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1812	100.0	1812	4	US-09-008-097-3
2	1808.4	99.8	3549	4	US-09-008-097-5
3	1763	97.3	4942	4	US-09-474-076-1
4	1519.8	83.9	4046	1	US-07-793-961A-1
5	1519.8	83.9	4046	1	US-08-240-357-1
6	1437.2	79.3	4131	3	US-08-726-214-11
7	895	49.4	4233	4	US-09-473-716-1
8	858.2	47.4	3924	3	US-08-726-214-9
9	436	24.1	3978	3	US-08-726-214-1
10	393.2	21.7	1652	3	US-08-726-214-17
11	335.6	18.5	4533	3	US-08-726-214-5
12	320.6	17.2	4601	3	US-08-726-214-15
13	311.2	17.2	5199	3	US-08-726-214-13
14	286	15.8	4008	3	US-08-307-896-5
15	286	15.8	4008	3	US-08-726-214-3
16	286	15.8	4008	5	PCT-US95-11808-5
17	284	15.7	3518	4	US-09-412-210-2
18	256.2	14.1	3357	3	US-08-726-214-7
19	216.8	12.0	4473	3	US-08-894-173-1
20	216.8	12.0	4473	4	US-09-398-193-1
21	209.4	11.6	4985	4	US-09-473-717-1
22	207.8	11.5	5515	4	US-09-398-193-98
23	73	4.0	7218	1	US-08-232-463-14
24	64.4	3.6	1259	2	US-08-997-080-123
25	64.4	3.6	1259	2	US-08-997-362-123
26	64.4	3.6	1259	4	US-09-095-855-123
27	64.4	3.6	1259	4	US-09-324-542-123

28	64.4	3.6	1259	4	US-09-205-426-123	Sequence 123, App
29	64.4	3.6	2013	2	US-08-997-080-176	Sequence 176, App
30	64.4	3.6	2013	2	US-08-997-362-176	Sequence 176, App
31	64.4	3.6	2013	4	US-09-095-855-176	Sequence 176, App
32	64.4	3.6	2013	4	US-09-324-542-176	Sequence 176, App
33	64.4	3.6	2013	4	US-09-205-426-176	Sequence 176, App
34	64.4	3.6	2172	2	US-08-997-080-173	Sequence 173, App
35	64.4	3.6	2172	2	US-08-997-362-173	Sequence 173, App
36	64.4	3.6	2172	4	US-09-095-855-173	Sequence 173, App
37	64.4	3.6	2172	4	US-09-324-542-173	Sequence 173, App
38	64.4	3.6	2172	4	US-09-205-426-173	Sequence 173, App
39	43	2.4	7218	1	US-08-232-463-14	Sequence 14, Appl
40	41.8	2.3	169	4	US-09-205-995-77	Sequence 77, Appl
41	41.8	2.3	190	4	US-09-205-995-77	Sequence 77, Appl
42	41.4	2.3	3784	1	US-07-623-033-1	Sequence 1, Appl
43	39.2	2.2	2028	4	US-09-634-920-1	Sequence 1, Appl
44	39.2	2.2	2734	3	US-09-135-021-79	Sequence 79, Appl
45	39.2	2.2	2821	4	US-09-135-021A-115	Sequence 115, App

## ALIGNMENTS

RESULT 1  
US-09-008-097-3  
; Sequence 3, Application US/09008097  
; Patent No. 6306830  
; GENERAL INFORMATION:  
; APPLICANT: Hammond, H. Kirk  
; APPLICANT: Insel, Paul A.  
; APPLICANT: Ping, Peipei  
; APPLICANT: Post, Steven R.  
; APPLICANT: Gao, Meihua  
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE  
; TITLE OF INVENTION: HEART FAILURE  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/008,097  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dylan, Tyler M  
; REGISTRATION NUMBER: 37,612  
; REFERENCE/DOCKET NUMBER: 22000-20567.21  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-813-5600  
; TELEFAX: 650-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1812 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Coding Sequence  
; LOCATION: 1..1812  
; OTHER INFORMATION:



, STREET: 755 PAGE MILL ROAD  
 , CITY: PALO ALTO  
 , STATE: CA  
 , COUNTRY: USA  
 , ZIP: 94304-1018  
 , COMPUTER READABLE FORM:  
 , MEDIUM TYPE: Diskette  
 , COMPUTER: IBM compatible  
 , OPERATING SYSTEM: DOS,  
 , SOFTWARE: FastSeq for Windows Version 2.0  
 , CURRENT APPLICATION DATA:  
 , APPLICATION NUMBER: US/09/008,097  
 , FILING DATE:  
 , CLASSIFICATION:  
 , PRIOR APPLICATION DATA:  
 , APPLICATION NUMBER:  
 , FILING DATE:  
 , ATTORNEY/AGENT INFORMATION:  
 , NAME: Dylan, Tyler M  
 , REGISTRATION NUMBER: 37,612  
 , REFERENCE/DOCKET NUMBER: 22000-20567.21  
 , TELECOMMUNICATION INFORMATION:  
 , TELEPHONE: 650-813-5600  
 , TELEFAX: 650-494-0792  
 , TELEX: 706141  
 , INFORMATION FOR SEQ ID NO: 5:  
 , SEQUENCE CHARACTERISTICS:  
 , LENGTH: 3549 base pairs  
 , TYPE: nucleic acid  
 , STRANDEDNESS: single  
 , TOPOLOGY: linear  
 , FEATURE:  
 , NAME/KEY: Coding Sequence  
 , LOCATION: 1...3501  
 , OTHER INFORMATION:  
 , SQS-09-008-097-5

Query Match	99.98;	Score 1808.4;	DB 4;	Length 3549;
Best Local Similarity	99.98;	Pred. No. 0;		
Matches 1809;	Conservative	0;	Mismatches	1; Indels 0; Gaps 0;
QY	3	TAACTGGTGGTCATCTGGGGCAGTGCAGGTCGGGGCGGCTTTCGGCAGCAGACCC	62	
Db	636	TAACTGGTGGTCATCTGGGGCAGTGCAGGTCGGGGCGGCTTTCGGCAGCAGACCC	695	
QY	63	GCAGAGCCCTCTCGGGCCCTCTGGTCCCTGTGCTCTTTATACATCGCATACAGCT	122	
Db	696	GCAGAGCCCTCTCGGGCCCTCTGGTCCCTGTGCTTTATACATCGCATACAGCT	755	
QY	123	CCTCCCATCCGATCGGGGCTGCGCTCTCAGGGGCTGGGCCCTCTCCACTTGCATTT	182	
Db	756	CCTCCCATCCGATCGGGGCTGCGCTCTCAGGGGCTGGGCCCTCTCCACTTGCATTT	815	
QY	183	GATCTTGGCTGGCACTTTAACCTGGTGATGCTTCTCTGGAAGCAGCTCGGTGCCAA	242	
Db	816	GATCTTGGCTGGCACTTTAACCTGGTGATGCTTCTCTGGAAGCAGCTCGGTGCCAA	875	
QY	243	TGTGCTGCTGTTCTCTGCACCACGTCATTAGCATCTGCACACACTATCCAGCAGAGT	302	
Db	876	TGTGCTGCTGTTCTCTGCACCACGTCATTAGCATCTGCACACACTATCCAGCAGAGT	935	
QY	303	GTCTACAGCCAGGCTTTTCAAGAGACCGCAGTTACATCCAGGCCCGGCTCCACCTGCA	362	
Db	936	GTCTACAGCCAGGCTTTTCAAGAGACCGCAGTTACATCCAGGCCCGGCTCCACCTGCA	995	
QY	363	GCATGAGAATCGGCAGCAGGACGGGCTGCTGCTCGGTATTTGCCCGCAGCAGCTTGCCAT	422	
Db	996	GCATGAGAATCGGCAGCAGGACGGGCTGCTGCTCGGTATTTGCCCGCAGCAGCTTGCCAT	1055	
QY	423	GGAGTGAAGAAGACATCAACACAAAAAGACATGTTTCCACAAAGATCTCATACACA	482	
Db	1056	GGAGTGAAGAAGACATCAACACAAAAAGACATGTTTCCACAAAGATCTCATACACA	1115	

Qy	483	GAAGCATGACAATGTG	CAGCATCCTGTTTG	CAGACATTTGAGGCTT	CACGACCTGGCATC	542
Db	1116	GAAGCATGACAATGTG	CAGCATCCTGTTTG	CAGACATTTGAGGCTT	CACGACCTGGCATC	1175
Qy	543	CCAGTGCAC	TGCGCAGGAGCTGGT	CATGACCCTGAATCAG	CTCTTGC	602
Db	1176	CCAGTGCAC	TGCGCAGGAGCTGGT	CATGACCCTGAATCAG	CTCTTGC	1235
Qy	603	GCTGGCTGCGGAGAAT	CAC	TGCCTGAGGATCAAGATCTT	GGGACCTGTTACTACTGTGT	662
Db	1236	GCTGGCTGCGGAGAAT	CAC	TGCCTGAGGATCAAGATCTT	GGGACCTGTTACTACTGTGT	1295
Qy	663	GTGAGGCTGCGGAGG	CCCGGCCGACATGCC	CACTGCTGTGTGGAGAT	TGGGGGTAGA	722
Db	1296	GTGAGGCTGCGGAGG	CCCGGCCGACCATGCC	CACTGCTGTGTGGAGAT	TGGGGGTAGA	1355
Qy	723	CATGATTGAGGCCAT	CTCCCTGGTACGTGAG	GTGACAGTGTGAATGT	GAAACATGCGCGT	782
Db	1356	CATGATTGAGGCCAT	CTCCCTGGTACGTGAG	GTGACAGTGTGAATGT	GAAACATGCGCGT	1415
Qy	783	GGGCATCCACAGCGG	CGCGTGCAC	TGCGGCGTCTTGGCTT	CGGAAATGGCAAGTTTCGA	842
Db	1416	GGGCATCCACAGCGG	CGCGTGCAC	TGCGGCGTCTTGGCTT	CGGAAATGGCAAGTTTCGA	1475
Qy	843	TGTTGGTCCAAATGAT	GTGACCTGCGCCAA	CCACATGGAAGCAG	GAAGCCGGGTGGCCG	902
Db	1476	TGTTGGTCCAAATGAT	GTGACCTGCGCCAA	CCACATGGAAGCAG	GAAGCCGGGTGGCCG	1535
Qy	903	CATCCACATCATTG	GGGGAACACTGAGT	ATCCTGAACGGGAC	TACGAAATGGAGCCAGG	962
Db	1536	CATCCACATCATTG	GGGGAACACTGAGT	ATCCTGAACGGGAC	TACGAAATGGAGCCAGG	1595
Qy	963	CCGTGTGGCAAGCG	CAACCGCTACTCA	AGAGCAGACACAT	TGAGACTTTTCCTCATCCT	1022
Db	1596	CCGTGTGGCAAGCG	CAACCGCTACTCA	AGAGCAGACACAT	TGAGACTTTTCCTCATCCT	1655
Qy	1023	GGGCGCAGCCAGAA	ACGGAAAGAGAGAA	AGGCATGCTGGCCAA	AGCTGACGCGGACTCG	1082
Db	1656	GGGCGCAGCCAGAA	ACGGAAAGAGAGAA	AGGCATGCTGGCCAA	AGCTGACGCGGACTCG	1715
Qy	1083	GGCCAACTCCATG	GGAAGGCTGATG	CCGCGATGGGTTCTCT	GATCGTGCTTCTCCCGGAC	1142
Db	1716	GGCCAACTCCATG	GGAAGGCTGATG	CCGCGATGGGTTCTCT	GATCGTGCTTCTCCCGGAC	1775
Qy	1143	CAMGACTCCAAAGC	CTCCGACATGGCAT	TTCATGATTC	CAGCAAGACACCGGG	1202
Db	1776	CAMGACTCCAAAGC	CTCCGACATGGCAT	TTCATGATTC	CAGCAAGACACCGGG	1835
Qy	1203	CACCCAAAGTGCCT	GAAACCTCAGGAT	GAGGTGATGAGTTCT	GAGCCGTGCAATCGA	1262
Db	1836	CACCCAAAGTGCCT	GAAACCTCAGGAT	GAGGTGATGAGTTCT	GAGCCGTGCAATCGA	1895
Qy	1263	TGCGCGCAGATTGAT	CAGTGGGAAGACCAT	GTGGCGGTTTGTGCT	CACCTTTCCA	1322
Db	1896	TGCGCGCAGATTGAT	CAGTGGGAAGACCAT	GTGGCGGTTTGTGCT	CACCTTTCCA	1955
Qy	1323	GAGAGAGATTGAGA	GAAGTACTCCCGA	AGGTGGATCCCGCT	TTCGAGGCTACGT	1382
Db	1956	GAGAGAGATTGAGA	GAAGTACTCCCGA	AGGTGGATCCCGCT	TTCGAGGCTACGT	2015
Qy	1383	TGCGTGGCCCTGTT	GGCTTCTGCTTCA	TCTATCTGCTTCAT	CACAGCTTCTAAATTTTCCAC	1442
Db	2016	TGCGTGGCCCTGTT	GGCTTCTGCTTCA	TCTATCTGCTTCAT	CACAGCTTCTAAATTTTCCAC	2075
Qy	1443	CTCCACCTGATGCT	TGGGAATTATG	CCAGACATCTTCTG	TGCTGCTTAATCACCGTGT	1502
Db	2076	CTCCACCTGATGCT	TGGGAATTATG	CCAGACATCTTCTG	TGCTGCTTAATCACCGTGT	2135
Qy	1503	GATCTGCTGTACT	CTCTGTGGTTC	TCTGTTCC	TAAAGCCCTGCAACGCTGTCCCG	1562
Db	2136	GATCTGCTGTACT	CTCTGTGGTTC	TCTGTTCC	TAAAGCCCTGCAACGCTGTCCCG	2195
Qy	1563	CAGCATTTGCGCT	CACGGGCACATAG	CACCGCAGTTGGCAT	CTTTTCCGCTCTGCTGTGT	1622

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Db 2196 CAGCATTTGTCGGCTCAGGGGCACATAGCACCAGCTGGCATCTTTTCCGTCCTGCTGTG 2255
Qy 1623 GTTTACTTCTGCCATTGCCAACATGTTACCTGTGAACACACACCCCCCATACGGAGCTGTGC 1682
Db 2256 GTTTACTTCTGCCATTGCCAACATGTTACCTGTGAACACACACCCCCCATACGGAGCTGTGC 2315
Qy 1683 AGCCCGGATGCTGAATTTAACACCTGCTGACATCACTGCTGCGCACTGCGAGCAGCTCAA 1742
Db 2316 AGCCCGGATGCTGAATTTAACACCTGCTGACATCACTGCTGCCACCTGCGAGCAGCTCAA 2375
Qy 1743 TTACTCTCTGGCGCTGGATGCTCCCTGCTGAGGGCACCAGTGCACCTGCAGCTTTCC 1802
Db 2376 TTACTCTCTGGCGCTGGATGCTCCCTGCTGAGGGCACCAGTGCACCTGCAGCTTTCC 2435
Qy 1803 TGAGGTGTTCC 1812
Db 2436 TGAGGTGTC 2445

RESULT 3
US-09-474-076-1
; Sequence 1, Application US/09474076
; Patent No. 6465237
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, James E.
; APPLICANT: COR Therapeutics, Inc.
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
; TITLE OF INVENTION: CYCLASE
; FILE REFERENCE: 44481-5028-01-US
; CURRENT APPLICATION NUMBER: US/09/474,076
; CURRENT FILING DATE: 1999-12-12
; PRIOR APPLICATION NUMBER: PCT/US98/13694
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/070,904
; PRIOR FILING DATE: 1997-07-01
; PRIOR APPLICATION NUMBER: 08/886,550
; PRIOR FILING DATE: 1997-07-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4942
; TYPE: DNA
; ORGANISM: human type VI adenylyl cyclase
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (145)..(3648)
US-09-474-076-1

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Qy	305	CTCAGCGCCAGGCGCTTTTCAGGAGACCCGCGAGTTTACATCCAGGCGCGGCTCCACCTGCAGC	364
Db	1082	CTCAGCGCCAGGCGCTTTTCAGGAGACCCGCGGTTTACATCCAGGCGCGGCTCCACCTGCAGC	1141
Qy	365	ATGAGAATCGCAGCAGGAGCGCTGCTGCTGTCGGTATTGCCCCAGCACGCTTGCCATGG	424
Db	1142	ATGAGAATCGCAGCAGGAGCGCTGCTGCTGTCGGTATTGCCCCAGCACGCTTGCCATGG	1201
Qy	425	AGATGAAGAAGACATCAACACAAAAAAGAAGAC---ATGTTCCACAAGATCTACATAC	481
Db	1202	AGATGAAGAAGACATCAACACAAAAAAGAAGACATGATGTTCCACAAGATCTACATAC	1261
Qy	482	AGAAGCATGACAAATGTCAGCATCTCTTTTGCAGACATTTGAGGGCTTCACAGCCTGGCAT	541
Db	1362	AGAAGCATGACAAATGTCAGCATCTCTTTTGCAGACATTTGAGGGCTTCACAGCCTGGCAT	1321
Qy	542	CCAGTCGACTGCGCAGGAGCTGGTCATCACCCTGAAATGAGCTCTTCCCGGTTTGACA	601
Db	1322	CCAGTCGACTGCGCAGGAGCTGGTCATCACCCTGAAATGAGCTCTTCCCGGTTTGACA	1381
Qy	602	AGCTGGCTGCGGAGAAATCACTGCTGAGGATCAAGATCTTTGGGGACTGTTTACTACTGTG	661
Db	1382	AGCTGGCTGCGGAGAAATCACTGCTGAGGATCAAGATCTTTGGGGACTGTTTACTACTGTG	1441
Qy	662	TGTCAGGGCTGCGGAGGCGCCGGCCGACCATGCCCCACTGCTGTGTGGAGATGGGGGTAG	721
Db	1442	TGTCAGGGCTGCGGAGGCGCCGGCCGACCATGCCCCACTGCTGTGTGGAGATGGGGGTAG	1501
Qy	722	ACATGATTGAGGCCATCTCGCTGGTAGTGAGGTGACAGGTGTGAATCTGAAACATGCGCG	781
Db	1502	ACATGATTGAGGCCATCTCGCTGGTAGTGAGGTGACAGGTGTGAATCTGAAACATGCGCG	1561
Qy	782	TGGGCATCCACAGCGGCGCGTSCACTGCGGCGTCTTGGCTTGGCGAAATGGCAGTTTCG	841
Db	1562	TGGGCATCCACAGCGGCGCGTSCACTGCGGCGTCTTGGCTTGGCGAAATGGCAGTTTCG	1621
Qy	842	ATGTGTGGTCCATGATGATGACCTCGGCCAACACACATGGAAGCAGGAGCCGGGCTGGCC	901
Db	1622	ATGTGTGGTCCATGATGATGACCTCGGCCAACACACATGGAAGCAGGAGCCGGGCTGGCC	1681
Qy	902	GCATCCACATCACTCGGGCAACACTGCAGTACTGAAAGGGGACTACGAAGTGGAGCCAG	961
Db	1682	GCATCCACATCACTCGGGCAACACTGCAGTACTGAAAGGGGACTACGAAGTGGAGCCAG	1741
Qy	962	GCCGTGTGTCACAGCGCAACGGGTACTTCAAGGAGCAGCACATTTGAGACTTTTCTCATCC	1021
Db	1742	GCCGTGTGTCACAGCGCAACGGGTACTTCAAGGAGCAGCACATTTGAGACTTTTCTCATCC	1801
Qy	1022	TGGGCGCCAGCCAGAACCGAAAGAGGAGAAAGCATGCTGGCCAAAGCTGCAGCGGACTC	1081
Db	1802	TGGGCGCCAGCCAGAACCGAAAGAGGAGAAAGCATGCTGGCCAAAGCTGCAGCGGACTC	1861
Qy	1082	GGGCGCAACTCCATGGAAGGGCTGATGCCCGATGGGTTCTTGATCGTGCCCTTCTCCCGGA	1141
Db	1862	GGGCGCAACTCCATGGAAGGGCTGATGCCCGCTGGGTTCTTGATCGTGCCCTTCTCCCGGA	1921
Qy	1142	CCAAGGACTCCAAGGCGCTTCCGCCAGATGGGCATTTGATGATTCACAAAGACAACCGGG	1201
Db	1922	CCAAGGACTCCAAGGCGCTTCCGCCAGATGGGCATTTGATGATTCACAAAGACAACCGGG	1981
Qy	1202	GCACCCCAAGATGCCCTGAACCCCTGAGGATGAGGTGGATGAGTTCTTGAGCCGTGCCATCG	1261
Db	1982	GCACCCCAAGATGCCCTGAACCCCTGAGGATGAGGTGGATGAGTTCTTGAGCCGTGCCATCG	2041
Qy	1262	ATGCCCCGACCATTTGATCAGCTGCGGAAGGACCATGTGGCGCGGTTTTTGTCTCACCCTTC	1321
Db	2042	ATGCCCCGACCATTTGATCAGCTGCGGAAGGACCATGTGGCGCGGTTTTTGTCTCACCCTTC	2101
Qy	1322	AGAGAGAGGATTTTGAGAGAAGACTACTCCCGGAAGGTGATCCCGGCTTCGGAGCCTACG	1381
Db	2102	AGAGAGAGGATTTTGAGAGAAGACTACTCCCGGAAGGTGATCCCGGCTTCGGAGCCTACG	2161
Qy	1382	TTGGCTGTGCCCTGTTGGTCTTCTGCTCATCTGCTTATCCAGCTTCTAAATTTTCCAC	1441

[illegible]

## RESULT 4

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US-07-793-961A-1
; Sequence 1, Application US/07793961A
; Patent No. 5334521
; GENERAL INFORMATION:
; APPLICANT: Yoshihiro Ishikawa
; TITLE OF INVENTION: Cloning and Character-
; TION OF INVENTION: ization of a Cardiac Adenylyl Cyclase-
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Alan M. Gordon
; ADDRESSEE: American Cyanamid Company
; STREET: 1937 West Main Street,
; STREET: P.O. Box 60
; CITY: Stamford
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06904
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: ASCII from DW4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/793-961A
; FILING DATE: 19911118
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gordon, Alan M.
; REGISTRATION NUMBER: 30,637
; REFERENCE/DOCKET NUMBER: 31,705
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203 321 2719
; TELEFAX: 203 321 2971
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4046 base pairs listed

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Qy	542	CCAGTGCAC	TGCGCAGGAGCTGGTGCATGACCCCTGAATGAGCTCTTTGCCGGTTTGACA	601
Db	1302	CCAGTGCAC	CCGCGAGGAGCTGGTGCATGATCCCTGAACGAGCTCTTGCCCGGTTTGACA	1361
Qy	602	AGCTGGCTGCGGAGAACTACTGCCTGAGGATCAAGATCTTGGGGAGCTGTACTACTGTG	661	
Db	1362	AGCTGGCTGCGGAAATCACTGCCGTAGGATCAAGATCTTAGGGGAGCTGTACTACTGTG	1421	
Qy	662	TGTCAGGGCTTGGCGAGGCCGCGCGACCACTGCCACTGCTGTGTGGAGATGGGGGTAG	721	
Db	1422	TGTCAGGGCTGCGGAGGCCGCGCGACCACTGCCACTGCTGTGTGGAGATGGGGGTG	1481	
Qy	722	ACATGATGAGGCCATCTCGCTGGTAGTGAGGTGACAGGTGTGAATGTGAACATGCGCG	781	
Db	1482	ACATGATGAGGCCATCTCGCTGGTAGTGAGGTGACAGGTGTGAAGGTGAACATCGCG	1541	
Qy	782	TGGGCATCACAGCGGGCGGTGCACCTCGGCGTCTTGGCTTGCAGAAATGGCAGTTGC	841	
Db	1542	TGGGCATCACAGCGGGCGGTGTGCACCTGTGTGTCTTGGCTTCGGAAATGGCAGTTGC	1601	
Qy	842	ATGTGTGGTCCAAATGATGTGACCTTGGCCAAACCACATGGAACGAGGAAAGCGGGCTGGCC	901	
Db	1602	ACGTGTGGTCCAAATGACGTGACTCTGGCCAAACCATATGAGGCGG--CCGCGCGCGCC	1658	
Qy	902	GCATCCACATCACTCGGGCAACACTGCACTGTAAGTCTGTAACGGGGACTACGAAGTGGAGCGAG	961	
Db	1659	GCATCCACATCAACCGGGCACGCTGCATGTAAGTCTGTAACGGGGACTACGAAGTGGAGCGG	1718	
Qy	962	GCCGTGTGGCAAGCGCAACGGTACCTCAAGGAGCAGCATTTGAGACATTTCTCTCATCC	1021	
Db	1719	GCCGTGTGGCAGCGGAACGGGTACCTCAAGGAGCAGCATCGAGACCTTCTCTCATCC	1778	
Qy	1022	TGGCGCCACGCGAGAAACGGAAGAGGAAAGGCATGCTGGCCAAAGCTGCAGCGGACTC	1081	
Db	1779	TGGGAGCGCCAGAAACGGAAGAGGAAAGGCATGCTGGCCAAAGCTGCAGCGGAGCG	1838	
Qy	1082	GGGCCAACTCCATGGAAGGGCTGATGCCGCGATGGTTCTCTGATGTCCTTCTCCCGGA	1141	
Db	1839	GGGCCAACTCCATGGAAGGGCTGATGCCACGCTGGGTGGCGGACGCGCTTCTCTCCGGA	1898	
Qy	1142	CCAAGACTCCAAGGCTTTCGCGCAGATGGGCATTGATGATTCAGACAAAGACAACCGGG	1201	
Db	1899	CCAAGACTCCAAGGCTTTCGCGCAGATGGGCATTGATGATTCAGACAAAGACAACCGGG	1958	
Qy	1202	GCACCAAGATGCCCTGAACCCCTGAGGATGAGGTGGATGAGTTCTCTGAGCCGTGCCCATCG	1261	
Db	1959	GTGCCCAAGATGCCCTGAACCCCGAGGATGAGTGCATGATGTTCTTGGCGCGTGGCATCG	2018	
Qy	1262	ATGCCCGCAGCATGATCAAGCTGCGGAGGAGGACCATGTGCGCGCGTTTGTCTCACTTCC	1321	
Db	2019	ATGCCCGCAGCATGATCAAGCTACGGAAGGACCATGTGCGCGCGTTTGTCTCACTTCC	2078	
Qy	1322	AGAGAGGATTTTGAAGAAGTAGTACTCCGGAAGTGGATCCCGCTTCGGAGCCTACG	1381	
Db	2079	AGAGAGGATTTTGAAGAAGTAGTACTCAAGGAGGTGGACCCCGCTTCGGAGCCTACG	2138	
Qy	1382	TTGCCCTGTGCCCTGTTTGGTCTTCTGCTTCATCTGTTTCATCCAGCTTCTTAATTTTCCAC	1441	
Db	2139	TGCGCTGTGCGCTGTTTGGTCTTCTGCTTCATCTGTTTCATCCAGCTCCTCGTCTTCCAC	2198	
Qy	1442	ACTCCACCCCTGATGCTGTGGGATTTATGCGAGCATGTTCCCTGCTGCTTAATCAACGCTGC	1501	
Db	2199	ACTCAACCCGCTGATGCTTGGGATCTACGCGAGTATCTTTGTGCTGTGTGATACCGCTGC	2258	
Qy	1502	TGATCTGTGCTGTGACTCTGTTCTGTTCTCTGTTCCCTTAAGGCCCTTCAAGCTCTGTCCC	1561	
Db	2259	TGACCTGTGCGGTGTACTCCTGTGGCTCTCTCTTCCCAAGGCCCTCGGAGCTCTTCCC	2318	
Qy	1562	GCAGCATGTGCGCTCACGGGCACATAGCAGCGAGTTGGCATCTTTTCGTCCTGCTTG	1621	
Db	2319	GCAGCATGTGCGCTCTCGGGCACACAGCATGTGGTTGGCATTTTTTTTCACTCTTGCTAG	2378	
Qy	1622	TGTTTACTTCTGCCATTTGCCAATGTTTCACTGTGAACCAACACCCCATACGAGAGCTGTG	1681	

[illegible]

RESULT 6  
 US-08-726-214-11  
 ; Sequence 11, Application US/08726214  
 ; Patent No. 6107076  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tang, Wei-Jen  
 ; APPLICANT: Gliman, Alfred G.  
 ; TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE  
 ; TITLE OF INVENTION: AND USES THEREFOR  
 ; NUMBER OF SEQUENCES: 31  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Arnold, White & Durkee  
 ; STREET: P.O. Box 4433  
 ; CITY: Houston  
 ; STATE: Texas  
 ; COUNTRY: United States of America  
 ; ZIP: 77210  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/726,214  
 ; FILING DATE: Concurrently Herewith  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 60/005,498  
 ; FILING DATE: 04-OCT-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Highlander, Steven L.  
 ; REGISTRATION NUMBER: 37,642  
 ; REFERENCE/DOCKET NUMBER: UTSD:450  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (512) 418-3000  
 ; TELEFAX: (512) 474-7577  
 ; INFORMATION FOR SEQ ID NO: 11:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 4131 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 US-08-726-214-11

Query Match	79.3%	Score 1437.2;	DB 3;	Length 4131;
Best Local Similarity	87.5%;	Pred. No. 0;		
Matches 1584;	Conservative	0;	Mismatches 223;	Indels 3;
Gaps 1;				

[illegible]

Db 807 TTCCCATTCGATGCGAGCGCGTCTCAGTGGCCCTGGGTCTTTCCACCCCTGCATTGGA 866  
QY 185 TCTTGGCCCTGGCAACTAAACGCTGGTGATGCTTCTCTCTGGAAGCAGCTCGGTGCCAATG 244  
Db 867 TTTTGGCCCTGGCAATCAACATGGTGACCCCTTCTCTTGGGAAGCAGCTCGGTGCTAAGC 926  
QY 245 TGTGCTGTCTCTCTGACCAACGTCATTAGCATCTGCACACACTATCCAGCAGAGGCTC 304  
Db 927 TGGTGCTCTCTCTGACCAATGCCATCGGTCTCTGCACGCACTACCCCGCTGAAGTGT 986  
QY 305 CTCAGCGCCAGGCTTTTCAGGAGACCCCGAGTTACATCCAGGCCCGGCTCCACCTGCAGC 364  
Db 987 CTCAGCGCCAGGCTTTTCAGGAGACCCCGTGGTTACATCCAGGCCCGGCTGCACCTGCAGC 1046  
QY 365 ATGAGAAATCGGAGCAGGAGCGGCTGCTGCTGCTCGGTATTGCCCGCCAGCAGCTTGCATCG 424  
Db 1047 ATGAGAAATCGAGCAGGAGGAGCGGCTGCTGCTGCTGGGTATTGCCCGCCAGCATTTGCCATGG 1106  
QY 425 AGATGAAAGAAAGACATCAACACAAAAAAGAAAGAC---ATGTTCACAAAGATCTACATAC 481  
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QY 482 AGAAGCATACAAATGTCAGCATCTCTGTCAGACATTCAGGCGCTTCACAGCCTGGGCAT 541  
Db 1167 AGAAGCATACAAATGTCAGCATCTCTGTCGCGACATCGAGGCGCTTCACAGCCTGGGCCT 1226  
QY 542 CCAGTGTCACTGCGCAGGAGCTGGTTCATGACCTGTAATGAGCTCTTTGCCCGGTTTGACA 601  
Db 1227 CCCAGTGTCACTGCGCAGGAGCTGGTTCATGACCTGTAATGAGCTCTTTGCCCGGTTTGACA 1286  
QY 602 AGCTGCTCGGAGAAATCACTGCCTGAGATCAAGATCTTTGGGGACTGTTACTACTGTG 661  
Db 1287 AGCTGCTCGGAGAAATCACTGCTGAGGATCAAGATCTTTAGAGACTGTTACTACTGTG 1346  
QY 662 TGTGAGGCTCGCGAGGCGCGGCGGACCATGCCACTGCTGCTGTGGAGATGGGGGTAG 721  
Db 1347 TGTGAGGCTCGCGAGGCGCGGCGGAGACCATGCCACTGCTGCTGTGGAGATGGGGGTAG 1406  
QY 722 ACATGATTCAGGCAATCTCGCTGGTACGTGAGTGCAGCTGTAATGTAACATGCGCGG 781  
Db 1407 ACATGATTCAGGCAATCTCGCTGGTACGTGAGTGCAGCTGTAATGTAACATGCGCGG 1466  
QY 782 TGGGATCCACAGCGCGCGCTGCATCGCGGCTCTTGGCTTGGCGAAATGGCAGTTGC 841  
Db 1467 TGGGATCCACAGCGCGCGCTGCATCGCGGCTCTTGGCTTGGCGAAATGGCAGTTGC 1526  
QY 842 ATGTGTGGTCCAAATGATGTACCTGGCCCAACCATGGAAGCAGGAGCCCGGGCTGGCC 901  
Db 1527 ATGTGTGGTCCAAATGATGTACCTGGCCCAACCATGGAAGCAGGAGCCCGGGCTGGCC 1586  
QY 902 GCATCCACATCACTCGGCGCAACACTGCAGTACCTGAACGGGACTACGAAGTGGAGCCAG 961  
Db 1587 GCATCCACATCACTCGGCGCAACACTGCAGTACCTGAACGGGACTATGAGTGGAGCCAG 1646  
QY 962 GCGGTGGTGGCAAGCGCAACCGCTACCTCAAGAGCAGACATGAGACTTTCCCTCATCC 1021  
Db 1647 GCGGTGGTGGCAAGCGCAACCGCTACCTCAAGAGCAGTGCATTTGAGACCTTTCCCTCATAC 1706  
QY 1022 TGGGCGCCAGCAGCAAAACGGAAGAGGAGAGGATGCTGCCAGCTGCAGCAGCACTC 1081  
Db 1707 TAGGAGCCAGCAGCAAAACGGAAGAGGAGAGGATGCTGCTCAAGCTGCAGCAGCGAGC 1766  
QY 1082 GGGCCAACTCCATGGAAGGCTGATGCCCGGATGGGTCTCTGATCGTGCCTTCTCCCGGA 1141  
Db 1767 GGGCCAACTCCATGGAAGGACTGATGCCCGGCTGGTCTCTGACCGTGCCTTCTCCCGGA 1826  
QY 1142 CCAAGACTCCAGGCTTTCCCGCAGATGGGCATTTGATGATTTCCAGCAAGAACCCGGG 1201  
Db 1827 CCAAGACTCTTAAGGCTTTCCGACAGATGGGCATGGCATGCTGACTAGCAAAAGAAACCCGG 1886  
QY 1202 GCACCCAGATCCCTGACCTGAGGATGAGTGGATGAGTTCCTTGAGCCGTGCCATCG 1261

Db 1887 GTGCCCAAGATGCTCTGAACCCCTGAGGATGAGTGGACAGAGTTTCTGGCCCGGACCATCG 1946  
QY 1262 ATGCCCGCAGCATGATCAGCTGCGAAGCACCATGCTGCGCGGTTTTCGCTCACCTTCC 1321  
Db 1947 ATGCCCGAAGCATGACCAAGCTGCGTAAGAACCATGTCGCGCGGTTCTCTGCTCACCTTCC 2006  
QY 1322 AGAGAGAGATTTTGAAGAAAGTACTCTCCGGAAGTGGATCCCGCTTTTCGGAGCGCTAGC 1381  
Db 2007 AGAGGAGGATCTCGAGAAGAAGTATTCACGGAAGATAGACCCCTCGTTTCGGAGCGCTAGC 2066  
QY 1382 TTGCTGTGCCCTGTGGTCTTCTGCTTCATCTGCTTCATCTGCTTCATCTGCTTCATCTGCTTC 1441  
Db 2067 TCGCTGTGCCCTGTGGTCTTCTGCTTCATCTGCTTCATCTGCTTCATCTGCTTCATCTGCTTC 2126  
QY 1442 ACTCCACCCGTGATGCTGGGATTTATGCCAGCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1501  
Db 2127 ACTCCGCCCTGATACTCGGGATTTATGCCGGGATCTTCTTTTGTCTGGTTCACCGGTGC 2186  
QY 1502 TGATCTGTCTGTACTCTCTGTGGTCTTCTTCTTCCCTAAGGCCCTTGCAACCTGCTGTCTCC 1561  
Db 2187 TCATCTGTCTGTCTCTCTCTGTGGTCTTCTTCCCAACCGCTTGCAAGCGCTGTCTCC 2246  
QY 1562 GCAGCATGTCTCGCTCAGCGGCACATAGCACCGCAGTTGGGATCTTTTCCGCTCTGCTGTG 1621  
Db 2247 GCAGTATCTGCTCGCTCAGCGGTCACAGCAGCGGCTGTTGGAGTCTTCTCGGTTCTGCTTG 2306  
QY 1622 TGTCTTACTTCTGCCATTCGCAACATGTTTCACCTGTAACACACACCCCATACGAGCTGTG 1681  
Db 2307 TGTCTTACTTCTGCCATTCGCAACATGTTTCACCTGTAACACACACCCCATACGAGCTGTG 2366  
QY 1682 CAGCCCGGATGCTGAATTTAACACCTGCTGACATCATGCTGCTGCCCTGCCACCTGCGAGCTCA 1741  
Db 2367 CCGCCCGGATGCTGAATTTAACACCTGCTGACATCATGCTGCTGCCCTGCCACCTGCGAGCTCA 2426  
QY 1742 ATTACTCTTGGGCTGGATGCTCCCTGCTGTGAGGGGACCAATGCCACCTGCAGCTTTC 1801  
Db 2427 ATTACTCTTGGGACTGGAAGCTCCCTGCTGTGAGGGGACCCACCCACCTGCAGCTTTC 2486  
QY 1802 CTGAGGTGT 1811  
Db 2487 CTGAGTACTT 2496

RESULT 7  
US-09-473-716-1  
; Sequence 1, Application US/09473716  
; Patent No. 6436672  
; GENERAL INFORMATION:  
; APPLICANT: Tomlinson, James  
; APPLICANT: Cor Therapeutics, Inc.  
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL  
; FILE OF INVENTION: CYCLASE  
; FILE REFERENCE: 44481-5027-01-US  
; CURRENT APPLICATION NUMBER: US/09/473,716  
; CURRENT FILING DATE: 1999-12-29  
; PRIOR APPLICATION NUMBER: PCT/US98/13540  
; PRIOR FILING DATE: 1998-07-01  
; PRIOR APPLICATION NUMBER: 60/070,901  
; PRIOR FILING DATE: 1997-07-01  
; PRIOR APPLICATION NUMBER: 08/886,362  
; PRIOR FILING DATE: 1997-07-01  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 4523  
; TYPE: DNA  
; ORGANISM: human type V adenylyl cyclase  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (139)..(3921)  
US-09-473-716-1

Query Match 49.4%; Score 895; DB 4; Length 4523;



MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/726,214  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/005,498  
FILING DATE: 04-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L.  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: UTSD:450  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3924 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-726-214-9

Query Match 47.4%; Score 858.2; DB 3; Length 3924;  
Best Local Similarity 68.6%; Pred. No. 1.5e-219;  
Matches 1254; Conservative 0; Mismatches 548; Indels 27; Gaps 4;

QY 5 ACGTGTGCTGGGCATCTGGGGCGAGTGCAGTGCAGGTGGGGCGCTTTTCGAGCAGACGCCG 64  
DB 421 ATGCGCTCATTTGACGTGGTGGCTGCGGTCCAGGTAGTGGGCTGTTGCTGCCACAGCCAC 480

QY 65 GCAGCCCTCTCGGGCCCTGCTGGTCCCTGTTCTTTATACATCGCATACACCTCC 124  
DB 481 GCAGCCCTCTCGGGCCCTGCTGGTCCCTGTTCTTTATACATCGCATACACCTCC 540

QY 125 TCCCATCTCGCATCGGGCTGCGCTCTCAGGGGCTGCGGCTCTCCACCTTGCATTGA 184  
DB 541 TGCCTGTGCGCATAGGGCTGCGGTGCTCAGGGGGTGTCTGTGCGGCTCTCCACTTG 600

QY 185 TCTTGGCTTGGCACTTAACGTGGTGGTATGCTTCTCTGGAAGCAGCTGGTGGCAATG 244  
DB 601 CCATCTCTCTGCACACCAACGCCAGGACGAGTCTTCTGTGAACAGCTTGTCTCCAAG 660

QY 245 TGTCTGTCTCTCTCACCACGTCATTAGCATCTGCACACTATCCAGCAGAGGTCT 304  
DB 661 TCCCTATCTCTTGCACCAACATCGTGGGTGTGTGCTACTACTACCCAGCGAGGTCT 720

QY 305 CTCAGCGCAGGCTTTTCAGGAGACCCGAGTTACATCCAGGCGCGGCTCCACCTGCAGC 364  
DB 721 CCAGAGACAAGCTTTCAGAGAGACCGGGAGTGCATCCAAAGCTCGGCTCCACTCACAGC 780

QY 365 ATGAGATCGGAGCAGGAGGCTGCTGCTGCTGGTATGCTCCAGGCGCGGCTTGCATGG 424  
DB 781 GGGAGAACAGCAACAGAGGCTGCTGCTGCTGCTTCCCGCTCATGTTGCCATGG 840

QY 425 AGATGAAGAAGACATCAACAAAAAAGAAGA ---CATGTTCCACAAGATCTACATAC 481  
DB 841 AGATGAAGACGACATCAACGCAACAGAGAGATATGATGTTCCACAAGATTTACATCC 900

QY 482 AGAAGCATGACATGTGACATCTCTGTTTCAGACATATTGAGGCTTTCACAGCCTGGCAT 541  
DB 901 AGAAATGACATGTGAGCATCTCTTTGCTGCATCGAAGGCTTTCACATAGCCTGGCAT 960

QY 542 CCCAGTGCATCGGAGGAGCTGGTCAATGACCTGAATGAGCTCTTTGGCCCGGTTTGACA 601  
DB 961 CCCAGTGTACTGCCAAGAACTGGTCAATGACCTCAACGAGCTCTTCGCGCGGTTTGACA 1020

QY 602 AGCTGGCTCGGAGAAATCACTGCTGAGATCAAGATCTTGGGGAGCTTACTACTGNG 661  
DB 1021 AGTTGGCTCGGAGAAATCACTGCTGAGATCAAGATCTTGGGGAGTGTACTACTGTG 1080

QY 662 TGTGAGGCTGCGGAGGCGCGGCGACATGCCCACTGCTGTGTGGAGATGGGGTAG 721  
DB 1081 TCTCGGGCTGCTGAAGCCAGAGCTGACCAAGCCCACTGCTGCGTAGAGATGGGAATGG 1140

QY 722 ACATGATTGAGGCCATCTCGTGTAGTGTGAGGTGACAGGTGTGAATGTGAACATCGCG 781  
DB 1141 ACATGATGAGGCCATCTCGTGGTCCGGAGGTGACAGGGTGAACGTGAACATCGCTG 1200

QY 782 TGGGCATCCACAGCGCGCGGTGCATCTGGGCGTCTTGGCTTGCAGAAATGGCACTTCG 841  
DB 1201 TGGGAATTCACAGCGGAGAGTACATCTGGGCTGCTTGGCTTGCAGAAATGGCACTTCG 1260

QY 842 ATGTGTGGTCCCAATGATGTGACCTGGCCCAACACATGGAAGCAGGAAGCGGGCTGGCC 901  
DB 1261 AGTGTGTGTACAGTGTACACTGGCCCAACACATGGAAGCTGCGCGCAGGAGGCC 1320

QY 902 GCATCCATCTACTCGGGCAACACTGCATCTGAAACGGGGACTACGAAGTGGAGCCAG 961  
DB 1321 GCATCCATCTACTCGGGCAACACTGCATCTGAAACGGGGACTACGAAGTGGAGCCAG 1380

QY 962 GCGTGGTGGCAGCGCAACGGGTGCTCAAGSAGCAGCACATTTGAGACTTTCTCTCATCC 1021  
DB 1381 GCTGTGGTGGCAGCGCAATGCTCACTCAAGSAGCAGCACATTTGAGACTTTCTCTCATCC 1440

QY 1022 TGGGCGCCAGCCAGAAACGGAAGAGGAAAGGATGCTGGCCAAAGCTCGAGCGGACTC 1081  
DB 1441 TGGCGTGTACCCAGAAAGCGGAAGAGAGAGGCGCATGATCGCCAAAGATGAACCGCCAGA 1500

QY 1082 GGGCCAACTCCATGGAAGGGCTGATGCCGCGATGGGTCTCTGATCGTGGCTTCTTCC --- 1137  
DB 1501 GAACCAACTCCATTTGGACACAACTCCGCTCACTGGGAGCTGAGCGCCCTTCTACAACC 1560

QY 1138 -----CGGACCAAGGACTCCAGGCGCTTCCGCCAGATGGGCAATTTGAGGACCCCA --- 1617  
DB 1561 ACTTGGGTGGCAGGAGTGTCCAGGAAGTGAAGAGGATGGGCTTTGAGGACCCCA --- 1617

QY 1190 AAGACAACCGGGGACCCCAAGATGCCCTGAACCCCTGAGGATGAGGTGGATTTCTCTGA 1249  
DB 1618 ---AGGACAAGAATGCCAGGAAGTGCACACCTGAGGATGAAGTGGAGTGTCTGG 1674

QY 1250 GCGTGGCATGATGCCCGCAGCATGTAGTACGTGGGGAAGACCATGTGCGCGGCTTTT 1309  
DB 1675 GTCGAGCCATCATGTCAGGAGTATTGACAGACTTGGCATCCGAACACGTCGGAAGTTCC 1734

QY 1310 TGTCACTTCCAGAGAGAGGATTTTGAAGAAGTACTCCCGGAAGTGGATCCCGCT 1369  
DB 1735 TCTTGACCTTAGGGAGCCGACTTAGAAGAGAGTACTCCAAAGCAGGTGGATGACCGAT 1794

QY 1370 TCGAGGCTTACGTTGCTGTGCGCTGTGGTCTTCTGCTTCTGCTTCTCATCTCCAGCTTC 1429  
DB 1795 TTTGGTCTTATGTGGCTGTGCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1854

QY 1430 TAATTTCCACACATCCACCTGATGCTTGGGATTTATGCCAGCATCTTCTCTGCTGCTG 1489  
DB 1855 CCATTTGCTCCACATCCCTGTTTCATGCTGAGCTTTTACCTGCTGCTGCTTCTTCTTCTG 1914

QY 1490 TAATCACCTGCTGATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1549  
DB 1915 CTTTGGTGTGTTTATATCTGTGATCTAGCCTGTGTGAGCTCTTCCCTACTCCCTGCTG 1974

QY 1550 AACGCTGTGCTCCGAGCATTTCCGCTCAGGGCAGATAGCACCGCAGTTGGCATCTTTT 1609  
DB 1975 AGACACTCTCCAGGAAGATAGTGGGATCAAGAAAGAACAGCAGCCCTGCTGCGGGTGTTC 2034

QY 1610 CCGTCTGCTGTTGTTTACTTCTGCCATTTGCCAATGTTCCACTTACACACACCCCA 1669  
DB 2035 CCATCACCCTGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2094

QY 1670 TACGAGCTGTGCAGCGCGGATGCTGAATTTTAAACCTGCTGACATCACTGCTGCTGCTG 1729  
DB 2095 TGGTGGTGTGCTGGCAGAGGAGCACACATCACGGTGAACAGGTGAACGATGTCATG 2154





1270 AAGGACGAGCAGTTCACACCATGTACATGTACCGCCATGAGAATGTGACGATCCTG 1329  
QY 508 TTGTCAGACATTTAGGCGCTTACCAGCCTGGCATCCAGTGCACCTGGCAGGAGCTGGTC 567  
Db 1330 TTGTCAGATATTTGGCGCTTACCAGCCTGGCATCCAGTGCACCTGGCAGGAGCTGGT 1389  
QY 568 ATGACCCCTGAATGAGCTCTTTGGCGGCTTTGACAAGCTGGCTGGGAGATCACTGCTG 627  
Db 1390 AAGCTACTCAACGAGCTCTTTGGCGGCTTTGACAAGCTGGCGCCCAATACACAGCTG 1449  
QY 628 AGATCAAGATCTTTGGGGGACTGTTACTACTGTGTGTCAGGCTGGCGGAGCCCGGCC 687  
Db 1450 AGATCAAGATCTTAGCGGACTGTTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1509  
QY 688 GACCATGCCACCTGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTGCTGGTA 747  
Db 1510 GACCATGCCCTGTGCTCCATCTGTGATGGGCTTTGCCATGTGAGGCCATCTGCTAGTG 1569  
QY 748 CGTGAGGTGACAGGTGTGAATGTGAACATCGCGTGGGCTATCCACAGCGCGGCTGCAC 807  
Db 1570 CGGAGAGACCAAGACCGGAGTGGACATCGTGTGGGGTGCACACAGGACTGTGCTA 1629  
QY 808 TGGCGGCTCTTGGCTTGGCGAATGACGATTCGATGTGTGGTCCCAATGATGACCCCTG 867  
Db 1630 GGTGGCTCTTGGCGGAGAGCGTGGCAGTATGATGTATGGTCTACCGATGTCACTGTG 1689  
QY 868 GCAACACATGGAAGCAGAGCGCGGCTGGCGGCTATCCACAGCGCGGCTGCACACTG 927  
Db 1690 GCAACAGATGAGGCTGGCGGCTATCCACAGCGCGGCTGCACATTTCCACAGACCATG 1749  
QY 928 CAGTACCTGAACGGGACTACGAGTGGAGCGGCGGCTGGGCGGCTGGGCGGCGGCTGAC 987  
Db 1750 GACTGCTGAAGGGAGTTCGATGTGCAACCTGGTTCATGCTGGCAGTCTGCTGCTGCT 1809  
QY 988 CTCAGGAGCAGCAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1047  
Db 1810 CTAGATGAGAGGGCAGTCAAGCTACCTCATCTGCTTCCCAAGCGGAGGTTGAAGAAG 1869

RESULT 12  
US-08-726-214-15  
Sequence 15, Application US/08726214  
Patent No. 610706  
GENERAL INFORMATION:  
APPLICANT: Tang, Wei-Jen  
APPLICANT: Gilman, Alfred G.  
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYL CYCLASE  
TITLE OF INVENTION: AND USES THEREFOR  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/726,214  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/005,498  
FILING DATE: 04-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L.  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: UTSD:450

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4601 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-726-214-15

Query Match 17.7%; Score 320.6; DB 3; Length 4601;  
Best Local Similarity 59.5%; Pred. No. 7.8e-76;  
Matches 567; Conservative 0; Mismatches 374; Indels 12; Gaps 1;

QY 79 GGCTCTGGTGGCCCTGTTGTTGATACATCGCATCGCATCGCTCCCTCCCATCCGCGATG 138  
Db 1575 GGCATAGGCTACGCTGCTTTTACACCTTCCGCCACCTACACAGCATGCTTCGCGCTGCTCTC 1634  
QY 139 CGGCTGCGCTCCTCGAGCGGCTCTCCACCTTGCATTTGATTTGATCTTTGGCTGGCAA 198  
Db 1635 ACCTGGCCATCTTGGCGGCTGGGACATCTTCTGCTGCAAGTCACACTTCAGTGCCTC 1694  
QY 199 CTTAACCGTGGTGTGATGCTTCTCTGGAAGCAGCTGGTCCCAATGCTGCTGCTTCCCTC 258  
Db 1695 ATACCCAGACTAGCGGCTTTTCCATCAACCCAGGCTCTGCCCGAGGTGGTCTTCTCATG 1754  
QY 259 TGACACCACTGATAGCATCTGCACACATNTCCACAGCAGAGTGTCTCAGCGCCAGGCC 318  
Db 1755 TGCATGAATACAGCAGCATCTTTCATCAGTTACCTTTTCAGACCGCGGCCAGCGCGGCC 1814  
QY 319 TTTTCAGAGACCGCAGCTTACATCCAGCGCGCTCCACCTGCAGCATGAGAAATCGGCAG 378  
Db 1815 TTCTTGAGACCGCGAGGTGTGGAGCGCAGGCTCGCTCGGACAGAGAACCAAGA 1874  
QY 379 CAGGAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 438  
Db 1875 CAGGAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1934  
QY 439 ATCAACACAAAAAAGAG-----ACATGTTCCACAGATCTACATACACAAG 486  
Db 1935 ATGACCAATGTGGAGGAGCAGCAGCTGACGATCAGTTCCACCGCATCTCATCATCGC 1994  
QY 487 CATGACAATGTGACATCTCTGTTGACAGATTTGAGGCTTTCACAGCGCTGGCATCCAG 546  
Db 1995 TAGGAGACCTGAGTATCTTTTGGAGATGCTCAAGAGATTACCAACCTCTCTACGACC 2054  
QY 547 TGACCTGCGCAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 606  
Db 2055 TTGCTGCTCAGGAGCTTGTGAGGATGCTCAACGAGCTCTTTCAGATTTGATCGGCTG 2114  
QY 607 GCTGCGGAGAACTCACTGCTGAGATCAAGATCTTGGGGGAGCTGTTACTACTGCTGCTCA 666  
Db 2115 GCGCATGAGCATCTGCTTTCGATTTAAATCTCGGGGAGCTGCTACTACTGCTGCTCA 2174  
QY 667 GGGCTGCGGAGGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 726  
Db 2175 GGACTGCTGAGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2234  
QY 727 ATTGAGGCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 786  
Db 2235 ATCAAAACTATCAGGTTTGTGAGGATCCAGAACGAGCATGATGTTGACATGCGAAATTTGA 2294  
QY 787 ATCCACAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 846  
Db 2295 ATCCATTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2354  
QY 847 TGGTCCAAATGATGTGACCTCGGCAACACATGGAAGCAGGAGCGGCGGCGGCGGCGGCGG 906  
Db 2355 TGGCTTGGGATGTGGACATCGCAAAACAACTTGAATCTGGAGGAATCCCTGGGAGATT 2414  
QY 907 CACATCACTCGGCGCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 966



Db 2415 CACATTTCCAAAGCCACACTGGAATTCCTCTACGTGTGACTATATAATGTGGAAGAGGGCCAC 2474

QY 967 GGTGCAAGCGCAAGCGGTACCTCAAGGAGCAGACATGTGACATTCCTCAT 1019

Db 2475 GGTAAAGGAGGAGGAATCTCTTGAGGAGCATAATATAGACACCTATTGTAT 2527

RESULT 13

US-08-726-214-13

; Sequence 13, Application US/08726214

; Patent No. 6107076

; GENERAL INFORMATION:

; APPLICANT: Tang, Wei-Jen

; APPLICANT: Gilman, Alfred G.

; TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE

; TITLE OF INVENTION: AND USES THEREOF

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: Texas

; COUNTRY: United States of America

; ZIP: 77210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/726,214

; FILING DATE: Concurrently Herewith

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/005,498

; FILING DATE: 04-OCT-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Highlander, Steven L.

; REGISTRATION NUMBER: 37,642

; REFERENCE/DOCKET NUMBER: UTSD:450

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (512) 418-3000

; TELEFAX: (512) 474-7577

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 5199 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-726-214-13

Query Match 17.2%; Score 311.2; DB 3; Length 5199;

Best Local Similarity 62.2%; Pred. No. 2.7e-73;

Matches 524; Conservative 0; Mismatches 288; Indels 30; Gaps 1;

QY 220 CTCTGGAAGCAGCTCGGTGCCAATGTGCTGTCTTCCCTGCAACCAAGCTATTAGCATC 279

Db 1210 CTGGGCTGCAGCTCTCTGSCCAATCCCGTTATCTCTCTGGTGGGAATTCACGGGTGCC 1269

QY 280 TGCACACACTATCCAGCAGAGAGGTGCTCAGCGCCAGGCTTTTCAGGAGACCCGCGAGTTAC 339

Db 1270 TTCCCAAGCAGCAGCTGCAGGACGCGTCCAGGGATCTCTTATCTACACCGTCAAAATGC 1329

QY 340 ATCCAGGCGCGCTCCAGCTGCAGCATGAGATCGGACGAGGCGGTGCTGCTGCTCG 399

Db 1330 ATCCAGATCCGTCGGAAGCTCTGCTGGGAGAGCCGCCAACAGCAACCTGCTCTGTCA 1389

QY 400 GTATTGCCCCAGCAGCTTGCCATGAGATGAAAGAGACATCA-----442

Db 1390 GTGCTCCAGCAGCACACTCTCCATGGGTATGAGCTGGCCATCATTTGAGCGCTCAAGAG 1449

QY 443 -----ACACAAAAAAGAACACATGTTTCCACAGATCTACATACGAAGCAT 489

Db 1450 GGTGTGACCGACACTACATGCCCGCAGCAACAACATTTTCACAGGCTCTATGTCAAGCGGCAC 1509

QY 490 GACAATGTACAGATCCTGTGTTGCAGACATTTAGGGCTTTCACCAGGCTTGGCATCCCAAGTGC 549

Db 1510 CAGAATGTACAGATCCTGTATGCAGACATCTGGGCTTTCACGAGGCTGCCAGCAGCTGC 1569

QY 550 ACTGCGCAGGAGCTGTGTCATGACCTGAATGAGCTCTTTGCCCCGTTTGTACAAAGTGGCT 609

Db 1570 TCTCCCAAGGAGCTGTGTGTGCTCAAGGAGCTGTTTGGGAAGCTTTCACCAAGATTGCT 1629

QY 610 CGGAGAAATCACTGCTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTGTGTCAGG 669

Db 1630 AAGGCCAATGATGTCATCGGATCAAGATCTCTGGTGACTGTTACTACTGCTGTCAGGC 1689

QY 670 CTGCGGAGGCGCGCGCGACCATGCCACTGCTGTGTGGAGATGGGATGGGATGACATGATT 729

Db 1690 CTGCGCGTATGCTGCCACACATGCCCGCAACTGTGTGAAGATGGGCTGGACATCTGC 1749

QY 730 GAGGCCATCTCGCTGTGACGTGACAGGTGAGTGAATGTGAACATGCGCTGGGCATC 789

Db 1750 GAGGCCAATTAAGCAGGTGCTGAGGCCAGCGGTGGACATCAGCATGCGTGTGGCATT 1809

QY 790 CACAGCGGCGGTGCTGCTGCGGCTGCTGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 849

Db 1810 CACTCCGGGAATGTCTATGTGGGCTCATCGGGCTCCGTAAGTGGCAGTATGATGTGTG 1869

QY 850 TCCAATGATGTGACCTGCGCAACACATGGAAGCAGGAAGCGGCTGGCGGCATCCAC 909

Db 1870 TCCCATGATGTCTCCCTGGCCACAGGATGGAGGAGCTGGAGTCCCTGGCCGGGTGCAC 1929

QY 910 ATCACTCGGGCAACACTGCACTGACGTACCTGAACGGGGACTACGAAGTGGAGCAGCGTGT 969

Db 1930 ATCAGAGGCAACATTAATCACTCCGCAAGCATACGAGGTGAGGATGGCATGGG 1989

QY 970 GCGAAGCGCAAGCGCTGCTGCTGAGGAGCAGCAGCATTTCTCTATCTGCGGCGGC 1029

Db 1990 GAGCAGCAGAGACCCCTATCTGAAAGAGATGAACATCCGAACCTACCTGCTGATCATCCC 2049

QY 1030 AG 1031

Db 2050 CG 2051

RESULT 14

US-08-307-896-5

; Sequence 5, Application US/08307896C

; Patent No. 6034071

; GENERAL INFORMATION:

; APPLICANT: Iyengar, Srinivas Ravi

; TITLE OF INVENTION: MUTANT ACTIVATED GSALPHA AND ADENYLYL

; TITLE OF INVENTION: CYCLASE 2 FOR USE AS THERAPEUTIC AGENTS

; FILE REFERENCE: 29770

; CURRENT APPLICATION NUMBER: US/08/307,896C

; CURRENT FILING DATE: 1994-09-16

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 5

; LENGTH: 4008

; TYPE: DNA

; ORGANISM: Rattus norvegicus

US-08-307-896-5

Query Match 15.8%; Score 286; DB 3; Length 4008;

Best Local Similarity 60.7%; Pred. No. 1.3e-66;

Matches 503; Conservative 0; Mismatches 295; Indels 30; Gaps 1;

QY 219 CCTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTCTGCTCTGCAACCAAGCTATTAGCAT 278

Db 624 CTTGTTCTGGCAGACTGCGCAATGTGATCATTTTTCATTTTGTGGAACTTGGCGGGAGC 683

QY 279 CTGCACACACTATCCAGCAGAGGTGCTCAGCGCCAGGCTTTCAGGAGAGCCCGCAGTTA 338

Db 684 CTACCACAAGCACCTTCATGGAGCTTGCCTTGACGAACACCTATTCGGGACACGCTGAATTG 743



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Qy 339 CATCCAGCCCGGCTCCACCTGCAGCATGAGAATCGGCAGCAGGCGGTGCTGCTGTC 398
Db 744 CATCAAGTCCCGGATCAAGCTGGATTTGAAAACGCGCAGCAGGAGCGCTCTGCTGTC 803
Qy 399 GGTATTGCCCGCAGCAGCTGTCATGGAGATGAAAGAACATCA----- 442
Db 804 CTGCTGCCAGCTCATCTGCATGCGATGGAGATGAAAGCTGAAATCATTCAGAGGCTGCAGGG 863
Qy 443 -----ACACAAAAGAGAGACATGTTCCACAAAGATCTACATACAGAAGCA 488
Db 864 CCCAAAGCAGGAGATGGAAACACAAACAACTTCCAAATCTGTATGTCAAAACGACA 923
Qy 489 TGACAATGTCAGCATCTGTTTGAGAGATGAGGGCTTCCAGCCTGGCAGTCCCAAGT 548
Db 924 CACCAAGTGAGCATATATACGCTGACATGTTGGCTTACCCGCCCTTGCAGCGGATTG 983
Qy 549 CACTGGCAGAGCTGTCATGACCCCTGAATGAGCTCTTCCCGCGTTTGACAGCTGGC 608
Db 984 CTCCTGTCGCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 983
Qy 609 TGCGGAGATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1043
Db 668 TGCGGAGATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 668
Db 1044 AAGAGAGATGAATGAGATGAGAAATTTAGGAGCTGCTATCTACTGTGTTCCGG 1103
Qy 669 GCTGCGGAGCCCGGCGCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 728
Db 1104 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1163
Qy 729 TGAGGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 788
Db 1164 GCGAGGCAATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1223
Qy 789 TGAGGCAATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 848
Db 1224 GATTTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1283
Qy 849 GTCCAAATGATGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 908
Db 1284 GTCTCATGATGTTACTCTGCGCAACCATGAAAGCTGGAGGAGTCCCTGGCGGTGTTCA 1343
Qy 909 CATCACTCGGCAACACTGAGTACCTGAAAGCAGGAGCGCGGCTGCGCCGATCCA 968
Db 1344 CATTTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1403
Qy 969 TGGCAAGCGCAACGCTACCTCAAGGAGCAGCAGCATGAGACTTTCCT 1016
Db 1404 TGAGTAAGACCCATATTTAAGCAGCAGCTTGGTGAACCTACTT 1451

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RESULT 15
US-08-726-214-3
; Sequence 3, Application US/08726214
; Patent No. 6107076
; GENERAL INFORMATION:
; APPLICANT: Tang, Wei-Jen
; APPLICANT: Gilman, Alfred G.
; TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYL CYCLASE
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/726,214
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/005,498
; FILING DATE: 04-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: UTSD:450
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4008 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-726-214-3

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Query Match 15.88; Score 286; DB 3; Length 4008;
Best Local Similarity 60.7%; Pred. No. 1.3e-66;
Matches 503; Conservative 0; Mismatches 295; Indels 30; Gaps 1;

Qy 219 CCTCTGGAAGCAGCTCGGTGCAATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 278
Db 624 CCTGCTGGCAGATAGTGGCCAAATGTGATCATTTTCATTTGTGGAACTTTGGCGGAGC 683
Qy 279 CTGCACACATATCCAGCAGAGGTGTCTCAGCGCCAGGCTTTCAGGAGACCCGAGTTA 338
Db 684 CTACCAAGCAGCTCATGGAGCTTGCCTTCAGCAAACTATCGGGACAGCTGTAATTG 743
Qy 339 CATCCAGCGCGCTCCACCTGCAGCATGAGAATCGGCAGCAGGCGCTGCTGCTGCTC 398
Db 744 CATCAAGTCCCGGATCAAGCTGGAATTTGAAAACGCGCAGGAGAACGCTCCTGCTCTC 803
Qy 399 GGTATTGCCCGCAGCAGCTTGCCTGAGATGAAAGAACATCA----- 442
Db 804 CTGCTGCCAGCTCATCTGCGCATGGAGATGAAAGCTGAAATCATTCAGAGGCTGCAGGG 863
Qy 443 -----ACACAAAAGAGAGACATGTTCCACAAAGATCTACATACAGAAGCA 488
Db 864 CCCAAAGCAGGAGATGGAAACACAAACAACTTCCAAATCTGTATGTCAAAACGACA 923
Qy 489 TGACAATGTCAGCATCTGTTTGAGAGATGAGGGCTTCCAGCCTGGCAGTCCCACTG 548
Db 924 CACCAAGTGAGCATATATACGCTGACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 983
Qy 549 CACTGCCAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 608
Db 984 CTCCTGTCGCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1043
Qy 609 TGCGGAGATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 668
Db 1044 AAGGAGAAATGAATGAGATGAGAAATTTTAGGAGAGCTGCTATCTACTGTTGCTCGG 1103
Qy 669 GCTGCGGAGCGCGCGCGCAGCAGTCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 728
Db 1104 GCTCCTTATATCACTTCCCTAACCATGCAAGAACTGTGTGAAATGGATTTGGATATG 1163
Qy 729 TGAGGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 788
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Qy 789 CCACAGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 848
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Qy 849 GTCCAAATGATGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 908
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QY 909 CATCACTCGGGCAACACTGCAGTACCTGAACGGGGACTACGAAAGTGGAGCCAGGCCGTGG 968  
Db 1344 CATTCTTCAGTCACTCTGGGACACTTGAATGGGGCTTATAAAGTGGAGGAGGAGATGG 1403  
QY 969 TGGCAAGCGCAACCGGTACCTCAAGGAGAGCAGCACATTGAGACTTTCCT 1016  
Db 1404 TGAGATAAGAGAGACCCATATTTAAAGCAGCACCTTGGTGAACCCTACTT 1451

Search completed: March 1, 2003, 04:05:16  
Job time : 85.382 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2003, 21:13:01 ; Search time 3111.21 Seconds  
(without alignments)  
16949.756 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 4109280

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Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 2: gb.htg.\*
- 3: gb.in.\*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1812	100.0	1812	6	AR174472	AR174472 Sequence
2	1812	100.0	1812	6	AX189759	AX189759 Sequence
3	1808.4	99.8	3549	6	AR174473	AR174473 Sequence
4	1808.4	99.8	3549	6	AX189761	AX189761 Sequence
5	1763.4	97.3	3552	6	AX189766	AX189766 Sequence
6	1763	97.3	6463	9	AF250226	AF250226 Homo sapi
7	1657.8	91.5	3582	6	AX189768	AX189768 Sequence
8	1604.2	88.5	5877	9	AB007882	AB007882 Homo sapi
9	1527.8	84.3	4046	4	DOGADENCYC	M94968 Canis faml
10	1519.8	83.9	4046	6	I29958	I29958 Sequence 1
11	1449.4	80.0	3465	10	MUSADNLCYC	M96653 Mus musc
12	1437.2	79.3	4131	6	AR106659	AR106659 Sequence
13	1437.2	79.3	4131	10	RATADCYB	M96160 Rattus norv
14	1431.8	79.0	5841	6	AX305965	AX305965 Sequence
15	1431.8	79.0	5841	10	MUSADCYC	M93422 Mouse adeny
16	1427.6	78.8	6036	10	RATADC	L01115 Rattus norv
17	906.2	50.0	4995	4	OCMRADCYV	Z29371 O.cuniculus
18	886.6	48.9	4545	4	DOGADENCYC	M88649 Canis faml
19	858.2	47.4	3924	6	AR106658	AR106658 Sequence
20	858.2	47.4	4847	10	RATADCYA	M96359 Rattus norv
21	811	44.8	2743	9	AF497517	AF497517 Homo sapi
22	799	44.1	3137	6	AX418303	AX418303 Sequence
23	798	44.0	2554	9	AK093840	AK093840 Homo sapi
24	780	43.0	4236	5	GGA293817	AJ293817 Gallus ga
25	667.2	36.8	2429	4	DOGADCYC	M97896 Canis faml
26	436	24.1	3978	4	BOVADC	M25579 Bovine aden
27	436	24.1	3978	6	AR106654	AR106654 Sequence
28	415.2	22.9	2857	10	AF053980	AF053980 Mus muscu
29	404	22.3	3811	6	AX418306	AX418306 Sequence
30	393.2	21.7	1652	6	AR106662	AR106662 Sequence
31	362.2	20.0	7546	3	DRORAC	M81887 Drosophila
32	340	18.8	6193	4	BTACILMR	Z49806 B.taurus mr
33	339	18.7	3563	9	AB011083	AB011083 Homo sapi
34	339	18.7	4080	9	AK027857	AK027857 Homo sapi
35	339	18.7	4142	9	AF033861	AF033861 Homo sapi
36	338.2	18.7	6005	9	HSADENCYR	Z35309 H.sapiens m
37	335.6	18.5	4533	6	AR106656	AR106656 Sequence
38	335.6	18.5	4533	10	RATADCY3	M55075 R.norvegicu
39	333.2	18.4	3674	10	AF458089	AF458089 Mus muscu
40	320.6	17.7	4601	6	AR106661	AR106661 Sequence
41	320.6	17.7	4601	10	RATACVII	L26986 Rat adenyly
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44	316.6	17.5	3243	6	AX463632	AX463632 Sequence
45	316.6	17.5	6196	6	AX463638	AX463638 Sequence

ALIGNMENTS

RESULT 1	AR174472	Sequence 3 from patent US 6306830.	1812 bp	DNA	linear	PAT 17-DEC-2001
LOCUS	AR174472	Sequence 3 from patent US 6306830.				
DEFINITION	AR174472	Sequence 3 from patent US 6306830.				
ACCESSION	AR174472	Sequence 3 from patent US 6306830.				
VERSION	AR174472.1	GI:17914792				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 1812)					
AUTHORS	Hammond,H.Kirk., Insel,P.A., Ping,P., Post,S.R. and Gao,M.					
TITLE	Gene therapy for congestive heart failure					
JOURNAL	Patent: US 6306830-A 3 23-OCT-2001;					
FEATURES	Location/Qualifiers					

source	1. .1812
BASE COUNT ORIGIN	361 a    539 c    507 g    405 t
Query Match	100.0%; Score 1812; DB 6; Length 1812;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 1812; Conservative	0; Mismatches 0; Indels 0; Gaps
Qy	1 GTTAACTGGTGCTGGGCATCCTCGGCGCACAGTCAGAGTCGGGGCGCTTTTCGACGACGAC 60
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Qy	1 GTTAACTGGTGCTGGGCATCCTCGGCGCACAGTCAGAGTCGGGGCGCTTTTCGACGACGAC 60
Db	
Qy	61 CCGCGCAGCCCTCTCGGGGCCCTCTGTGCCCCTGTGTTCTTTGTATACATTCGATACAG 120
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Db	
Qy	181 TTGATCTTGGCTGGCAACTTAACCCGTGGTGATGCCCTTCTCTGGAAGCAGCTCGGTGCC 240
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Qy	361 CAGCATGAGATCGGCAGCAGGAGCGGCTGCTGCTGCGTATTTGCCCAGACAGTTGGC 420
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Qy	421 ATGGAGATGAAAGAAGACATCAACAAAAAAGAGACATGTTCCACAAGATCTACATA 480
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Qy	541 TCCCAGTGCACTGCGCAGGAGCTGGTCATGACCCCTGAATGAGCTCTTTGCCCGGTTTGAC 600
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Qy	541 TCCCAGTGCACTGCGCAGGAGCTGGTCATGACCCCTGAATGAGCTCTTTGCCCGGTTTGAC 600
Db	
Qy	601 AAGCTGGCTCGGAGAACTACTGCCTGAGGATCAAGATCTTTGGGGACACTGTTACTACTGT 660
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Qy	601 AAGCTGGCTCGGAGAACTACTGCCTGAGGATCAAGATCTTTGGGGACACTGTTACTACTGT 660
Db	
Qy	661 GTGTCAGGGCTGCGGAGGCCCGGCGACCATGCCCACTGCTGTGTGGAGATGGGGGTA 720
Db	
Qy	721 GACATGATGAGGCCATCTCGCTGGTACGTGAGGTGACAGGTGTGAATGTGRAACATGCCG 780
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Qy	781 GTGGGCATCCACAGCGGGCGGTGCATCTGGCGGCTGCTTTGGCTTTCGGGAAATGGCAATTC 840
Db	
Qy	841 GATGTGTGTTCCAATGATGTGACCCCTGGCCAACCCATGGAAGCAGGAAGCCGGGCTGGC 900
Db	
Qy	901 CGCATCCACATCACTCGGCGAAACACTGCACTACTGAAACGGGACCTACGAAGTGGAGCCA 960
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Db	841	GATGTGTGGTCCAATGATGTACCCCTGGCCCAACACACATGGAAGCAGGAGCCGGCTGGC	900
QY	901	CGCATCCACATCACTCTGGGCAACACTCGATACCTGAACGGGGGACTACGAAGTGGAGCCA	960

Db 901 CGCATCCACATCACTCGGGCAACACTGCGAGTACCTGAACGGGGACTACGANGGAGCCA 960

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Db 961 GGCCGTGGCAAGCGCACGGCGTACCTCAAGGAGCAGCACATTGAGACTTTCCTCATC 1020

QY 1021 CTGGGCGCCAGCCAGAAACGGAAAGAGGAGAGGATCTGSCCAAGTCACAGCGGACT 1080  
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Db 1021 CTGGGGCCAGCCAGAAACGAAAGGAGAGGATGTCGGCCAGCTGCAGCGGACT 1080

QY 1081 CGGGCCAACTCCATGGAAGGCTGATCCCGGATGGGTTCTCTGATCGTGCCTTCTCCCGG 1140

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Db 1441 CACTCACCCCTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGCTGCTAATCACCGTG 1500

Qy 1501 CTGATCTGTGTGTGTACTCCTGTGCTTCTGTCCCTAAGGCCCTGCAAGTCTGTCC 1560

Db 1501 CTGATCTGTGCTGTGTA

Qy 1561 CGCAGCATTGCCGCTCAGCGGCACATAGCACCGCAGTTGCATCTTTTCGGTCCCTGCTT 1620

Db 1561 CGCAGATTGTCGGCTACGGGCACATAGCACCGCAGTTGGCATCTTTTCCGTCCTGCTT 1620

Qy 1621 GTGTTTACTTCTGCGCATTCGCAACATGTTCACTGTAAACACCCCCCATACGGAGCTGT 1680

Db 1621 GTGTTACTTCTGCCATTGCCAACATGTTACCTGTAAACACACCCCCCATACGGAGCTGT 1680

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Db 1681 GCAGCCGGATGCTGAATTTAACACCTGCTGACATCACTGCCCTGCCACCTGCAGCAGTC 1740

QY 1741 AATTACTCTCTGGGGCTGGATGCTCCCCCTGTGTGAGGGCACCATGCCACCTGCACCTTT 1800

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Qy 1801 CCTGAGGTGTTT 1812  
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Db 1801 CCTGAGGTGTC 1812

### RESULT 3

AR174473	AR174473	3549 bp	DNA	linear	PAT 17-DEC-2001
LOCUS					

DEFINITION Sequence 5 from patent US 6306830.  
ACCESSION ARI74473

VERSION AR174473.1 GI:17914793

RESULT 3	AR174473	LOCUS	AR174473	3549 bp	DNA	linear	PAT 17-DEC-2001
DEFINITION	Sequence 5 from patent US 6306830.	ACCESSION	AR174473				
VERSION	AR174473.1	GI:	17914793				

LOCUS	AR174473	3549 bp	DNA	linear	PAT 17-DEC-2001
DEFINITION	Sequence 5 from patent US 6306830.				
ACCESSION	AR174473				
VERSION	AR174473.1	GI:17914793			

KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 3549)
AUTHORS	Hammond,H.Kirk., Insel,P-A., Ping,P., Post,S.R. and Gao,M.
TITLE	Gene therapy for congestive heart failure
JOURNAL	Patent: US 6306830-A 5 23-Oct-2001;
FEATURES	Location/Qualifiers
source	1..3549
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ORIGIN	/organism="unknown"
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Best Local Similarity	99.9%; Pred. No. 0;
Matches 1809; Conservative	0; Mismatches 1; Indels 0; Gaps
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Qy 63	GCGCAGCCCCCTCTGCGGGCCTCTGGTGCCTCTGTTCTTTGTATACATCGCATACACGCT 122
Db 696	GCGCAGCCCCCTCTGCGGGCCTCTGGTGCCTCTGTTCTTTGTATACATCGCATACACGCT 755
Qy 123	CCTCCCATCCGATCGGGCTGCCGCTCTCAGCGCCTGGGCTCTCCACCTTGCATTT 182
Db 756	CCTCCCATCCGATCGGGCTGCCGCTCTCAGCGCCTGGGCTCTCCACCTTGCATTT 815
Qy 183	GATCTTGGCTTGCACACTTAACCGTGGTGATGCCTTCTCTGGAAGCAGCTCGGTGCCAA 242
Db 816	GATCTTGGCTTGCACACTTAACCGTGGTGATGCCTTCTCTGGAAGCAGCTCGGTGCCAA 875
Qy 243	TGTGCTGCTGTTCTCTGCACCAACGTCATTAGCATCTCCACACACTATCCAGCAGAGGT 302
Db 876	TGTGCTGCTGTTCTCTGCACCAACGTCATTAGCATCTCCACACACTATCCAGCAGAGGT 935
Qy 303	GTCTCAGCGCCAGGCTTTTCAGGAGACCCGCGAGTTACATCCAGGCCGGCTCCACCTGCA 362
Db 936	GTCTCAGCGCCAGGCTTTTCAGGAGACCCGCGAGTTACATCCAGGCCGGCTCCACCTGCA 995
Qy 363	GCATGAGAATCGGCAGCAGAGCGGCTGCTGCTCGGTATTGCCCCAGCAGCTTGGCCAT 422
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Qy 423	GGAGATGAAGAAGACATCAACACAAAAAAGAAGACATGTTCCACAGATCTACATACA 482
Db 1056	GGAGATGAAGAAGACATCAACACAAAAAAGAAGACATGTTCCACAGATCTACATACA 1115
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Qy 543	CCAGTGCACCTCGCAGAGCTGTCATGCCCTGAATGAGCTCTTTGCCCGGTTTGACAA 602
Db 1176	CCAGTGCACCTCGCAGAGCTGTCATGCCCTGAATGAGCTCTTTGCCCGGTTTGACAA 1239
Qy 603	GCTGGCTCGGAGAACTACATGCTCTGAGGATCAAGATCTTTGGGGGACTGTTACTACTGTGT 662
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Qy 663	GTCAGGCTCCCGAGGCCCGGCCACCATGCCACTGCTGTGTGGAGATGGGGGTAGA 722
Db 1296	GTCAGGCTCCCGAGGCCCGGCCACCATGCCACTGCTGTGTGGAGATGGGGGTAGA 1355
Qy 723	CATGATTTAGGCCATCTCGCTGTGTAGCTGAGGTGACAGGTGTGAATGTGAACATCGCGGT 782
Db 1356	CATGATTTAGGCCATCTCGCTGTGTAGCTGAGGTGACAGGTGTGAATGTGAACATCGCGGT 1415
Qy 783	GGGCATCCACAGCGGGCGGTGCATCTGCGGCTTCCTTTGGCTTGCAGAAATGGCAGTTCGA 842
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Dn	2436	TGAGGTGTCC	2445
RESULT 5 AX189766			
LOCUS	AX189766	3552 bp	DNA linear PAT 08-AUG-2001
DEFINITION	Sequence 10 from Patent WO0148164.		
ACCESSION	AX189766		
VERSION	AX189766.1	GI:15143139	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 3552)		
AUTHORS	Hammond,H.K. and Gao,M.		
TITLE	Gene therapy for congestive heart failure		
JOURNAL	Patent: WO 0148164-A 10 05-JUL-2001;		
FEATURES	THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US) Location/Qualifiers 1..3552		
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Qy	3	TAACGTGTGTGGGCATCTCGGGCAGTGCAGTCGGGGCGCTTTCCGACGAGACC 62	
Dn	636	TTACGTGTGTGGCATCTCGGGCAGTGCAGTCGGGGCGCTTCGACGAGACC 695	
Qy	63	GCGAGCCCCCTCTCGGGCCCTCTGGGCCCTCTGTTTGTATACATCGATACAGCT 122	
Dn	696	GCGAGCCCCCTCTCGGGCCCTCTGGGCCCTCTGTTTGTATACATCGATACAGCT 755	
Qy	123	CCTCCCATCGCATCGGGCTGGCTCTCAGCGGCTGGGCTCTCCACTTGCAATT 182	
Dn	756	CCTCCCATCGCATCGGGCTGGCTCTCAGCGGCTGGGCTCTCCACTTGCAATT 815	
Qy	183	GATCTGGCCCTGGCAACTTAACCGTGTGTATGCTCTCTCGGAAGCAGCTCGGTGCCAA 242	
Dn	816	GATCTGGCCCTGGCAACTTAACCGTGTGTATGCTCTCTCGGAAGCAGCTCGGTGCCAA 875	
Qy	243	TGTGCTGTCTCTGTCACCAACAGCTATTAGCATCTGCACACTATCCAGCAGAGGT 302	
Dn	876	TGTGCTGTCTCTGTCACCAACAGCTATTAGCATCTGCACACTATCCAGCAGAGGT 935	
Qy	303	GTCTCACGCCAGGCCTTTACAGAGACCCGAGTACATCCAGGCCCGGCTCCACCTGCA 362	
Dn	936	GTCTCACGCCAGGCCTTTACAGAGACCCGAGTACATCCAGGCCCGGCTCCACCTGCA 995	
Qy	363	GCATGAGAATCGGCAGCAGGAGCGGCTGCTGCTCTCGGTATTGCCCCAGCAGCTTGCCAT 422	
Dn	996	GCATGAGAATCGGCAGCAGGAGCGGCTGCTGCTCTCGGTATTGCCCCAGCAGCTTGCCAT 1055	
Qy	423	GGAGATGAAGAAGACATCAACAACAAAAGAAC---ATGTTCCACAAGATCTACAT 479	
Dn	1056	GGAGATGAAGAAGACATCAACAACAAAAGAACATGATGTTCCACAAGATCTACAT 1115	
Qy	480	ACAGAAGCATACAAATGTCAGCATCTGTTTGCAGACANTTACGGCTTCACGACCTGGC 539	
Dn	1116	ACAGAAGCATACAAATGTCAGCATCTGTTTGCAGACANTTACGGCTTCACGACCTGGC 1175	
Qy	540	ATCCAGTGTACTCGCAGGAGCTTGGTCATGACCCCTGAATGAGCTCTTTGGCCGGTTGA 599	
Dn	1176	ATCCAGTGTACTCGCAGGAGCTTGGTCATGACCCCTGAATGAGCTCTTTGGCCGGTTGA 1235	
Qy	600	CAAGCTGGCTGCGGAGAAATCACTGCCCTGAGATCAAGATCTTTGGGGACTGTTACTACTG 659	
Dn	1236	CAAGCTGGCTGCGGAGAAATCACTGCCCTGAGATCAAGATCTTTGGGGACTGTTACTACTG 1295	



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Qy 1740 CAATTACTCTCTGGCCTGGATGCTCCCTGTGTGAGGCGACCATGCCCACCTGCAGCTT 1799
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Db 2376 CAATTACTCTCTGGCCTGGATGCTCCCTGTGTGAGGCGACCATGCCCACCTGCAGCTT 2435

Qy 1800 TCCTGAGGTGTC 1812
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Db 2436 TCCTGAGTATTC 2448

RESULT 6
AF250226
LOCUS AF250226 6463 bp mRNA linear PRI 15-SEP-2000
DEFINITION Homo sapiens adenylyl cyclase type VI mRNA, complete cds.
ACCESSION AF250226
VERSION AF250226.1 GI:9049782
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 6463)
Wicker, R., Catalan, A.G., Caillaux, A., Starenki, D., Stengel, D.,
Sarasin, A. and Suarez, H.G.
Cloning and expression of human adenylyl cyclase type VI in normal
thyroid tissues
Biochim. Biophys. Acta 1493 (1-2), 279-283 (2000)
JOURNAL
MEDLINE 20435313
PUBMED 10978539
REFERENCE
2 (bases 1 to 6463)
Wicker, R., Gascon Catalan, A., Caillaux, A.-F., Starenki, D.,
Stengel, D., Sarasin, A. and Suarez, H.G.
Direct Submission
Submitted (28-MAR-2000) Lab Etude des Relations - Instabilite
genetique et Cancer UPR 2169, Institut de Recherches sur le Cancer
CNRS IFR 1221, 7 rue Guy Moquet, Villejuif 94801, France
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ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1
AUTHORS	Ishikawa, K., Nagase, T., Nakajima, D., Seki, N., Ohira, M., Miyajima, N., Tanaka, A., Kotani, H., Nomura, N. and Ohara, O.
TITLE	Prediction of the coding sequences of unidentified human genes. VIII. 78 new cDNA clones from brain in which code for large proteins in vitro
JOURNAL	DNA Res. 4 (5), 307-313 (1997)
MEDLINE	98116653
PUBMED	9455477
REFERENCE	2 (bases 1 to 5877)
AUTHORS	Ohara, O.
TITLE	Direct Submission
JOURNAL	Submitted (06-OCT-1997) Osamu Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba 292-0812, Japan (E-mail: cdnainfo@kazusa.or.jp. Tel: +81-438-52-3913, Fax: +81-438-52-3914)
COMMENT	On May 9, 2002 this sequence version replaced gi:2887418. Sequence updated (05-Jan-1998).
FEATURES	Location/Qualifiers 1..5877 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="hh01205s1" /sex="male" /tissue_type="brain" /clone_lib="pBluescriptII SK plus" /note="This sequence was obtained by subcloning of the DNA fragments derived from two cDNA clones (1..1352 was derived from pg00161 and 1353..5877 was derived from hh01205)." 1..5877 /gene="KIAA0422" <1..3484 /codon_start=2 /gene="KIAA0422" /db_xref="GI:20521045" /translation="GRRTAGGTATRLGGRPRGAGRSPPRRGGGPGQASRRASGS NMSWESGLLVPKVDERTKANGERNCKRRCTRAGGCTPRYMSCLRDAEPSPPTP AGPFCPQDDAERIRGGCKGKELGVALGDETEVTITAGGTAEVADPVRPSG RCQRRLVQFSQCKPSAKLERLYQRFQMNSSLTLMVLVLLTAVLLAFHAA ARFPYAVALLACAAFLVGLVYCNRHFSFRQDSMMVSYVILGILAAQVGGAAL PRSPAGLWCPVFPIYATLLPIRMRAVLSGLSLSTLHLI LAWLNRGDAFLWQL GANVLLCTNIGICTHYPAEVSQRFQETRGYIQARLHLOHERNQERLLLSVLP QHVAMEMKEDINTKKEDMPHKIYIQKHNVSLIFADIEGFTSLASQCTAQELVMTLN ELFARDKLAENHKLRKILKGDCYCVSGLPPEARADHCCVGMGDMIEALSLR VLPQVNMVRGTHSGRHVCGVLGRKQWFDVNSDVTLANHMEAGGRAGRIHTRATL QYNGSYEVEPGRGNGRYALKQHIETETLILGASQKREKAMLAQLQTRANSEG LMPWVDPRAFSTKDSKAFROMGIDDSKDRNQTALNPEDEVDFLSRAIDAKSI DOLRKHVRRELLTFQRELDCKYSRKVPDFCAVACALLVFCFICFQLLFPFHS LMGIYASIFRLLLLIVLICAVYSCGSLPKAQLRSLRSIVSRHASTAVGICFVLLY FTSIANMVFIGNMLLSLASSVFLHISIGKLAMIFVLGILYLVLLGLGPPATIFDN YDLLGLHGLASNETFDGLDQPAAGRVALKYPTVPIYFALYLYHHQQVSTEAR DYLLKQATQGEKEMEELQYNNRLLHNTLPKDVAAFLHARNRNDELXYQSCCVAV MPASIANSEFYVVELPANNEGVCLRLNEIADDFEITSEERFROLEKTKTIGTSYV AASGLNASTYDQVGRSHITADLYAMRMEQMKHINEHSEFNQMKIGLNGMPVAGY IGARKEQYDINQVNSVSRMSDSTVPDRIVQVTTDLYQVLAAGQYQLECGVVYKVGK GEMTTFYFLNGPSS"
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## RESULT 9

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ACCESSION M94968  
VERSION M94968.1 GI:163896  
KEYWORDS adenyllyl cyclase type VI.  
SOURCE Canis familiaris cardiac muscle cDNA to mRNA.  
ORGANISM Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Canis; Canidae; Canis.  
REFERENCE 1 (Bases 1 to 4046)  
AUTHORS Katsushika,S., Chen,L., Kawabe,J., Nilakantan,R., Hainon,N.J.,  
Homcy,C.J. and Ishikawa,Y.  
TITLE Cloning and characterization of a sixth adenyllyl cyclase isoform:  
types V and VI constitute a subgroup within the mammalian adenyllyl  
cyclase family  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (18), 8774-8778 (1992)  
MEDLINE 92409599  
PUBMED 1528892  
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Db 1719 GCGCGGTGGCAGCGCAACGCGTACTCTCAAGGAGCAGGCACATTCGAGACTTCTCATCC 1778  
QY 1022 TGGGCGCCAGCCAGAACCGGAAGAGGAGAAAGGCATGTGCGCAAGCTGCAGCGGACTC 1081  
Db 1779 TGGGCGCCAGCCAGAACCGGAAGAGGAGAAAGGCATGTGCGCAAGCTGCAGCGGAGCG 1838  
QY 1082 GGGCAACTCCATGGAAGGCTGTATGCCGCGATGGTCTCTCATGCTGCTTCTCCCGA 1141  
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Db 1839 GGGCCAACCTCCATGGAAGGCTGTATGCCAGCTGGGTGGCGAGCCGCGCTTCTTCGGA 1898  
QY 1142 CCAGGACTCAAGGCTTCCGCCAGATGGGCATTGATGATTCAGAAAACACACGCGG 1201  
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QY 1202 GCACCCAAGATGCCCTGAACCCCTGAGGATGAGTGGAGTTCCTGAGCGGTGCCATCG 1261  
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QY 1262 ATGCCCCAGCATGTATCAGCTCGGGAAGGACCATGTCGCCCGTTTTTGTCTACCTTCC 1321  
Db 2019 ATGCCCCAGCATGTATCAGCTACGGAAGGACCATGTCGCCCGTTTTTGTCTACCTTCC 2078  
QY 1322 AGAGAGAGGATTTTGAAGAAGTACTCCCGGAAGTGGATCCCGCTTCGGAGCCTACG 1381  
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QY 1382 TTGCTGTGCCCTGTGGTCTTCTGTCTCATCTGCTTCATCTCCAGCTTCTTAATTTCCAC 1441  
Db 2139 TGGCTGTGGCGTGTGGTCTTCTGTCTCATCTGCTTTATCCAGCTCCTCGTCTTCCAC 2198  
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Db 2559 CTGAGTACTTC 2569

RESULT 11  
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LOCUS Mus musculus adenylyl cyclase type 6 mRNA linear ROD 27-APR-1993  
DEFINITION M96653  
ACCESSION M96653  
VERSION GI:191726  
KEYWORDS adenylyl cyclase type VI  
SOURCE Mus musculus CDNA to mRNA.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 3465)  
AUTHORS Premont, R. T.  
TITLE Multiple mechanisms underlying desensitization of the liver  
adenylyl cyclase system. Structure and cAMP regulation of liver  
adenylyl cyclases  
JOURNAL Unpublished (1992)  
REFERENCE 2 (bases 1 to 3465)  
AUTHORS Premont, R. T., Jacobowitz, O. and Iyengar, R.  
TITLE Lowered responsiveness of the catalyst of adenylyl cyclase to  
stimulation by GS in heterologous desensitization: a role for  
adenosine 3',5'-monophosphate-dependent phosphorylation



JOURNAL MEDLINE PUBMED FEATURES	Endocrinology 131 (6), 2774-2784 (1992) 93076707 1332848	Location/Qualifiers 1. .3465 /organism="Mus musculus" /db_xref="taxon:10090" /cell_line="549 lymphoma cell (UNC variant)" 1. .3465 /partial /EC_number="4.6.1.1" /citation=[2] /citation=[1] /codon_start=1 /evidence=experimental /product="adenylyl cyclase, type 6" /protein_id="AAA37182.1" /db_xref="GI:191727" /translation="LLVPKVDKRTAWGERNGOKRPHANRSGFCAPRYMSCLNNAE PPSPTAAHTRCPQWDEAFIRRRAGPARGVELGLRSVALGFDDETEVTPMGTAEPDPT SPRSGSCHRLVQVQSKQFRSAKLERLYQRYFFQMNQSSLLHMAVLVLLMAVLLT FHAAPQSPAYVALLTFCASVLFVLLMVNCRNSFRQDSMWVSYVYVLGILAAVQGG ALAAHPSPAGLWPCVPFFVYITLLPIRMAAVLSGLSLHLHLAWLNSSDPF LWQLGANVYLFCTNAIGVCTHYPAEVRSQRAFQETRGVYQARLHLQHENRQOERLL LSVLPQHVAEMEKEDINTKKEDMMFKIYIQKHNVSYILFADTEGFTSLASQCTAOEL VMTNELFAFEDKLAENHCLRIKILGDCVYCVSGLPPEARADHAHCCVEMGVMIKAI SLVRETVGNVNRVGTSHGRVHCVGLGKROFDVWSNDVTLANHEAGRGRIHI TRATLOYLNGDIYEVFGRGGERNAYLKEQIEFTLLIGASQKRREKAMUKALQRTNA NSMGLMPRWPRFASRTKDSKAFROMGIDSSKONRGAQDALNDEVEDEFELGRAI DAISIQLRKHRRVRLTFQREDLEKKYKRDVPRFYAYVACALLVFCFICITQLLV FPYTLTISALNAFTQNTPIRTCAARMNLTPADVTACHLOQLNYSLGIDAPLCEGT SVLLVFSLANFTQNTPIRTCAARMNLTPADVTACHLOQLNYSLGIDAPLCEGT APCSRPPEVGNVLLSLASSVFLHTSSIGKIAMTFILGFTVYLLVLLGLPPRAIPDN YDLILGVHGLASSNEDFGDQCPAVGRVALKYPTVYLLVFLALALYHQAQVSTARL DPLWKQATGEKEMBELQAINRLLNHLNIDVAAHFLARENRNDELXYTQSCCEVAV MFASIANFSDYQENSHITALADYAMRLMEQMKHINEHSFNFMQKITGLNMGPVAVG AGSLNASTYDQVLRSHITALADYAMRLMEQMKHINEHSFNFMQKITGLNMGPVAVG IGARKPOYDIWGNVTNVNSRMDSTGVPDRIQVTTDLYVLAARKQYLECRGVVVKRG GEMTYPFN"	BASE COUNT 715 a 998 c 980 g 772 t ORIGIN
Query Match	80.08; Score 1449.4; DB 10; Length 3465;		
Best Local Similarity	87.99; Pred. No. 0;		
Matches 1592; Conservative	0; Mismatches 216; Indels 3; Gaps 1;		
Qy 5	ACGTGGTCTGGGCATCTCGCGGCAGTGCAGGTGCGGGGGCGCTTCGCCACGACACCGGC 64		
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Qy 65	GCAGCCCTCTCGCGGCCTCTGGTCCCTGTCTTTGTATACATGCATACACGCTCC 124		
Db 674	ACAGCCCTCTCGCGGCCTCTGGTCCCTGTCTTTGTATACATGCATACACGCTCTTC 733		
Qy 125	TCCCATCCGATCGGGCTCCGCTCTCGCGGCCTGGGCTCTCCACCTTGCATTGA 184		
Db 734	TTCCCATTCGATCGAGCCGAGTACTACGCGCCTGGGCTCTCTACTCTGCATTGA 793		
Qy 185	TCTTGGCTGCACTTAACCGTGGTGATGCCCTTCCTTGAAGCAGCTCGGTGCGCAATG 244		
Db 794	TTTTGGCTGCGAGCTCAACAGCAGCGACCCCTTCCTTTGGAAGCAGCTCGGTGCTACG 853		
Qy 245	TGCTGTCTTCTCTGACCAACGCTCATTAGCATCTGCACACATATCCAGCAGAGTGT 304		
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Qy 305	CTCAGCCGACGCGCTTTTCAGGAGACCGCGAGTTACATCCAGCGCGGCTCCACCTGCGAG 364		
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Qy 425	AGATGAAGAGACATCAACACAAAAAAGAGAC---ATGTTCCACAAGATCTACATAC 481		
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Qy 662	TGTCAGGCTGCCGAGGCGCCGCGGACCATGCCACTGCTGTGTGAGATGGGGTAG 721		
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Qy 842	ATGTGTGTCATGATGTGACCTTGGCCAAACACATGGAAGCAGGAGAGCGGCGGCTGCGC 901		
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Qy 962	GCCGTGTGGCAAGCGCAACCGCTACCTTCAAGGAGCAGACATTTGAGACTTTCCTCATCC 1021		
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Qy 1022	TGGCGCCAGCCAGAAACGGAGAGAGAGAGATGCTGGCCAAAGCTGAGCGGAGTCC 1081		
Db 1634	TGGCGCCAGCCAGAAACGGAGAGAGAGAGATGCTGGCCAAAGCTTTCAGCGGAGAC 1693		
Qy 1082	GGGCCAACTCCATGGAAGGCTGATGCCCGATGGGTTCCTGATCGTGCCTTCTCCCGGA 1141		
Db 1694	GGGCCAACTCCATGGAAGGACTGATGCCCGCTGGGTTCCTGACCGTGCCTTCTCCCGGA 1753		
Qy 1142	CCAAGGACTCCCAAGGCTTCGCCAGATGGCATTTGATGATTCAGCAAAAGACAACCGGG 1201		
Db 1754	CCAAGGACTCTAAGGCATTCGCCAGATGGCATTTGATGATTTAGCAAAAGACAACCGGG 1813		
Qy 1202	GCACCCAGATGCGCTGAACCCCTGAGGATGAGGTGAGTTCCTGAGCGCTGCCATTCG 1261		
Db 1814	GTGCCAAGATGCTCTGAACCTGAAGCTGAGGTGAGTTCCTGAGCGGAGCCATTCG 1873		
Qy 1262	ATGCCCGCAGCATTTGATCAGCTGCGGAGGAGCACCATGCGCGCGGTTTTTGTCTACCTTCC 1321		
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Qy 1322	AGAGAGGATTTTGAAGAAGTACTCCCGAAGGTGATCCCGCTTCGGAGGCTACG 1381		
Db 1934	AGAGAGGATTTTGAAGAAGTATTCACGGAAGATGATCTCGCTTCGGAGGCTACG 1993		
Qy 1382	TGCGCTGCGCTTGTGCTTCTGCTTCATCTGCTTCATCCAGCTTCTAAATTTTCCAC 1441		
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RESULT 12  
AR106659  
LOCUS AR106659 4131 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 11 from patent US 6107076.  
ACCESSION AR106659  
VERSION AR106659.1 GI:12821189  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 4131)  
AUTHORS Tang, W.-J. and Gilman, A. G.  
TITLE Soluble mammalian adenylyl cyclase and uses therefor  
JOURNAL Patent: US 6107076-A 11 22-AUG-2000;  
FEATURES  
Location/Qualifiers  
1..4131  
Source /organism="unknown"  
BASE COUNT 835 a 1190 c 1182 g 924 t  
ORIGIN

Query Match 79.3%; Score 1437.2; DB 6; Length 4131;  
Best Local Similarity 87.5%; Pred. No. 3.2e-311;  
Matches 1584; Conservative 0; Mismatches 223; Indels 3; Gaps 1;

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DEFINITION	Mouse adenylyl cyclase type VI mRNA, complete cds.		ROD 27-APR-1993
ACCESSION	M93422		
VERSION	M93422.1	GI:191690	
KEYWORDS	adenylyl cyclase; adenylyl cyclase type VI.		
SOURCE	Mus musculus	cdna to mRNA.	
ORGANISM	Mus musculus		
REFERENCE			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
TITLE	Yoshimura, M. and Cooper, D.M.		
JOURNAL	Cloning and expression of a Ca(2+)-inhibitable adenylyl cyclase		
MEDLINE	Proc. Natl. Acad. Sci. U.S.A. 89 (15), 6716-6720 (1992)		
PUBLISHED	92357702		
FEATURES	1379717		
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BASE COUNT	1214 a	1558 c	1673 g
ORIGIN	1396 t		
Query Match	79.08;	Score 1431.8;	DB 10; Length 5841;
Best Local Similarity	87.7%;	Pred. No.5.le-310;	
Matches 1586;	Conservative	0; Mismatches 217;	Indels 6; Gaps 2;
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Db	727	ATGTGGTCTGGGCATCTCTACAGCCGTGCAAGTGGGGGGTGCCTCGCAGCCATCCAC	786
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QY 482 AGAAGCATGACAAATGTACGATCCTGTTTTCAGACATTTGAGGCTTTCACGAGCTGGCAT 541  
Db 1207 AGAAGCATGATAATGTACGATCCTGTTTTCGCGACATTCAGGCTTTCACGAGCTGGCCT 1266  
QY 542 CCCAGTGCATCGGAGGAGCTGGTCATGATGACCTGTAATGAGCTCTTTGGCCCGTTTGACA 601  
Db 1267 CCCAGTGCATGCACAGGAACTGGTCATGACCTTGAATGAGCTCTTTGGCCCGTTTGACA 1326  
QY 602 AGCTGCTCGGAGAACTACCTGCTGAGATCAAGATCTTGGGGACTGTTACTACTG 661  
Db 1327 AGCTGCTCGGAGAACTACCTGCTGAGATCAAGATCTTGGGGACTGTTACTACTG 1386  
QY 662 TGTACGGGCTCGGGAGGCGCGGCGACCATGCCACTGCTGTGTGAGATGGGGGTAG 721  
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QY 782 TGGGCATCCACAGCGGCGCTGCACTCGGCGTCTCTGCTTGGGAAATGCGAGTTG 841  
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QY 842 ATGTCTGGTCCAAATGATGTACCCCTGGCCAAACCATGGAAGCAGGAGCGGCTGGCC 901  
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QY 1202 GCACCCAAAGATGCCTGAACCTGAGGATGAGTGGATGAGTTCTCTGAGCGGTGCCATCG 1261  
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QY 1322 AGAGAGAGATTTTGAAGAAGTACTCCCGGAAGTGTATCCCGCTTCGGAGCCTAGC 1381  
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QY 1802 CTGAGGTGTTTC 1812  
Db 2524 CTGAGTACTTC 2534

Search completed: March 1, 2003, 02:24:10  
Job time : 3154.21 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 28, 2003, 21:14:01 ; Search time 1740.16 Seconds  
(without alignments)  
16964.108 Million cell updates/sec

**Title:** US-09-750-240-3  
**Perfect score:** 1812  
**Sequence:** 1 gttaacgtggtgctgggcat.....gcagctttctctgaggtgttc 1812

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST: \*

1: em\_estba:\*  
2: em\_esthum:\*  
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4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estum:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES							
Result No.	Score	Query Match	Length	DB	ID	Description	
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2	540.2	28.8	581	13	BG993320	BG993320	MR3-HT099
3	463.4	25.6	565	12	BG872335	BG872335	602792616
4	442.4	24.4	525	13	BM090325	BM090325	505523 MA
5	418.6	23.1	682	14	BQ180663	BQ180663	UI-N-EX0-
c 6	393.2	21.7	442	9	A1905602	A1905602	CM-BT094-

C	7	393.2	21.7	466	9	A1905641	A1905641	CM-BT094-
C	8	392.8	21.7	453	12	BE83164	CM1-FN011	
C	9	387.8	21.4	417	12	BE840138	QVO-FN018	
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C	11	372	20.5	1016	14	BO881496	BO881496	AGENCOURT
C	12	361.8	20.0	625	12	BF369868	BF369868	QV4-GN012
C	13	347.2	19.2	611	12	BG004182	QV4-GN012	
C	14	345.8	19.1	673	14	BQ370134	QV4-GN012	
C	15	342.4	18.9	367	10	BE0011572	PM2-BN008	
C	16	332.2	18.3	1039	14	BM811640	AGENCOURT	
C	17	316.6	17.5	2661	11	BC028085	BC028085	Homo sapi
C	18	311	17.2	567	13	BI739363	BI739363	603359680
C	19	296.8	16.4	1076	13	BM548851	AGENCOURT	
C	20	293.6	16.2	515	14	BQ370137	QV4-GN012	
C	21	289.4	16.0	944	9	AL558455	AL558455	
C	22	285.4	15.8	770	13	BI562576	BI562576	603256509
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C	24	277.2	15.3	3369	11	BC020148	BC020148	Homo sapi
C	25	276.6	15.3	630	14	BQ442310	BQ442310	UI-M-EXO-
C	26	271.2	15.0	813	12	BF582692	BF582692	602094103
C	27	260	14.3	729	13	BI823791	BI823791	603038930
C	28	247.8	13.7	627	10	BB616087	BB616087	
C	29	243.4	13.4	834	14	BM963626	BM963626	UI-M-EQO-
C	30	238.6	13.2	721	10	BE546643	BE546643	601073694
C	31	232.4	12.8	1075	12	BF982389	BF982389	602308826
C	32	227	12.5	600	13	BJ118754	BJ118754	BJ118754
C	33	223	12.3	243	12	BF817426	RC5-CT014	
C	34	218.4	12.1	733	12	BF988269	BF988269	CM0-GN016
C	35	216.8	12.0	201	17	AZ991711	AZ991711	2M0276006
C	36	216.6	12.0	377	9	A1944903	A1944903	tr27c01.x
C	37	209.8	11.6	517	12	BG731141	daellb03.	
C	38	208.6	11.5	464	9	AA672242	AA672242	v112b09.r
C	39	201.2	11.1	431	10	BB863676	BB863676	
C	40	199.8	11.0	448	9	AI218521	qhl6h12.x	
C	41	196.2	10.8	583	10	BE504143	BE504143	h585h09.x
C	42	190.8	10.5	575	12	BG295901	BG295901	602393432
C	43	182.8	10.1	554	13	BJ104077	BJ104077	BJ104077
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## ALIGNMENTS

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LOCUS	676 bp mRNA linear EST 22-SEP-2000
DEFINITION	QV0-FN0181-100800-335-d08 FN0181 Homo sapiens cDNA, mRNA sequence.
ACCESSION	BE840188
VERSION	BE840188.1 GI:10272566
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 676)
AUTHORS	Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE	20202663
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001

RESULT 2	BG993320	581 bp	linear	EST 13-JUN-2001
LOCUS	MR3-HT0999-070201-003-h04	hm0999	Homo sapiens	CDNA, mRNA sequence.
DEFINITION	RG993320			
ACCESSION	GI:14397390			
VERSION	EST.			
KEYWORDS	human.			
SOURCE	Homo sapiens			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1 (bases 1 to 581)			
AUTHORS	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.			
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	97 (7),	3491-3496	(2000)
MEDLINE	200202663			
COMMENT	COMMENT			

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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.hwdw3.org.br/scripts/gethtml2.pl?tl=MR3&t2=MR3-HT0999-
070201-003-h04&t3=2001-02-07&t4=1)
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High quality sequence stop: 581.
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    /clone_lib="HT0999"
    /dev_stage="Adult"
    /note="Organ: head neck; Vector: puc18; Site_1: SmaI;
        Site_2: SmaI; A mini-library was made by cloning products
        derived from ORESTES PCR (U.S. Letters Patent application
        NO. 196,716 - Ludwig Institute for Cancer Research)
        profiles into the pUC 18 vector. Reverse transcription of
        tissue mRNA and cDNA amplification were performed under
        low stringency conditions."
BASE COUNT      118 a   157 c   199 g   106 t       1 others
ORIGIN

Query Match          29.8%; Score 540.2; DB 13; Length 581;
Best Local Similarity 98.2%; Pred. No. 8.3e-119;
Matches 556; Conservative 0; Mismatches 1; Gaps 1;

QY  623 GCCTGAGGATCAAGATCTTGGGGACTGTGTACTGTGTGTGCAGGCTCCCGAGGCC 682
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Db   17 GCCTGAGATCAAGATCTTGGGGAC-GTTACTACTGTGTGTGCAGGCTCCCGAGGCC 75
      |||||||

QY  683 GGCCCGACCATGCCCACTGCTGTGTGGAGATGGGGGTAGACATGATTAGGCCATCTCGC 742
      |||||||
Db   76 GGCCCGACCATGCCCACTGCTGTGTGGAGATGGGGGTAGACATGATTAGGCCATCTCGC 135
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QY  743 TGTACTGTCAGGTGCACAGGTGTCAATGTGAACATGCGGTGGCATCCACAGCGGGCGC 802
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Db   136 TGTACTGTCAGGTGCACAGGTGTGAATGTGAACATGCGGTGGCATCCACAGCGGGCGC 195
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QY  803 TGCACTGCGGCGTCCTTGGCTTGCGAAATGGCAGTTCCGATGTGTGTCCAATGATGTGA 862
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BASE COUNT	118 a	157 c	199 g	106 t	1 others
ORIGIN					
Query Match	29.8%;	Score 540.2;	DB 13;	Length 581;	
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Matches 556;	Conservative 0;	Mismatches 9;	Indels 1;	Gaps 1.	
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QY	743	TGCTACGTGAGGTGACAGGTGTGAATGTGAACATGGCGCGTGGGCATCCACAGCGGGCGC	802		
Db	136	TGCTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGGCGC	195		
QY	803	TGCATGCGGGCTCCTTGGCTTCGCGAAATGCGAGTTTCGATGTGGTCCAAATGATGTGA	862		
Db	196	TGCATGCGGGCTCCTTGGCTTCGCGAAATGCGAGTTTCGATGTGGTCCAAATGATGTGA	255		
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QY 923 CACTGCAGTACCTGAACGGGGACTACGAAGTGGAGCGAGCGCGTGGTGGCAAGCGCAACG 982
Db 316 CACTGCAGTACCTGAACGGGGACTACGAAGTGGAGCGAGCGCGTGGTGGCGAGCGCAACG 375
QY 983 CGTACCTCAAGGAGCAGCACATGAGACTTTCCTCATCTCTGGGCGCCAGCCAGAAACGGA 1042
Db 376 CGTACCTCAAGGAGCAGCACATGAGACTTTCCTCATCTCTGGGCGCCAGCCAGCAAGCGGA 435
QY 1043 AAGAGGAAAGGATGCTGGCCAAAGCTGCAGGGAGCTCGGGGCCAACTCCATGGAAAGGC 1102
Db 436 AAGAGGAAAGGATGCTGGCCAAAGCTGCAGGGAGCTCGGGGCCAACTCCATGGAAAGGC 495
QY 1103 TGATGCGCGATGGTTCCTGATGCTGCTCTCCCGGACCAAGGACTCCAAAGCCCTTCC 1162
Db 496 TGATGCGCGATGGTTCCTGATGCTGCTCTCCCGGACCAAGGACTCCAAAGCCCTTCC 555
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Db 556 GNCAGATGGGCATTGATGATTCAGC 581

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LOCUS
DEFINITION
602792616F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4923890 5',
mRNA sequence.
ACCESSION
BG872335
VERSION
BG872335.1 GI:14222875
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 565)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapps-femail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10845 row: p column: 03
High quality sequence start: 11
High quality sequence stop: 565.
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Location/Qualifiers
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1. 565
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Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 133 a 141 c 174 g 117 t
ORIGIN
Query Match 25.6%; Score 463.4; DB 12; Length 565;
Best Local Similarity 91.2%; Pred. No. 2.1e-100;
Matches 515; Conservative 0; Mismatches 46; Indels 4; Gaps 2;
QY 434 AAGACATCAACACAAAAAAGAGAC---ATGTTCCAAAGATCTACATACAGAAGCATG 490
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QY 551 CTGCGCAGGAGCTGGTTCATGACCTCAATGAGCTCTTTGCCCGTTTTCACAAAGCTGGCTG 610
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Db 121 CTGCACAGGAACTGGTTCATGACCTTGAATGAGCTCTTTGCCCGTTTTCACAAAGCTGGCTG 180
QY 611 CGGAGAACTACTGCTCTGAGGATCAAGATCTTTGGGGGACTGTTACTACTGTGTGTCAGGGC 670
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QY 851 CCAATGATGTACCTCGCGCAACACACATGGAGCAGGAGCCGCGGCGCATCCACA 910
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QY 911 TCACTCGGGCAACACTGCAGTACCTGAACGGGGGACTACGA-AGTGGAGCCAGGCGGTGGT 969
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505523 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION
BM090325
VERSION
BM090325.1 GI:17000953
KEYWORDS
EST.
SOURCE
Bos taurus
ORGANISM
Bos taurus
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 525)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-Mckown,C.G.,
Perlea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
Keele,J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
21180013
CONTACT: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCAGTCACGCG
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/note="Vector: pCMV SPORT6; Site\_1: NotI; Site\_2: SalI;  
Library made from pooled tissue from marrow, alveolar  
macrophage, ovary, fetal semitendinosus muscle, and fetal  
longissimus muscle."

BASE COUNT 112 a 162 c 133 g 117 t 1 others

## ORIGIN

Query Match 24.4%; Score 442.4; DB 13; Length 525;  
Best Local Similarity 91.4%; Pred. No. 2.2e-95;  
Matches 480; Conservative 0; Mismatches 42; Indels 3; Gaps 1;  
QY 90 CCTGTGTTCTTTATACATCGCATACACGCTCTCCCTCCATCCGATCGGGCTGCCGT 149  
Db 1 CCTGTGTTCTTTATACATCGCATACACGCTCTCCCTCCATCCGATCGGGCTGCCGT 60  
QY 150 COTCAGCGCCCTGGGCTCTCCACCTTGATTTGATTTGGCTGGCAACTTAACCGTGG 209  
Db 61 CTTTACAGCGCCCTGGGCTCTCCACCTGCTGTTGGCTGGCAGCTCAACCGTGG 120  
QY 210 TGATGCTTCTTCTGGAAGCAGCTGGTGCCAAATGTGCTGCTGCTCTGACCAAGCT 269  
Db 121 TGACGCTTCTTCTGGAAGCAGCTGGTGCCAAATGTGCTGCTGCTCTGACCAAGCT 180  
QY 270 CATTAGCATCTGCACACATATCCAGCAGAGGTGCTCAGCGCCAGCGCTTTCAGGAGAC 329  
Db 181 CATTGCGATCTGCACACATATCCGCTGAGGTGCTCAGCGCCAGGCAATTCAGAGAC 240  
QY 330 CGCAGTTTACATCCAGGCGCGCTCCACTGCAGCATGAGATCGSCAGCAGGCGGCT 389  
Db 241 CGCGGTTTACATCCAGGCGCGCTCCACTGCAGCATGAGATCGSCAGCAGGCGGCT 300  
QY 390 GCTGCTGCTGATGCCCCAGCAGCTTCCCATGAGATGAAGAGAGACATCAACACAA 449  
Db 301 GCTGCTGCTGATGCCCCAGCAGCTTCCCATGAGATGAAGAGAGACATCAACACAA 360  
QY 450 AAAAGAAGAC---ATGTTTCCACAAGATCTACATACAGAGCATGCAATGTTCAGCATCT 506  
Db 361 GAAAGAAGACATGATGTTTCATAAGATCTACATCCAGAGCAGCAATGTTCAGCATCT 420  
QY 507 GTTTCAGACATGAGGGCTTACCAGCTGCGATCCAGTCCAGTCCGCGCAGGAGCTGT 566  
Db 421 GTTTCGGGACATGAGGGCTTACCAGCTGCGCTCCAGTCCAGCAGCGCANGAGCTGT 480  
QY 567 CATGACCTTGAATGAGCTCTTTGCCCGGTTTACAAAGCTGGCTGC 611  
Db 481 CATGACCTTGAACGAGCTCTTTGCCCGGTTTACAAAGCTGGCTGC 525

## RESULT 5

BQ180663

LOCUS

DEFINITION UI-M-EX0-bxb-n-18-0-UI.r1 NIH\_BMAP\_EX0 Mus musculus cDNA clone  
IMAGE:5706065 5', mRNA sequence.

ACCESSION BQ180663

VERSION BQ180663.1

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 682)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

## COMMENT

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Dr. James Lin, University of Iowa

cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

This clone was contributed by the Brain Molecular Anatomy Project

(BMAP)

Seq primer: pYX-5.

Location/Qualifiers

1. 682

/organism="Mus musculus"

/strain="C57BL/6"

/db\_xref="taxon:10090"

/clone="IMAGE:5706065"

/clone\_lib="NIH\_BMAP\_EX0"

/tissue\_type="whole brain"

/dev\_stage="embryo 15.5 dpc"

/lab\_host="DH10B (T1 phage resistant)"

/note="Organ: brain; Vector: pYX-Asc; Site\_1: EcoR I;

Site\_2: Not I; The library was constructed according to

Bonaldo, Lennon and Soares, Genome Research, 6:791-806,

1996. Denatured mRNA was size fractionated on a 1% agarose

gel. First strand cDNA synthesis was primed with an

oligo-dT primer containing a Not I site. Double stranded

cDNA was size selected according to mRNA size fraction,

ligated with EcoR I adaptor, digested with Not I, and then

cloned directionally into pYX-Asc vector. The library tag

sequence located between the Not I site and the polyA tail

, is GTGCGTGAA. This library was created for the

University of Iowa Mouse Brain Molecular Anatomy Project

(BMAP): 'Gene Discovery in the Developing Mouse Nervous

System', supported by National Institutes of Mental Health

(NIMH), Hemin Chin, Ph.D., program coordinator."

BASE COUNT 142 a 195 c 187 g 156 t 2 others

## ORIGIN

Query Match

Best Local Similarity 23.1%; Score 418.6; DB 14; Length 682;

Matches 529; Conservative 0; Mismatches 146; Indels 4; Gaps 2;

QY 146 CGGTCTCTCAGCGCTCGGGCTCTCCACTTGCCTTTGATCTTGGCTGCAACTTAACC 205

Db 1 CGGTCTCTCAGCGGTGCTCTGCTGGCTCTCCACTTGGCCATCTCTGCGACACCACT 60

QY 206 GTGGTGATGCCCTTCTCTGGAAGCAGCTCGGTGCGCAATGTGCTGTGCTCTCTGCACCA 265

Db 61 CCCAGGACCACTTCTGCTGTAACACAGCTTGTCTCCAATGTCTCATCTCTCTCTGCACCA 120

QY 266 AGTCTATTAGCATCTGCACACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCTTTCAGG 325

Db 121 ACATTGGGGTGTGTGCTACTACTACCAGCTGAGGTCTCCAGAGACAGGCTTCCAGG 180

QY 326 AGACCCGCGAGTTACATCCAGGCGCGCTCCACTCGCATGAGATCGGACGAGGAGGAGC 385

Db 181 AGACCCGCGAGTTATCCAGGCTCGCTCCATCCAGCGGGAGAACACAGCAGGAGGAGC 240

QY 386 GGCTGCTGCTGCTGATGTCGCCAGCAGAGTTCGATGAGATGAAGAAGACATCAACA 445

Db 241 GTCTCTGCTGCTGCTCTCTCCCGCTCATGTTGCCATGGAGATGAAGAGCAGACATCAAGC 300

QY 446 CAAAAAAGAAGA---CATGTTCCACAAGATCTACATACAGAGCATGACATGTCAGCA 502

Db 301 CCNAGCAGGAGATGATGTTCCACAAGATCTATCATCCAGAGCATGACATGTCAGCA 360

QY 503 TCCTCTTTTCGACATTTAGGGCTTTCACAGCTGGCATCCGATCCGATCCGCTGCGCAGGAGC 562

Db 361 TCCTCTTTTCGACATCGAGGCTTTCACAGCTGGCTTCCAGTGTACTGCTCCCAAGAC 420

QY 563 TGGTCATGACCCCTGAATGAGCTCTTTTGGCCGGTTTGTACAAAGCTGGCTGCGGAGATCACT 622



[illegible]

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/organism="Homo sapiens"  
/db_xref="taxon:9606"  
/clone_lib="BT094"  
/sex="female"  
/dev_stage="Adult"  
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:  
SmaI; A mini-library was made by cloning products derived  
from ORESTES PCR (U.S. Letters Patent application No. 196  
716 - Ludwig Institute for Cancer Research) profiles  
into the pUC 18 vector. Reverse transcription of tissue  
mRNA and cDNA amplification were performed under low  
stringency conditions." 91 t
```

BASE COUNT 107 a 125 c 143 g 91 t

Query Match 21.7%; Score 393.2; DB 9; Length 466;

Best Local Similarity 96.7%; Pred. No. 1.4e-83;

Matches 412; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

QY 1069 CTGCAGCGACTCGGGCCAACTCCATGAAGGC-TGATGCCGCGATGGTTCTCTGATCG 1127

Db 456 CAGCAGCGACTCGGGCCAACTCCATGAAGGCTTGATCGCGCTGGTTCTCTGATCG 397

QY 1128 TGCCTTCTCCGGACCAAGGACTCAAGGCTTCGCCAGATGGGCATGATGATCCAG 1187

Db 396 TGCCTTCTCCGGACCAAGGACTCAAGGCTTCGCCAGATGGGCATGATGATCCAG 337

QY 1188 CAAAGACAACGGGGCACCCCAAGATGCCCTGAACCTCAGGATGAGGTGATGCTTCT 1247

Db 336 CAAAGACAACGGGGCACCCCAAGATGCCCTGAACCTCAGGATGAGGTGATGCTTCT 277

QY 1248 GAGCGGTGCCATCGATCGCCGACGATTCATGATGATGCGGAGGACCATGTGCGCGGTT 1307

Db 276 GAGCGGTGCCATCGATCGCCGACGATTCATGATGATGCGGAGGACCATGTGCGCGGTT 217

QY 1308 TTTGCTGACCTTCCAGAGAGGATTTGAGNAGATCTCCCGAAGGTGGATCCCG 1367

Db 216 TCTGCTGACCTTCCAGAGAGGATTTGAGNAGATCTCCCGAAGGTGGATCCCG 157

QY 1368 CTTGCGAGCGTACGTTGCTGTGCCCTGTGCTCTTCCTTCATCTCATCCAGCT 1427

Db 156 CTTGCGAGCGTACGTTGCTGTGCCCTGTGCTCTTCCTTCATCTCATCCAGCT 97

QY 1428 TCTAATTTCCACACTCCACCTGATGCTGGGATTTATGCCAGCATCTTCTGCTGCT 1487

Db 96 TCTAATTTCCACACTCCACCTGATGCTGGGATTTATGCCAGCATCTTCTGCTGCT 37

QY 1488 GCTAAT 1493

Db 36 GGAAT 31

#### RESULT 8

BE838164/c

LOCUS

DEFINITION CMI-FN0105-200600-280-f02 FN0105 Homo sapiens cdna, mRNA sequence.

ACCESSION BE838164

VERSION BE838164.1

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 453)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare

M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

#### MEDLINE

##### COMMENT

20202663

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Frudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-CMI-FN0105-200

600-280-f02&t3=2000-06-20&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 9

High quality sequence stop: 453.

##### FEATURES

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1..453

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="FN0105"

/dev\_stage="Adult"

/note="Organ: prostate\_normal; Vector: puc18; Site\_1: SmaI

; Site\_2: SmaI; A mini-library was made by cloning

products derived from ORESTES PCR (U.S. Letters Patent

application No. 196.716 - Ludwig Institute for Cancer

Research) profiles into the pUC 18 vector. Reverse

transcription of tissue mRNA and cDNA amplification were

performed under low stringency conditions."

BASE COUNT 75 a 141 c 134 g 103 t

##### ORIGIN

Query Match 21.7%; Score 392.8; DB 12; Length 453;

Best Local Similarity 96.7%; Pred. No. 1.7e-83;

Matches 433; Conservative 0; Mismatches 12; Indels 3; Gaps 3;

QY 881 AAGCAGGAAGCGGCTGGCGCATCCACATCCTCGGGCAACACTGCAGTACCTGAACG 940

Db 453 AGTTTGAGTTCGGGCTGGCGCATCCACATCCTCGGGCAACACTGCAGTACCTGAACG 394

QY 941 GGGACTACGAAGTGGAGCCAGGCGGTGGCAAGCGCAACCGTACCTCAAGGAGCAGC 1000

Db 393 GGGACTACGAAGTGGAGCCAGGCGGTGGCAAGCGCAACCGTACCTCAAGGAGCAGC 334

QY 1001 ACATTGAGACTTCTCATCTTGGCGCCAGCCAGCAAGAAAGAGGAAAGCATGTC 1060

Db 333 ACATTGAGACTTCTCATCTTGGCGCCAGCCAGCAAGAAAGAGGAAAGCATGTC 274

QY 1061 TGGCCAAAGCTGCAGCGGACTCGGGCCAACTCCATGGAAGGCTGATGCCGCGATGGGTT 1120

Db 273 TGGCCAAAGCTGCAGCGGACTCGGGCCAACTCCATGGAAGGCTGATGCCGCGATGGGTT 214

QY 1121 CTGATCGTCCCTTCCTCCCGGACCAAGGACTCCAAAGCGCTTCGCCAGATGGGCATTGATG 1180

Db 213 CTGATCGTCCCTTCCTCCCGGACCAAGGACTCCAAAGCGCTTCGCCAGATGGGCATTGATG 154

QY 1181 ATTCCAGCAAAAGACAAACCGGGGCACCCCAAGATGCCCTTGAACCCCTGAGGATGAGGTGGATG 1240

Db 153 ATTCCAGCAAAAGACAAACCGGGGCACCCCAAGATGCCCTTGAACCCCTGAGGATGAGGTGGATG 94

QY 1241 AGTTCTCGAGCGGTGCCATCGATGCCCGCAGCAATTGATCGCGGAAGGACCATGTGTC 1300

Db 93 AGTTCTCGAGCGGTGCCATCGATGCCCGCAGCA-TGATCAGCTGCGGAAGGAC-CATGTGTC 36

QY 1301 GCCGGTTTTTGTCTACCTTCCAGAGAGA 1328

Db 35 GCC-GTTTCTGTCTACCTTCCAGAGAGA 9

##### RESULT 9

BE840138/c

LOCUS

DEFINITION QVO-FN0181-280700-321-d07 FN0181 Homo sapiens cdna, mRNA sequence.

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ACCESSION BE840138
VERSION BE840138.1 GI:10272516
KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 417)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-QV0-FN0181-280
700-321-d07&ts=2000-07-28&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 10
High quality sequence stop: 415.
FEATURES
Location/Qualifiers
1..417
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="FN0181"
/dev_stage="Adult"
/note="Organ: prostate_normal; Vector: puc18; Site_1: SmaI
; Site_2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the puc 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
BASE COUNT 88 a 119 c 124 g 86 t
ORIGIN
Query Match 21.4%; Score 387.8; DB 12; Length 417;
Best Local Similarity 97.8%; Pred. No. 2.6e-82;
Matches 404; Conservative 0; Mismatches 7; Indels 2; Gaps 1;
QY 1033 CAGAAACGGAAGAGAGAGAGCATGTCGGCCAAAGCTGCAGCGGACTGGGGCAACTCC 1092
Db 417 CAGAAACGGAAGAGAGAGAGAGGCATGCTGGCCAAAGCTGCAGCGGACTGGGGCAACTCC 358
QY 1093 ATGGAAGGGCTGATGCCGGCATGGGTTCCTGATCGTGCCTTCCTCCCGGACCAAGGACTCC 1152
Db 357 ATGGAAGGGCTGATGCCGGCTGGGTTCCTGATCGTGCCTTCCTCCCGGACCAAGGACTCC 298
QY 1153 AAGGCTTCGCCAGATGGGCATTGATGATTCAGCAAAAGACACACCGGGACCCCAAGAT 1212
Db 297 AAGGCTTCGCCAGATGGGCATTGATGATTCAGCAAAAGACACACCGGGACCCCAAGAT 238
QY 1213 GCCTGAACCTCAGATGAGGTGGATGAGTTCCTGAGCGGTGCCATCGATGCCCGCAGC 1272
Db 237 GCCTGAACCTCAGATGAGGTGGATGAGTTCCTGAGCGGTGCCATCGATGCCCGCAGC 178
QY 1273 ATTGATCAGCTGGGAAGACCATGTCGCCGGTTTTTGTACACTTCACAGAGAGAGGAT 1332
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QY 1393 CTGTTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCACACTC 1445
Db 57 CTGTTGGTCTTCTGCTTCATCTGCTTCATC--GCTTCTCATCTTCCACACTC 7
RESULT 10
BI873142 603397792F1 NTH_MGC_94 939 bp mRNA linear EST 11-OCT-2001
LOCUS BI873142 Mus musculus cDNA clone IMAGE:5401415 5',
DEFINITION BI873142.1 GI:16046817
ACCESSION BI873142
VERSION BI873142
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL 1 (bases 1 to 939)
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@rsr@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12023 row: h column: 24
High quality sequence stop: 638.
FEATURES
Location/Qualifiers
1..939
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:5401415"
/clone_lib="NIH_MGC_94"
/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT 208 a 271 c 256 g 204 t
ORIGIN
Query Match 20.8%; Score 377; DB 13; Length 939;
Best Local Similarity 75.6%; Pred. No. 1.1e-79;
Matches 521; Conservative 0; Mismatches 160; Indels 8; Gaps 4;
QY 133 CGCATGCGGCTCCGCTCCCTCAGCGCTCGGCTCTCCACCTTGCATTTGATCTTGCC 192
Db 12 CGCATGAGGCTCGGCTGCTCAGCGGGTGCTTCTGTGCGCTCTCCACTTGGTCACTCT 71
QY 193 TGGCAACTTAACGCTGGTGATGCTTCCTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTG 252
Db 72 CTGCACACCAACTCCAGGACCAAGTTTCTGCTGAAACAGCTTGTCTCCAATGCTCTCATC 131
QY 253 TTCCTCTGCACCAACCTCATTCATCTGCACACACTATCCAGCAGAGGTGTCTCAGCGC 312
Db 132 TTCCTCTGCACCAACCTCATTCATTCGCTGTGTGCACCTACTACCCAGCTGAGGTCTCC 191
QY 313 CAGGCTCTTCAGGAGACCCGCACTTACATCCAGCGCGGCTCCACCTGCACGATGAGAAT 372
Db 192 CAGGCTCTTCAGGAGACCCGCGGAGTGTATCCAGGCTCGGCTCCATTCGCCAGCGGAGA 251
QY 373 CGGCAGCAGGAGCGGCTGCTGCTGTGCTGTTGCGGTATTCGCCCCAGCAGCTTGCCATGG 432
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Db 370 TCCTCCCGTCACTGTTGGCATGAGATGAAGCAGACATCAACGCCAAGCAGGAGATA 311
QY 460 --ATGTTCCACAGACTTACATACAGAAGCATGACAAATGTCAGCATCCTGTTTGCAGACA 517
Db 310 TGATGTTCCATAGATTACATCCAGAACATGACAACTGAGCATCCCTGTTTGTGAGACA 251
QY 518 TTGAGGGCTTCCACAGCCTGGCATCCAGTGCACCTGCAGGAGAGCTGGTTCATGACCCCTGA 577
Db 250 TCAGGGCTTCCACAGCCTGGCTCCAGTGCACCTGCAGGAGAGCTGGTTCATGACCCCTGA 191
QY 578 ATGAGCTCTTGGCCGGTTTGACAAGCTGGCTGGCGGAGAAATCACTGCTGAGGATCAAGA 637
Db 190 ACAGAGCTCTTGGCCGGTTTGACAAGCTGGCGGAGAGAAATCACTGTTTACGTAATTAAGA 131
QY 638 TCTTGGGGACCTGTTACTACTGTTGTCAGGCTGCGGAGGCGCGGCGGCGGCGGCGGCGG 697
Db 130 TCCTGGGAGTGTATTACTGCTGCTGGGCTGCTGGAAGCAGGCGGCTGAGCCAGCGCC 71
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RESULT 14
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT
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BO370134  
BO370134.1 GI:21045648  
EST.  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 673)  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,  
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=QV4st2-QV4-GN0122-  
250900-424-a04&t3=2000-09-25&t4=1)  
Seg primer: puc 18 forward  
High quality sequence stop: 556.  
High quality sequence stop: 556.  
Location/Qualifiers  
1. 673  
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/db\_xref="taxon:9606"  
/clone\_lib="GN0122"  
/dev\_stage="Adult"  
/note="Organ: placenta\_normal; Vector: puc18; Site\_1: SmaI  
; Site\_2: SmaI; A mini-library was made by cloning  
products derived from ORESTES PCR (U.S. Letters Patent  
application No. 196,716 - Ludwig Institute for Cancer  
Research) profiles into the pUC 18 vector. Reverse  
transcription of tissue mRNA and cDNA amplification were

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BASE COUNT 144 a 171 c 214 g 144 t
ORIGIN
Query Match 19.1%; Score 345.8; DB 14; Length 673;
Best Local Similarity 76.4%; Pred. No. 3.3e-72;
Matches 438; Conservative 0; Mismatches 132; Indels 3; Gaps 1;
QY 165 CCTTCCACCTTGCATTTGATCTTGGCTTGGCAACTTAACCGTGGTGATGCTCTCTCTG 224
Db 590 CTTGTCGCGCTTCCACCTTGGCCATGCGCTGCGCACCACGCCCGACGAGTCTCTGCT 531
QY 225 GAAGCAGCTCGGTGCAATGTGCTGCTCTCTGTCACCAACAGTCATTAGCATCTGCAC 284
Db 530 GAAGCAGCTTGTCTCCAATGTTCTCATTTCTCTGCAACACATCGTGGGTGTCGAC 471
QY 285 ACACATATCAGCAGAGGTGCTCAGCGCCAGCCCTTTCAGGAGACCCGAGTTACATCA 344
Db 470 CCACATATCGGCTGAGGTCTCCAGAGACAGGCTTTCAGGAGACCCGAGAGTGCATCCA 411
QY 345 GCGCGGCTCCACCTTGCACATGAGANTCGGAGAGGAGCGGCTGCTGCTGGTATT 404
Db 410 GCGCGGCTCCACCTTGCACATGAGANTCGGAGAGGAGCGGCTGCTGCTGGTCTCT 351
QY 405 GCGCGGCTCCACCTTGCATGAGATGAAAGAGACATCAACACAAAAAAGAGAC---AT 461
Db 350 TCCCGTCAATGTTGCTGAGATGAAGACACATCAACGCCAGCAGGAGATATGAT 291
QY 462 GTTCCACAGATCTACATACAGAAGCATGACAATGTACAGATCCTGTTTTCAGACATGA 521
Db 290 GTTCCATAAGATTACATCCAGAAACATGACAACGTGAGCATCTGTTGCTGACATCA 231
QY 522 GGGCTTCCACCTTGGCATCCAGTGCACATCGGAGAGGCTGGTCAATGACCTGAATCA 581
Db 230 GGGCTTCCACCTTGGCATCCAGTGCACATCGGAGAGGCTGGTCAATGACCTCAACA 171
QY 582 GCTCTTGGCCGGTTTGACAACTGCTGCGGAGATCACTGCCTGAGATCAAGATCTT 641
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RESULT 15
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LOCUS
DEFINITION
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KEYWORDS
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AUTHORS
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JOURNAL
MEDLINE
COMMENT
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BE001572  
PM2-BN0080-180400-004-g02 BN0080 Homo sapiens cDNA, mRNA sequence.  
BE001572  
BE001572.1 GI:8261805  
EST.  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 367)  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,  
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics







GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2003, 21:13:01 ; Search time 6093.65 Seconds  
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Total number of hits satisfying chosen parameters: 4109280

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Listing first 45 summaries

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- 5: gb.ov.\*
- 6: gb.pat.\*
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- 41: em.htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	3549	100.0	3549	6	AR174473	AR174473 Sequence
2	3549	100.0	3549	6	AX189761	AX189761 Sequence
3	3484.8	98.2	3552	6	AX189766	AX189766 Sequence
4	3478.4	98.0	6453	9	AF250226	AF250226 Homo sapi
5	3379.2	95.2	3582	6	AX189768	AX189768 Sequence
6	3356.8	88.9	5877	9	AB007882	AB007882 Homo sapi
7	2996.8	84.4	4046	4	DOGADENCYC	M94968 Canis famill
8	2990.4	84.3	4046	6	I29958	I29958 Sequence 1
9	2765	77.9	5841	6	AX305965	AX305965 Sequence
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13	2743.2	77.3	6036	10	RATADC	L01115 Rattus norv
14	2734	77.0	3465	10	MUSADNLCYC	M96653 Mus musculu
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19	1655.2	46.6	4847	10	RATADCYA	M96159 Rattus norv
20	1648.2	46.4	3924	6	AR106658	AR106658 Sequence
21	1475.4	41.6	2743	9	AF497517	AF497517 Homo sapi
22	1431.6	40.3	4236	5	GGA293817	AJ293817 Gallus ga
23	854.6	24.1	205248	2	AC117498	AC117498 Homo sapi
24	853	24.0	193283	2	AC021647	AC021647 Homo sapi
25	843	23.8	3137	6	AX418303	AX418303 Sequence
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27	841.8	23.7	2554	9	AK093840	AK093840 Homo sapi
28	806.6	22.7	2429	4	DOGADCYC	M97886 Canis famill
29	597.4	16.8	139619	2	AC074028	AC074028 Mus muscu
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34	553.6	15.6	2857	10	AF053980	AF053980 Mus muscu
35	545	15.4	3811	6	AX418306	AX418306 Sequence
36	522.4	14.7	6193	4	BTAC11MR	Z49806 B.taurus mR
37	505.2	14.2	3518	6	AX107094	AX107094 Sequence
38	503.6	14.2	3266	9	AF497516	AF497516 Homo sapi
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ALIGNMENTS

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LOCUS	Sequence 5 from patent US 6306830.					
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ACCESSION	AR174473					
VERSION	AR174473.1	GI:17914793				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 3549)					
AUTHORS	Hammond,H.Kirk., Insel,P.A., Ping,P., Post,S.R. and Gao,M.					
TITLE	Gene therapy for congestive heart failure					
JOURNAL	Patent: US 6306830-A 5 23-OCT-2001;					
FEATURES	Location/Qualifiers					





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ACCESSION AX189766  
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REFERENCE 1 (bases 1 to 3552)  
AUTHORS Hammond, H.K. and Gao, M.  
TITLE Gene therapy for congestive heart failure  
JOURNAL Patient: WO 0148164-A 10 05-JUL-2001;  
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)  
FEATURES  
Location/Qualifiers  
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Matches 3517; Conservative 0; Mismatches 32; Indels 3; Gaps 1;  
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SOURCE	Homo sapiens		
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REFERENCE	1 (bases 1 to 5463)		
AUTHORS	Wicker, R., Catalan, A.G., Cailieux, A., Starenki, D., Stengel, D., Sarasin, A. and Suarez, H.G.		
TITLE	Cloning and expression of human adenylyl cyclase type VI in normal thyroid tissues		
JOURNAL	Biochim. Biophys. Acta 1493 (1-2), 279-283 (2000)		

MEDLINE	20435313		
PUBMED	10978539		
REFERENCE	2 (bases 1 to 5463)		
AUTHORS	Wicker, R., Gascon Catalan, A., Cailieux, A.-F., Starenki, D., Stengel, D., Sarasin, A. and Suarez, H.G.		
TITLE	Direct Submission		
JOURNAL	Submitted (28-MAR-2000) Lab Etude des Relations - Instabilite genetique et Cancer upr 2169, Institut de Recherches sur le Cancer CNRS IFR 1221, 7 rue Guy Moquet, Villejuif 94801, France		
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AUTHORS  
Hammond H.K. and Gao M.  
TITLE  
Gene therapy for congestive heart failure  
JOURNAL  
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2 (bases 1 to 5877)  
Ohara, O.  
Direct Submission  
Submitted (06-OCT-1997) Osamu Ohara, Kazusa DNA Research Institute,  
Laboratory of DNA Technology, Yana 1532-3, Kisarazu, Chiba  
292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, tel:++81-438-52-3913,  
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On May 9, 2002 this sequence version replaced gi:2887418.  
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QY	1198	GTCATGACCTGAAATGAGTCTTTGCCCGGTTTGACAGCTGGCTGGGAGAATCACTGC	1257
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VERSION	AX305965.1 GI:17645322		
KEYWORDS	house mouse.		
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AUTHORS	Ishikawa,K., Asai,S., Takahashi,Y., Nagata,T. and Ishii,Y.		
TITLE	Method for examining ischemic conditions		
JOURNAL	Patent: WO 0188188-A 716 22-NOV-2001;		
FEATURES	School Juridical Person Nihon University (JP)		
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QY	121	CCCGGCTATAGCTGCTCCGGGATGAGAGCCACCCAGCCCTCGGGGCC	180
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QY	1198	GTCAATCACCTGAATGAGCTCTTTGCGCGGTTTGACAAGCTGGTGGAGATCACTGC	1257
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AUTHORS Yoshimura,M. and Cooper,D.M.
TITLE Cloning and expression of a Ca(2+)-inhibitable adenylyl cyclase
from NCB-20 cells
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (15), 6716-6720 (1992)
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AR174472

LOCUS AR174472 1812 bp DNA linear PAT 17-DEC-2001

DEFINITION Sequence 3 from patent US 6306830.

ACCESSION AR174472

VERSION AR174472.1 GI:17914792

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1812)

AUTHORS Hammond,H.Kirk., Insel,P.A., Ping,P., Post,S.R. and Gao,M.

TITLE Gene therapy for congestive heart failure

JOURNAL Patent: US 6306830-A 3 23-OCT-2001;

FEATURES

source Location/Qualifiers

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23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.\*  
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3549	100.0	3549	22	AAD08563 Human cardiac aden
2	3484.8	98.2	3552	22	AAD08567 Human cardiac aden
3	3478.4	98.0	4942	20	AA000461 Human type VI aden
4	3379.2	95.2	3582	22	AAD08568 Human modified car
5	2996.8	84.4	4046	14	AAQ42525 Cardiac adenyl cycl
6	2765	77.9	5841	24	ABT99680 Mouse ischaemic co
7	2751.2	77.5	4131	21	AA53923 Type vi adenyl cycl
8	1808.4	51.0	1812	22	AAD08562 Human partial card
9	1808.4	51.0	2127	19	AAV23246 Human adenyl cycl

10	1703.4	48.0	4523	20	AA000462 Human type V aden
11	1690	47.6	4356	16	AAQ95540 Cardiac adenyl cycl
12	1688.4	47.6	4356	14	AAQ37543 Cardiac adenyl cycl
13	1648.2	46.4	3924	21	AA53922 Type V adenyl cycl
14	843	23.8	3137	24	AAD28058 Human adenyl cycl
15	595	16.8	3978	21	AA53918 Adenyl cyclase t
16	586	16.5	837	22	AA530177 DNA encoding rena
17	545	15.4	3811	24	AAD28061 Human adenyl cycl
18	529.6	14.9	915	22	AA530223 DNA encoding rena
19	529.6	14.9	915	22	AA527146 cDNA encoding nove
20	505.2	14.2	3518	22	AA502694 Human adenyl cycl
21	495.8	14.0	6470	24	AAAD31191 Human adenyl cycl
22	494.2	13.9	4011	22	AAD06820 Human adenyl cycl
23	475.2	13.4	5873	24	AAAD31190 Human adenyl cycl
24	463.6	13.1	4601	21	AA53925 Type viii adenyl cycl
25	460.2	13.0	3769	24	AAD28057 Human adenyl cycl
26	459	12.9	4008	17	AAAT14528 Rat adenyl cyclase
27	459	12.9	4008	21	AA53919 Adenyl cyclase t
28	449.4	12.7	4827	23	ABLO7501 Drosophila melanog
29	446.6	12.6	3312	24	ABN89298 Human adenyl cycl
30	441.6	12.4	4533	21	AA53920 Type iii adenyl cycl
31	433	12.2	5199	21	AA53924 Type vii adenyl cycl
32	428	12.1	3357	21	AA53921 Type iv adenyl cycl
33	412	11.6	4355	24	ABL39754 Human NS cDNA sequ
34	407.6	11.5	3505	24	AAD34078 Human secreted pro
35	395.8	11.2	2601	21	AAAC99124 Human pancreatic c
36	393.2	11.1	1652	21	AA53926 Adenyl cyclase C
37	388.6	10.9	4080	22	AAH16647 Human cDNA sequenc
38	362.2	10.2	7005	23	ABL15355 Drosophila melanog
39	343.8	9.7	3239	22	AAF33100 Human secreted pro
40	295.2	8.3	314	22	AAD08561 Human partial card
41	288.2	8.1	2092	17	AAAT14529 Human adenyl cycl
42	284.4	8.0	1180	22	AAH46933 Human secreted pro
43	277	7.8	5046	23	ABLO2755 Drosophila melanog
44	273.6	7.7	320	24	ABL90026 Human polynucleoti
45	267.6	7.5	5201	23	ABL29627 Drosophila melanog

ALIGNMENTS

RESULT 1	
AAD08563	
ID	AAD08563 standard; DNA; 3549 BP.
XX	
AC	AAD08563;
XX	
DT	04-SEP-2001 (first entry)
XX	
DE	Human cardiac adenylcyclase VI (ACVI) isoform #1 DNA.
XX	
KW	Human; cardiant; beta-adrenergic signalling protein; beta-ASP;
KW	myocardium; gene therapy; beta-adrenergic receptor; beta-AR;
KW	adenylcyclase; adenylyate cyclase; cAMP synthetase;
KW	G-protein receptor kinase; GRK; heart disease; congestive heart failure;
KW	cardiac adenylcyclase VI; ACVI isoform; beta-ASP transgene; ds.
XX	
OS	Homo sapiens.
XX	
FH	Key
CDS	Location/Qualifiers
FT	1..3504
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FT	/product= "Human cardiac adenylcyclase VI isoform #1"
FT	/EC_number= "4.6.1.1"
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PN	WO200148164-A2.
XX	
PD	05-JUL-2001.
XX	
PF	26-DEC-2000; 2000WO-US35411.
XX	
PR	27-DEC-1999; 99US-0472667.
XX	



(REGC ) UNIV CALIFORNIA.  
Hammond HK, Gao M;  
WPI: 2001-418260/44.  
P-PSDB; AAE04310.  
Novel polynucleotide encoding a modified adenylyl cyclase polypeptide  
useful for enhancing cardiac function in mammalian hearts, and for  
treating heart disease, especially congestive heart failure -  
Example 5; Page 122-129; 153pp; English.  
The present invention relates to methods and compositions for enhancing  
cardiac function in mammalian hearts by inserting transgenes encoding  
beta-adrenergic signalling proteins (beta-ASP) which increase  
beta-adrenergic responsiveness within the myocardium using in vivo  
gene therapy. The beta-ASPs of the invention include beta-adrenergic  
receptors (beta-AR), adenylyl cyclases (also referred as adenylylase,  
adenylate cyclase and cAMP synthetase) and G-protein receptor kinase  
(GRK) inhibitors. The beta-ASP is used for enhancing cardiac function  
in mammalian hearts and for treating heart disease, especially  
congestive heart failure. The present DNA sequence encodes human  
cardiac adenylyl cyclase VI (ACVI) isoform which is used for generating  
a third beta-ASP transgene, used in the exemplification  
of the invention.  
Sequence 3549 BP; 699 A; 1025 C; 1061 G; 764 T; 0 other;

Query Match 100.0%; Score 3549; DB 22; Length 3549;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 ATGTGATGTTAGTGGCTCTCTGTCCTAAAGTGGATGAACGGAACACGCTGGGGT 60  
QY 61 GAACGCAATGGCAGAAAGCTTCGCGGCGCCGTGCACCTCGGCGAGGTGCTTCGCAG 120  
DB 61 GAACGCAATGGCAGAAAGCTTCGCGGCGCCGTGCACCTCGGCGAGGTGCTTCGCAG 120  
QY 121 CCCCGCTATATAGCTGCTCCGGGATGCAGAGCCACCCAGCCGCCCTCGGGCCGC 180  
DB 121 CCCCGCTATATAGCTGCTCCGGGATGCAGAGCCACCCAGCCGCCCTCGGGCCGC 180  
QY 181 CCTCGTGGCCCTGGCAGGATGACGCTTCATCCGGAGGGCGGCCAGGCAAGGCAAG 240  
DB 181 CCTCGTGGCCCTGGCAGGATGACGCTTCATCCGGAGGGCGGCCAGGCAAGGCAAG 240  
QY 241 GAGCTGGGGCTCGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACACGACAGG 300  
DB 241 GAGCTGGGGCTCGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACACGACAGG 300  
QY 301 GCGGGACGGCTGAGGTGGCGCCGACGGGTGCCAGAGGTGGCGATCTGCTGGCGC 360  
DB 301 GCGGGACGGCTGAGGTGGCGCCGACGGGTGCCAGAGGTGGCGATCTGCTGGCGC 360  
QY 361 CGTTTGGTGCAGGTGTTCCAGTGAAGAGTTCCTGTCGGCCAAAGCTGGAGCGCTGTAC 420  
DB 361 CGTTTGGTGCAGGTGTTCCAGTGAAGAGTTCCTGTCGGCCAAAGCTGGAGCGCTGTAC 420  
QY 421 CAGCGGTACTTTTCCAGATGAACAGAGCAGCCTGACGCTGCTGGTGGCGTGTGTG 480  
DB 421 CAGCGGTACTTTTCCAGATGAACAGAGCAGCCTGACGCTGCTGGTGGCGTGTGTG 480  
QY 481 CTGCTCAGAGCGGTGCTGCTGCTTCCAAAGCCGACCGCCGCCCTCAGCCTGCCAT 540  
DB 481 CTGCTCAGAGCGGTGCTGCTGCTTCCAAAGCCGACCGCCGCCCTCAGCCTGCCAT 540  
QY 541 CTGCGCACTGTTGGCTGTGCCCGCCCTGTTCTGTTGGGCTCATGTTGGTGTGAACCGG 600  
DB 541 CTGCGCACTGTTGGCTGTGCCCGCCCTGTTCTGTTGGGCTCATGTTGGTGTGAACCGG 600

QY 601 CATAGCTTCGCGCAGGACTCCATGTGGTGTGAGTAACCTGTGCTGGCATCTCTGGCG 660  
DB 601 CATAGCTTCGCGCAGGACTCCATGTGGTGTGAGTAACCTGTGCTGGCATCTCTGGCG 660  
QY 661 GCAGTGCAGGTGCGGGGCGCTTTCGACAGACACCGCGAGCCCTCTCTCGGGCGCTTGG 720  
DB 661 GCAGTGCAGGTGCGGGGCGCTTTCGACAGACACCGCGAGCCCTCTCTCGGGCGCTTGG 720  
QY 721 TGGCCCTGTGTTTGTATATACATCGACGCTCTCCCATCGGATCGGGGCTGCG 780  
DB 721 TGGCCCTGTGTTTGTATATACATCGACGCTCTCCCATCGGATCGGGGCTGCG 780  
QY 781 GTCCTCAGCGGCTGGGCTCTCCACCTTGCATTTGATCTTGGCTGGCAACTTAACCT 840  
DB 781 GTCCTCAGCGGCTGGGCTCTCCACCTTGCATTTGATCTTGGCTGGCAACTTAACCT 840  
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DB 841 GGTGATGCTTCTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTTCTCTGCACCAAC 900  
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DB 901 GTCATTAGCATCTGCACACACTATCCAGCAGAGTGTCTCAGCGCCAGGCTTTTCAGGAG 960  
QY 961 ACCCGCAGTTACATCCAGGCGCGCTCCACCTGCAGCATGAGAATCGGCGAGCAGGCG 1020  
DB 961 ACCCGCAGTTACATCCAGGCGCGCTCCACCTGCAGCATGAGAATCGGCGAGCAGGCG 1020  
QY 1021 CTGCTGCTGTGGTATATGCCCCAGCAGCTGTCATGAGATGAAAGAGACATCAACACA 1080  
DB 1021 CTGCTGCTGTGGTATATGCCCCAGCAGCTGTCATGAGATGAAAGAGACATCAACACA 1080  
QY 1081 AAAAAGAGACATGTTCCACAAGATCTACATACAGAGCATGACAATGTACGATCCTG 1140  
DB 1081 AAAAAGAGACATGTTCCACAAGATCTACATACAGAGCATGACAATGTACGATCCTG 1140  
QY 1141 TTTGCAGACATTTAGGGCTTCCACAGCCTGGCATCCAGTGCACCTGCGCAGAGCTGGTC 1200  
DB 1141 TTTGCAGACATTTAGGGCTTCCACAGCCTGGCATCCAGTGCACCTGCGCAGAGCTGGTC 1200  
QY 1201 ATGACCTTGAATGAGCTCTTTGCCCGGTTTGACAGCTGGCTGCGGAGAACTCACTGCCTG 1260  
DB 1201 ATGACCTTGAATGAGCTCTTTGCCCGGTTTGACAGCTGGCTGCGGAGAACTCACTGCCTG 1260  
QY 1261 AGGATCAAGATCTTGGGGACTGTTACTACTGTGTGTCAGGGCTGCCGAGGCCCGGGCC 1320  
DB 1261 AGGATCAAGATCTTGGGGACTGTTACTACTGTGTGTCAGGGCTGCCGAGGCCCGGGCC 1320  
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DB 1321 GACCATGCCACTGCTGTGGAGATGGGGGTAGACATGATTTGAGGCCATCTCGCTGGTA 1380  
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DB 1381 CGTGAGGTGACAGGTGTGAATGTGAACATGCCGCTGGCATCCAGCGGGCGCTGAC 1440  
QY 1441 TCGCGCTCTTGGCTTGGGAAATGGCAGTTCGATGTGTGTCCTCAATGATGTGACCTG 1500  
DB 1441 TCGCGCTCTTGGCTTGGGAAATGGCAGTTCGATGTGTGTCCTCAATGATGTGACCTG 1500  
QY 1501 GCCAACACATGGAAGCAGGAGCGGGCTGGCGCATCCACATCACTCTCGGCAACACTG 1560  
DB 1501 GCCAACACATGGAAGCAGGAGCGGGCTGGCGCATCCACATCACTCTCGGCAACACTG 1560  
QY 1561 CAGTACCTGAACGGGGACTACGAAGTGGAGCGCCCTGGTGGCAAGCGCAACCGCTAC 1620  
DB 1561 CAGTACCTGAACGGGGACTACGAAGTGGAGCGCCCTGGTGGCAAGCGCAACCGCTAC 1620  
QY 1621 CTCAGGAGCAGCATTGAGACTTTCCTCATCTCTGGCGCCAGCAGCAAAACGGAAGAG 1680  
DB 1621 CTCAGGAGCAGCATTGAGACTTTCCTCATCTCTGGCGCCAGCAGCAAAACGGAAGAG 1680  
QY 1681 GAGAAAGCATGCTGGCCAAAGCTGCAGCGGACTCGGGGCCAACTCCATGGAAGGGCTGATG 1740



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Db 1681 |GAGAAAGCATGCTGGCCAAAGCTCAGCGGACTCGGGCCAACTCCATGGAGGGCTGATG| 1740
Qy 1741 |CCGCGATGGGTTCTGATGCTGGCCCTTCTCCCGGACCAAGGACTCCAAGGCCCTTCGCGCAG| 1800
Db 1741 |CCGCGATGGGTTCTGATGCTGGCCCTTCTCCCGGACCAAGGACTCCAAGGCCCTTCGCGCAG| 1800
Qy 1801 |ATGGCGATTGATGATTCAGCAAAAGACAACCGGGGACCCAAAGATGCCCTGAACCCCTGAG| 1860
Db 1801 |ATGGCGATTGATGATTCAGCAAAAGACAACCGGGGACCCAAAGATGCCCTGAACCCCTGAG| 1860
Qy 1861 |GATGAGTGGATGATGATTCCTGAGCCGTGCCATCGATGCCCGCAGCATTTGATCAGCTGGG| 1920
Db 1861 |GATGAGTGGATGATGATTCCTGAGCCGTGCCATCGATGCCCGCAGCATTTGATCAGCTGGG| 1920
Qy 1921 |AAGGACCATGTGCGCCCGTTTTTGGCTCAACCTTCCAGAGAGAGGATTTTGAGAAAGTAC| 1980
Db 1921 |AAGGACCATGTGCGCCCGTTTTTGGCTCAACCTTCCAGAGAGAGGATTTTGAGAAAGTAC| 1980
Qy 1981 |TCCCGGAAGTGGATCCCGGCTTCGAGACCTACGTTGCCGTGTCCTGTTGGTCTTCTGC| 2040
Db 1981 |TCCCGGAAGTGGATCCCGGCTTCGAGACCTACGTTGCCGTGTCCTGTTGGTCTTCTGC| 2040
Qy 2041 |TTGATCTGCTTCATCCAGCTTCTAAATTTTCCACACTCCACCCTGATGCTTGGGATTTAT| 2100
Db 2041 |TTGATCTGCTTCATCCAGCTTCTAAATTTTCCACACTCCACCCTGATGCTTGGGATTTAT| 2100
Qy 2101 |GCCAGCATCTTCCGTGCTGCTAATCACCCTGCTGATCTGTGCTGTGTAATCTCTGTTGGT| 2160
Db 2101 |GCCAGCATCTTCCGTGCTGCTAATCACCCTGCTGATCTGTGCTGTGTAATCTCTGTTGGT| 2160
Qy 2161 |TCTCTGTTCCTAAGGCCCTGCAACGCTGTGTCGCCAGCATTTGTCGCTCACGGGACAT| 2220
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Qy 2221 |AGCACCGAGTTGCACTTTTCCGTCCTGCTGCTGTTTACTTCTGCAATGCCCCAATG| 2280
Db 2221 |AGCACCGAGTTGCACTTTTCCGTCCTGCTGCTGTTTACTTCTGCAATGCCCCAATG| 2280
Qy 2281 |TTCACCTGTAAACACACCCCATAGGAGCTGTGCACCGGAGTCTGAATTTAACACCT| 2340
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Qy 2341 |GCTGACATCACTGCTGCCACCTGACAGCTCAATTTACTCTTGGCCCTGGATGCTCCC| 2400
Db 2341 |GCTGACATCACTGCTGCCACCTGACAGCTCAATTTACTCTTGGCCCTGGATGCTCCC| 2400
Qy 2401 |CTGTGTAGGCGCACCATGCCACCTGACGCTTCTGAGGTGTCATCGGGAACATGCTG| 2460
Db 2401 |CTGTGTAGGCGCACCATGCCACCTGACGCTTCTGAGGTGTCATCGGGAACATGCTG| 2460
Qy 2461 |CTGAGTCTCTTGGCCAGCTCTGCTCTCTGCACATCAGCAGCATCGGGAAGTTGGCCATG| 2520
Db 2461 |CTGAGTCTCTTGGCCAGCTCTGCTCTCTGCACATCAGCAGCATCGGGAAGTTGGCCATG| 2520
Qy 2521 |ATCTTTGCTTGGGCTCATCTATTGCTGCTGCTTCTGCTGGGTCCCGGAGCCCATC| 2580
Db 2521 |ATCTTTGCTTGGGCTCATCTATTGCTGCTGCTTCTGCTGGGTCCCGGAGCCCATC| 2580
Qy 2581 |TTTGACAACTATGACCTACTGCTTGGCGTCCATGGCTTGGCTTCTTCCAAATGAGACCTTT| 2640
Db 2581 |TTTGACAACTATGACCTACTGCTTGGCGTCCATGGCTTGGCTTCTTCCAAATGAGACCTTT| 2640
Qy 2641 |GATGGCTGGACTCTCAGCTGAGGGGAGGCTGGCCCTCAATATATGACCCCTGTGATT| 2700
Db 2641 |GATGGCTGGACTCTCAGCTGAGGGGAGGCTGGCCCTCAATATATGACCCCTGTGATT| 2700
Qy 2701 |CTGCTGTGTTGGCTGGGCTGCTATCTGATGCTCAGAGGTGGAATCAGCTGCCGCG| 2760
Db 2701 |CTGCTGTGTTGGCTGGGCTGCTATCTGATGCTCAGAGGTGGAATCAGCTGCCGCG| 2760
Qy 2761 |CTAAACTTCTCTGGAACCTACAGGCAACAGGGGAAAGAGGAGATGGAGGACTACAG| 2820
Db 2761 |CTAAACTTCTCTGGAACCTACAGGCAACAGGGGAAAGAGGAGATGGAGGACTACAG| 2820
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Db 2761 |CTAAACTTCTCTGGAACCTACAGGCAACAGGGGAAAGAGGAGATGGAGGACTACAG| 2820
Qy 2821 |GCATACACCGGAGGCTGCTGCATAACATTTGCCCAGAGACGCTGGGGGCCCATCTTCTCTG| 2880
Db 2821 |GCATACACCGGAGGCTGCTGCATAACATTTGCCCAGAGACGCTGGGGGCCCATCTTCTCTG| 2880
Qy 2881 |GCCGGGAGGCGCCCAATGATGAATCTCTACTATCAGTCGTGTGATGTGTGGCTGTTATG| 2940
Db 2881 |GCCGGGAGGCGCCCAATGATGAATCTCTACTATCAGTCGTGTGATGTGTGGCTGTTATG| 2940
Qy 2941 |TTTSCCTCCATGTCACAACTTCTCTGAGTTCTCTGAGCTGGAGCTGGAGGAAACAATGAGGGT| 3000
Db 2941 |TTTSCCTCCATGTCACAACTTCTCTGAGTTCTCTGAGCTGGAGCTGGAGGAAACAATGAGGGT| 3000
Qy 3001 |GCCGAGTGCCTGCGGCTGCTCAACAGATCATCTGACTTTGATGATGATTTATCAGCGAG| 3060
Db 3001 |GCCGAGTGCCTGCGGCTGCTCAACAGATCATCTGACTTTGATGATGATTTATCAGCGAG| 3060
Qy 3061 |GAGCGGTTCCGGCAGCTGGAAGAGATCAAGACGATTTGGTAGCAGCTACATGGCTGCCTCA| 3120
Db 3061 |GAGCGGTTCCGGCAGCTGGAAGAGATCAAGACGATTTGGTAGCAGCTACATGGCTGCCTCA| 3120
Qy 3121 |GGGCTGAACGCCAGCAGCTAGCATCAGGTGGCGCTCCACACATCACTGCCCTGGCTGAC| 3180
Db 3121 |GGGCTGAACGCCAGCAGCTAGCATCAGGTGGCGCTCCACACATCACTGCCCTGGCTGAC| 3180
Qy 3181 |TACGCCATGGGCTTCATGGAGCAGATGAAGCACATCAATGAGCACTCCTTCAACAATTC| 3240
Db 3181 |TACGCCATGGGCTTCATGGAGCAGATGAAGCACATCAATGAGCACTCCTTCAACAATTC| 3240
Qy 3241 |CAGATGAAGATTGGGCTGAACATGGGCCAGTGTGCGAGGTGTCTATCGATGGAGCAGCGGG| 3300
Db 3241 |CAGATGAAGATTGGGCTGAACATGGGCCAGTGTGCGAGGTGTCTATCGATGGAGCAGCGGG| 3300
Qy 3301 |CCACAGTATGACATCTGGGGGAACACAGTGAATGTCTCTAGTCGTATGGACAGCAGCGGG| 3360
Db 3301 |CCACAGTATGACATCTGGGGGAACACAGTGAATGTCTCTAGTCGTATGGAGCAGCGGG| 3360
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Db 3361 |GTCCCCACCAATCCAGTGACCGACCTGTACAGAGTTCTAGCTGCCAAGGGGTAC| 3420
Qy 3421 |CAGCTGAGTGTGAGGGGTGGTCAAGGTGAAGGGCAAGGGGAGATGACCACCTACTTC| 3480
Db 3421 |CAGCTGAGTGTGAGGGGTGGTCAAGGTGAAGGGCAAGGGGAGATGACCACCTACTTC| 3480
Qy 3481 |CTCAATGGGGCCCCAGCAGTTAACAGGGCCCCAGCCACAAATTCAGCTGAAGGACCAAG| 3540
Db 3481 |CTCAATGGGGCCCCAGCAGTTAACAGGGCCCCAGCCACAAATTCAGCTGAAGGACCAAG| 3540
Qy 3541 |GTGGGCACT 3549
Db 3541 |GTGGGCACT 3549

RESULT 2
AAD08567
ID AAD08567 standard; DNA; 3552 BP.
XX
AC AAD08567;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human cardiac adenylylase VI (ACVI) isoform #2 DNA.
XX
KW Human; cardiant; beta-adrenergic signalling protein; beta-ASP;
KW myocardium; gene therapy; beta-adrenergic receptor; beta-AR;
KW adenylylase; adenylate cyclase; cAMP synthetase;
KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;
KW cardiac adenylylase VI; ACVI isoform; beta-ASP transgene; ds.
XX
OS Homo sapiens.
XX
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Key	Location/Qualifiers
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PD	05-JUL-2001.
XX	
PF	26-DEC-2000; 2000WO-US35411.
XX	
PR	27-DEC-1999; 99US-0472667.
XX	
PA	(REGC ) UNIV CALIFORNIA..
XX	
PI	Hammond HK, Gao M;
XX	
DR	WPI; 2001-418260/44.
XX	
DR	P-PSDB; AAE04311.
XX	
PT	Novel polynucleotide encoding a modified adenylylase polypeptide
PT	useful for enhancing cardiac function in mammalian hearts, and for
PT	treating heart disease, especially congestive heart failure -
XX	
PS	Claim 6; Page 134-140; 153pp; English.
XX	
CC	The present invention relates to methods and compositions for enhancing
CC	cardiac function in mammalian hearts by inserting transgenes encoding
CC	beta-adrenergic signalling proteins (beta-ASP) which increase
CC	beta-adrenergic responsiveness within the myocardium using in vivo
CC	gene therapy. The beta-ASPs of the invention include beta-adrenergic
CC	receptors (beta-AR), adenylylases (also referred as adenylylase,
CC	adenylylase and CAMP synthetase) and G-protein receptor kinase
CC	(GRK) inhibitors. The beta-ASP is used for enhancing cardiac function
CC	in mammalian hearts and for treating heart disease, especially
CC	congestive heart failure. The present DNA sequence encodes human
CC	cardiac adenylylase VI (ACVI) isoform which is used for generating
CC	a fourth beta-ASP transgene, used in the exemplification
CC	of the invention.
XX	
SQ	Sequence 3552 BP; 686 A; 1037 C; 1068 G; 761 T; 0 other;

Db	361	CGTCTGTTGCAAGTGTTTCCAGTCCGAAGCAGTTCCTCGTTTCGGCCCAAGCTGGAGCGCCTGTAC	420
Qy	421	CAGCGGTACTTTTTTCCAGATGAACACAGACAGCCTCAGCCTCTGCTGGTGGCGGTGCTGGTG	480
Db	421	CAGCGGTACTTCTTCAGATGAACACAGACAGCCTGACGCTGCTCATGGCGGTGCTGGTG	480
Qy	481	CTGCTCAACAGGGTGCTGCTGGGCTTTTCCAAGCGCGACCCGCCGCCCTCAGCCTGCGCTAT	540
Db	481	CTGCTCAACAGGGTGCTGCTGGGCTTTTCCAAGCGCGACCCGCCGCCCTCAGCCTGCGCTAT	540
Qy	541	GTGCACTGTGTGGCTGTGCCCGCGCCCTGTCTGTGGGGCTCATGGTGGTGTGAACCGG	600
Db	541	GTGCACTGTGTGGCTGTGCCCGCGCCCTGTCTGTGGGGCTCATGGTGGTGTGAACCGG	600
Qy	601	CATAGCTTCGCCAGGACTCCATGTGGGTGGTGAAGCTGGTCTGGGCATCTGCGG	660
Db	601	CATAGCTTCGCCAGGACTCCATGTGGGTGGTGAAGCTGGTCTGGGCATCTGCGG	660
Qy	661	GCATGTGAGTTCGGGGCGCTTTTCGACAGACACCGCGAGCCCTCTGTCGGGGCTCTGG	720
Db	661	GCATGTGAGTTCGGGGCGCTTCGACAGACACCGCGAGCCCTCTGTCGGGGCTCTGG	720
Qy	721	TGCCCTGTGTCTTTGTATACATCGCATACAGCTTCTCCCATCCGCATCGCGGCTGCC	780
Db	721	TGCCCTGTGTCTTTGTATACATCGCATACAGCTTCTCCCATCCGCATCGCGGCTGCC	780
Qy	781	GCTCTCAGCGCCTGGGCCCTCCACCTTGCATTTGATCTTGGCTGGCAACTTAAACGT	840
Db	781	GCTCTCAGCGCCTGGGCCCTCCACCTTGCATTTGATCTTGGCTGGCAACTTAAACGT	840
Qy	841	GGTGATGCCCTTCTCTGGAAAGCAGCTCGGTGGCAATGTCTGCTTCTCTGCACCAAC	900
Db	841	GGTGATGCCCTTCTCTGGAAAGCAGCTCGGTGGCAATGTCTGCTTCTCTGCACCAAC	900
Qy	901	GTCAATTAGCATCTGCACACACTATCAGACAGAGTGTCTCAGCGCCAGCGCTTTCAGGAG	960
Db	901	GTCAATTAGCATCTGCACACACTATCAGACAGAGTGTCTCAGCGCCAGCGCTTTCAGGAG	960
Qy	961	ACCCGCGAGTTACATCCAGGCCCGGGCTCCACCTGCAGCATGAGAATCGCAGCAGAGCGG	1020
Db	961	ACCCGCGAGTTACATCCAGGCCCGGGCTCCACCTGCAGCATGAGAATCGCAGCAGAGCGG	1020
Qy	1021	CTGCTGCTGTCGGTATTTGCCCAAGCAGCTTGCATGGAGATGAAGAAGACATCAACACA	1080
Db	1021	CTGCTGCTGTCGGTATTTGCCCAAGCAGCTTGCATGGAGATGAAGAAGACATCAACACA	1080
Qy	1081	AAAAAACAAGAC--ATGTTTCCACAAGATCTACATACAGAAGCATGACAATGTCAAGATC	1137
Db	1081	AAAAAACAAGACATGATTTTCCACAAGATCTACATACAGAAGCATGACAATGTCAAGATC	1140
Qy	1138	CTGTTTTCAGACATTTAGGGCTTTCACCGACCTGGCATCCCACTGCATCTGCAGAGAGCTG	1197
Db	1141	CTGTTTTCAGACATTTAGGGCTTTCACCGACCTGGCATCCCACTGCATCTGCAGAGAGCTG	1200
Qy	1198	GTCATGACCTGAAATGAGCTCTTTTGCCCGGTTTGACAAGCTGGCTGGGAGAACTACTGC	1257
Db	1201	GTCATGACCTGAAATGAGCTCTTTTGCCCGGTTTGACAAGCTGGCTGGGAGAACTACTGC	1260
Qy	1258	CTGAGGATCAAGATCTTGGGGAGCTGTACTACTGTGTGTGAGGGCTGCCGAGGCCCGG	1317
Db	1261	CTGAGGATCAAGATCTTGGGGAGCTGTACTACTGTGTGTGAGGGCTGCCGAGGCCCGG	1320
Qy	1318	GCCGACCATGCCACTGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTG	1377
Db	1321	GCCGACCATGCCACTGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTG	1380
Qy	1378	GTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGGCGCTG	1437
Db	1381	GTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGGCGCTG	1440
Qy	1438	CACGTGGGGCTCCTTGGCTTGGGAAATGGCAGTTTCGATGTGTGGTCCAATGATGTGACC	1497
Db	1441	CACGTGGGGCTCCTTGGCTTGGGAAATGGCAGTTTCGATGTGTGGTCCAATGATGTGACC	1500

Qy	1498	CTGCCAACCACATGGAAGCAGGAAGCCGGCGTGC	CAGATCATCAATCATCTGGGCAACA	1557
Db	1501	CTGCCAACACATGAGAGCAGAGCGCGGTGC	CAGATCATCAATCTGGGCAACA	1560
Qy	1558	CTGCAGTACCTGAACGGGACTACGAAGTGGA	GCCAGCGCTGTGTGSCAGCGAACGCG	1617
Db	1561	CTGCAGTACCTGAACGGGACTACGAAGTGGA	GCCAGCGCTGTGTGSGAGCGAACGCG	1620
Qy	1618	TACCTCAAGGAGCAGCACATTGAGACTTTTC	TATCTTCATCTTGGCGCCAGCAGAAACGAAA	1677
Db	1621	TACCTCAAGGAGCAGCACATTGAGACTTTTC	TATCTTCATCTTGGCGCCAGCAGAAACGAAA	1680
Qy	1678	GAGGAGAAGGCATGTGGCCAAAGCTGACGG	AATCTCGGGCCAATCCATGGAAGGCGTG	1737
Db	1681	GAGGAGAAGGCATGTGGCCAAAGCTGACGG	AATCTCGGGCCAATCCATGGAAGGCGTG	1740
Qy	1738	ATGCCGGATGGGTTCCTGATCGTGCTTCTCC	CGSACCAAGGACTCCAAGGCCCTCCCG	1797
Db	1741	ATGCCGGCTGGGTTCCTGATCGTGCTTCTCC	CGSACCAAGGACTCCAAGGCCCTCCCG	1800
Qy	1798	CAGATGGGCATTGATGATTCAGAACAAACAC	CCGGGCAACCAAGATGCCCTGAACCCCT	1857
Db	1801	CAGATGGGCATTGATGATTCAGAACAAACAC	CCGGGCAACCAAGATGCCCTGAACCCCT	1860
Qy	1858	GAGATGAGGTGATGAGTTCCTGAGCCGTGC	ATCGATCGATCCCGAGCATTTGATCAGTG	1917
Db	1861	GAGATGAGGTGATGAGTTCCTGAGCCGTGC	ATCGATCGATCCCGAGCATTTGATCAGTG	1920
Qy	1918	CGAAGGACCATGTGCGCGGTTTTTGCTACCT	TCCAGAGAGGATTTTGAGAAAG	1977
Db	1921	CGAAGGACCATGTGCGCGGTTTTTGCTACCT	TCCAGAGAGGATTTTGAGAAAG	1980
Qy	1978	TACTCCCGAAGTGGATCCCGCTTCGGAGCCT	ACGTTGCCTGTGCCCTGTGGTCTTC	2037
Db	1981	TACTCCCGAAGTGGATCCCGCTTCGGAGCCT	ACGTTGCCTGTGGTCTTC	2040
Qy	2038	TGCTTATCTGCTTCATCCAGCTTCTAATTTT	CCCACACTCCACCCTGATCTGGGATT	2097
Db	2041	TGCTTATCTGCTTCATCCAGCTTCTAATTTT	CCCACACTCCACCCTGATCTGGGATT	2100
Qy	2098	TATGCCAGCATCTTCTGCTGCTGCTTAATCA	CCGTCGTACTGTGCTGTACTCCCTGT	2157
Db	2101	TATGCCAGCATCTTCTGCTGCTGCTTAATCA	CCGTCGTACTGTGCTGTACTCCCTGT	2160
Qy	2158	GGTTCCTGTTCCCTAAGCCCTGCAAGCTGTG	TCCCGCAGCATTTGCCCTCACGGGCA	2217
Db	2161	GGTTCCTGTTCCCTAAGCCCTGCAAGCTGTG	TCCCGCAGCATTTGCCCTCACGGGCA	2220
Qy	2218	CATGACACCGCAGTTGGCATTTTCCGTCCTG	CTGTGTACTCTGTCATCTGGCATTGC	2277
Db	2221	CATGACACCGCAGTTGGCATTTTCCGTCCTG	CTGTGTACTCTGTCATCTGGCATTGC	2280
Qy	2278	ATGTTACCTGTAAACCACACCCCCCATAGG	AGCTGTGCAGCCCCGGATGCTGAATTTAA	2337
Db	2281	ATGTTACCTGTAAACCACACCCCCCATAGG	AGCTGTGCAGCCCCGGATGCTGAATTTAA	2340
Qy	2338	CCTGCTGACATCACTGCCCTGCCACCTGCA	GCATTAATCTCTCTGGGCGCTGGATGCT	2397
Db	2341	CCTGCTGACATCACTGCCCTGCCACCTGCA	GCATTAATCTCTCTGGGCGCTGGATGCT	2400
Qy	2398	CCCTGTGTGAGGGACCATGCCACCTGCAGCT	TTCTCCTGAGGTGCCATCGGGAACATG	2457
Db	2401	CCCTGTGTGAGGGACCATGCCACCTGCAGCT	TTCTCCTGAGGTGCCATCGGGAACATG	2460
Qy	2458	CTGCTGAGTCTCTTGGCCAGCTCTGCTTCT	TCTGTGCACATCAGCAGCATCGGGAAGTTG	2517
Db	2461	CTGCTGAGTCTCTTGGCCAGCTCTGCTTCT	TCTGTGCACATCAGCAGCATCGGGAAGTTG	2520
Qy	2518	ATGATCTTTGCTTTGGGCTCATCATTAATTT	TGGTGCTTCTGCTGCGGTCCCGACGCGC	2577
Db	2521	ATGATCTTTGCTTTGGGCTCATCATTAATTT	TGGTGCTTCTGCTGCGGTCCCGACGCGC	2580

RESULT 3  
AAX00461  
ID AAX  
XX

AC AAX00461;  
XX  
DT 21-MAY-1999 (first entry)  
XX  
DE Human type VI adenylyl cyclase cDNA.  
XX  
KW Adenylyl cyclase type VI; human; hAC6; therapy; diagnosis; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 145..3651  
FT /\*tag= a  
XX  
PN WO9901547-A1.  
XX  
PD 14-JAN-1999.  
XX  
PF 01-JUL-1998; 98MO-US13694.  
XX  
PR 01-JUL-1997; 97US-0886550.  
PR 01-JUL-1997; 97US-0070904.  
XX  
PA (CORT-) COR THERAPEUTICS INC.  
XX  
PI Tomlinson JA;  
XX  
DR WPI; 1999-106049/09.  
DR P-PSDB; AAW30599.  
XX  
PT Newly isolated and purified human type VI adenylyl cyclase (hAC6)  
PT polypeptide - useful for identifying potential therapeutic agents  
PT that modulate hAC6 activity, and for the diagnosis of  
PT hAC6-associated diseases and disorders  
XX  
PS Claim 3; Fig 1A-I; 42pp; English.  
XX  
CC This DNA sequence encodes human type VI adenylyl cyclase (hAC6, see  
CC AAW30599) that is expressed mainly in the heart and brain. hAC6 has  
CC a similar putative structure to other adenylyl cyclase isoforms  
CC but, like type V, is distinguishable in that it has a larger  
CC N-terminus and a relatively shorter C-terminus as it lacks the C2b  
CC region. hAC6 cDNA was initially isolated from a human heart cDNA  
CC library using an adenylyl cyclase PCR fragment as probe. It was  
CC used to design primers that were used in a PCR-based RACE to obtain  
CC the full-length cDNA sequence. The invention relates to the hAC6  
CC gene, methods for the recombinant production of purified hAC6 and  
CC the proteins made by these methods, antibodies against hAC6,  
CC vectors, probes and host cells (especially HEK-293) transformed by  
CC genes encoding polypeptides having hAC6 activity, along with  
CC diagnostic and therapeutic uses for these various reagents. hAC6  
CC can be used as a tool to screen for agonists and antagonists that  
CC stimulate/inhibit hAC6. Such compounds have therapeutic utility  
CC in treating diseases caused by aberrant activity of this enzyme,  
CC and diseases whose symptoms can be ameliorated by stimulating or  
CC inhibiting the activity of hAC6.  
XX  
SQ Sequence 4942 BP; 953 A; 1404 C; 1512 G; 1073 T; 0 other;  
Query Match 98.0%; Score 3478.4; DB 20; Length 4942;  
Best Local Similarity 98.9%; Pred. No. 0;  
Matches 3513; Conservative 0; Mismatches 36; Indels 3; Gaps 1;  
Oy 1 ATGTCATGGTTAGTGGCTCTCTGGTCCCTAAAGTGGATGAACGAAACACACCCCTGGGGT 60  
Db 145 ATGTCATGGTTAGTGGCTCTCTGGTCCCTAAAGTGGATGAACGAAACACACCCCTGGGGT 204  
Oy 61 GAACCAATGGGCAAGAGCGTTTCGGCGCGGTGGCACTCGGGCAGGTGGCTTCTGCACG 120  
Db 205 GAACCAATGGGCAAGAGCGTTTCGGCGCGGTGGCACTCGGGCAGGTGGCTTCTGCACG 264  
Oy 121 CCCGCTATATAGTGGCTCGGGATGCAGAGCCACCCAGCCCAACCCCTCGGGGGCCCC 180  
Db 1345 GTCATGACCCCTGAATGAGCTCTTTGCCCGGGTTTGCACAGCTGGCTGGCGGAGAACTACCTGC 1404

Db 265 CCCGCTATATAGTGGCTCGGGATGCAGAGCCACCCAGCCCCCCTCTCGGGGGCCCC 324  
Oy 181 CTTGGTCCCTTGGCAGGATGACGCTTTCATCCGGAGGGGGCCAGCAAGGCAAG 240  
Db 325 CTTGGTCCCTTGGCAGGATGACGCTTTCATCCGGAGGGGGCCAGCAAGGCAAG 384  
Oy 241 GAGCTGGGGCTTCGGGCGAGTGGCCCTTGGGCTTCGAGGATACCGAGGTGACACGACGCG 300  
Db 385 GAGCTGGGGCTTCGGGCGAGTGGCCCTTGGGCTTCGAGGATACCGAGGTGACACGACGCG 444  
Oy 301 GCGGGAGGCTGAGGTGGCGCGGACGCGGTGGCCAGCTCGGCAAGCTGAGCGCTGTAC 360  
Db 445 GCGGGAGGCTGAGGTGGCGCGGACGCGGTGGCCAGCTCGGCAAGCTGAGCGCTGTAC 504  
Oy 361 CGTTGGTGCAGGTGTTCCAGTGAAGCAGTTCCTTCGGCAAGCTGAGCGCTGTAC 420  
Db 505 CGTCTGGTGCAGGTGTTCCAGTGAAGCAGTTCCTTCGGCAAGCTGAGCGCTGTAC 564  
Oy 421 CAGCGGTACTTTTCCAGATGAACAGAGACCTGACGCTGCTGGTGGCGGTGCTGGT 480  
Db 565 CAGCGGTACTTTTCCAGATGAACAGAGACCTGACGCTGCTGATGGCGGTGCTGGT 624  
Oy 481 CTGCTCAGAGCGGTGCTGCTGGCTTTCAGCGCGCACCCGCCCTCAGCGTGCCTAT 540  
Db 625 CTGCTCAGAGCGGTGCTGCTGGCTTTCAGCGCGCACCCGCCCTCAGCGTGCCTAT 684  
Oy 541 GTGCACGTGTTGGCTGTGCGCGCGCCCTGTTCTGGGGCTCATGGTGGTGTAAACGG 600  
Db 685 GTGCACGTGTTGGCTGTGCGCGCGCCCTGTTCTGGGGCTCATGGTGGTGTAAACGG 744  
Oy 601 CATAGCTTCCGCCAGGACTCCATGTGGTGGTGAAGTGGTGGTGGGCTGCTGGCG 660  
Db 745 CATAGCTTCCGCCAGGACTCCATGTGGTGGTGAAGTGGTGGTGGGCTGCTGGCG 804  
Oy 661 GCAGTGCAGGTGCGGGGGCGCTTTCGACAGACACCGCGCGCCCTCTGCGGGGCTCTGG 720  
Db 805 GCAGTGCAGGTGCGGGGGCGCTTTCGACAGACACCGCGCGCCCTCTGCGGGGCTCTGG 864  
Oy 721 TGCCCTGTGTTCTTTGTATACATCGCATACAGCTTCCTCCCATCCGATCGGGGCTGCC 780  
Db 865 TGCCCTGTGTTCTTTGTATACATCGCATACAGCTTCCTCCCATCCGATCGGGGCTGCC 924  
Oy 781 GTCCTCAGCGGCTGGGCTCTCCACCTTGCATTTGATCTTGGCTGGCAACTTAACCGT 840  
Db 925 GTCCTCAGCGGCTGGGCTCTCCACCTTGCATTTGATCTTGGCTGGCAACTTAACCGT 984  
Oy 841 GGTATGCTTCTCTGGAAGCAGCTCGGTGCAATGCTGCTGCTTCTCTGCACCAAC 900  
Db 985 GGTATGCTTCTCTGGAAGCAGCTCGGTGCAATGCTGCTGCTTCTCTGCACCAAC 1044  
Oy 901 GTCATTAGCATCTGCACACACTATCCAGCAGAGGTGTCTCAGCGCGAGGCTTTTCAGGAG 960  
Db 1045 GTCATTAGCATCTGCACACACTATCCAGCAGAGGTGTCTCAGCGCGAGGCTTTTCAGGAG 1104  
Oy 961 ACCCGCAGTTATATCCAGGCGCGGCTCCACCTGCAGCATGAGAATCGCAGCAGGAGCGG 1020  
Db 1105 ACCCGCAGTTATATCCAGGCGCGGCTCCACCTGCAGCATGAGAATCGCAGCAGGAGCGG 1164  
Oy 1021 CTGCTGCTGTCGGTATTGCCCGCAGCAGCTTGCATGGAGATGAAGAAGACATCAACACA 1080  
Db 1165 CTGCTGCTGTCGGTATTGCCCGCAGCAGCTTGCATGGAGATGAAGAAGACATCAACACA 1224  
Oy 1081 AAAAAAGAGAC---ATGTTCCACAAGATCTACATACAGAAGCATGACAATGTGACGATC 1137  
Db 1225 AAAAAAGAGACATGATGTTCCACAAGATCTACATACAGAAGCATGACAATGTGACGATC 1284  
Oy 1138 CTGTTTGCAGACATTGAGGGGCTTCAACAGCTGGCATCCCACTGCCAGTGCAGGAGCTG 1197  
Db 1285 CTGTTTGCAGACATTGAGGGGCTTCAACAGCTGGCATCCCACTGCCAGTGCAGGAGCTG 1344  
Oy 1198 GTCATGACCCCTGAATGAGCTCTTTGCCCGGGTTTGCACAGCTGGCTGGCGGAGAACTACCTGC 1257  
Db 1345 GTCATGACCCCTGAATGAGCTCTTTGCCCGGGTTTGCACAGCTGGCTGGCGGAGAACTACCTGC 1404



|||||  
Db 3565 TACCAGCTGGAGTGTGAGGGGTGCTCAAGGTGAAGGGCAAGGGGAGATGACACCTAC 3624  
Qy 3478 TTCCCTCAATGGGGGCCCGAGCAGTTTAACAGGGGCCCGAGCCACAAATTCAGCTGAAGGGACC 3537  
Db 3625 TTCCTCAATGGGGGCCCGAGCAGTTTAACAGGGGCCCGAGCCACAAATTCAGCTGAAGGGACC 3684  
Qy 3538 AAGGTGGGCACT 3549  
Db 3685 AAGGTGGGCATT 3696  
RESULT 4  
AAD08568  
ID AAD08568 standard; cDNA: 3582 BP.  
XX  
XX  
AC AAD08568;  
XX  
DT 04-SEP-2001 (first entry)  
XX  
DE Human modified cardiac adenylylase VI (ACVI) isoform cDNA.  
XX  
KW Human; cardiant; beta-adrenergic signalling protein; beta-ASP;  
KW myocardium; gene therapy; beta-adrenergic receptor; beta-AR;  
KW adenylylase; adenylylase; adenylylase; adenylylase;  
KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;  
KW cardiac adenylylase VI; ACVI isoform; beta-ASP transgene; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT CDS 22..3525  
FT /\*tag= a  
FT /product= "Human modified cardiac ACVI isoform"  
XX  
PN WO200148164-A2.  
XX  
PD 05-JUL-2001.  
XX  
PF 26-DEC-2000; 2000WO-US35411.  
XX  
PR 27-DEC-1999; 99US-0472667.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Hammond HK, Gao M;  
XX  
PI  
XX  
DR WPI; 2001-418260/44.  
DR P-PSDB; AAE04312.  
XX  
PT Novel polynucleotide encoding a modified adenylylase polypeptide  
PT useful for enhancing cardiac function in mammalian hearts, and for  
PT treating heart disease, especially congestive heart failure -  
XX  
PS Claim 4; Page 143-150; 153pp; English.  
XX  
CC The present invention relates to methods and compositions for enhancing  
CC cardiac function in mammalian hearts by inserting transgenes encoding  
CC beta-adrenergic signalling proteins (beta-ASP) which increase  
CC beta-adrenergic responsiveness within the myocardium using in vivo  
CC gene therapy. The beta-ASPs of the invention include beta-adrenergic  
CC receptors (beta-AR), adenylylases (also referred to as adenylylase,  
CC adenylylase cyclase and CAMP synthetase) and G-protein receptor kinase  
CC (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function  
CC in mammalian hearts and for treating heart disease, especially  
CC congestive heart failure. The present cDNA sequence encodes human  
CC modified cardiac adenylylase VI (ACVI) isoform which is used for  
CC generating a beta-ASP transgene, used in the exemplification of the  
XX invention.  
XX  
SQ Sequence 3582 BP; 703 A; 1036 C; 1067 G; 776 T; 0 other;

Query Match 95.2%; Score 3379.2; DB 22; Length 3582;  
Best Local Similarity 97.4%; Pred. NO. 0;  
Matches 3458; Conservative 0; Mismatches 88; Indels 6; Gaps 2;  
Qy 1 ATGTCATGTTAGTGGCTCTCTGCTCCCTAAAGTGGATGAACGGAACACACCCCTGGGT 60  
Db 22 ATGTCATGTTAGTGGCTCTCTGCTCCCTAAAGTGGATGAACGGAACACACCCCTGGGT 81  
Qy 61 GAAACCAATGGCAGAAAGCGTTTCGGGGCGCGCTGCACCTCGGGCAGGTGGCTTCGACG 120  
Db 82 GAAACCAATGGCAGAAAGCGTTTCGGGGCGCGCTGCACCTCGGGCAGGTGGCTTCGACG 141  
Qy 121 CCCCCTATATGAGCTGCTCCGGGATGCAGAGCCACCCAGCCACCCCTCGGGCCCC 180  
Db 142 CCCCCTATATGAGCTGCTCCGGGATGCAGAGCCACCCAGCCACCCCTCGGGCCCC 201  
Qy 181 CCTCGGTGCTGCGGCGAGTACGCCCTTCATCCGGAGGGGGGGCCAGGCGCAAG 240  
Db 202 CCTCGGTGCTGCGGCGAGTACGCCCTTCATCCGGAGGGGGGGCCAGGCGCAAG 261  
Qy 241 GAGCTGGGGCTGCGGCGAGTGGCCCTTCGAGGATACCGAGTGAACAACGACAGCG 300  
Db 262 GAGCTGGGGCTGCGGCGAGTGGCCCTTCGAGGATACCGAGTGAACAACGACAGCG 321  
Qy 301 GCGGGAGCGGTGAGTGGCGCGCGCGAGCGGTGCCAGAGTGGCGATCTCTGCTGGCG 360  
Db 322 GCGGGAGCGGTGAGTGGCGCGCGCGAGCGGTGCCAGAGTGGCGATCTCTGCTGGCG 381  
Qy 361 CGTTTGGTGCAGGTGTTCCAGTGAAGAGTTCCTTTCGGCCAAAGCTGAGGCGCTGTAC 420  
Db 382 CGTCTGGTGCAGGTGTTCCAGTGAAGAGTTCCTTTCGGCCAAAGCTGAGGCGCTGTAC 441  
Qy 421 CAGCGGTACTTTTCCAGATGAACAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
Db 442 CAGCGGTACTTTTCCAGATGAACAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 501  
Qy 481 CTGCTCACAGCGGTGCTGCTGCTTTCACAGCGCGCGCGCGCGCGCGCGCGCGCTAT 540  
Db 502 CTGCTCACAGCGGTGCTGCTGCTTTCACAGCGCGCGCGCGCGCGCGCGCGCTAT 561  
Qy 541 GTGGCAGTGTGGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600  
Db 562 GTGGCAGTGTGGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 621  
Qy 601 CATAGCTTCGCGCAGGACTTCCATGTGGTGGTGAAGTGAAGTGGTGGTGGTGGTGG 660  
Db 622 CATAGCTTCGCGCAGGACTTCCATGTGGTGGTGAAGTGAAGTGGTGGTGGTGGTGG 681  
Qy 661 GCAGTGCAGGTGCGGGCGCTTTCGACAGACCGCGCGCGCGCGCGCGCGCGCGCGCTG 720  
Db 682 GCAGTGCAGGTGCGGGCGCTTTCGACAGACCGCGCGCGCGCGCGCGCGCGCGCGCTG 741  
Qy 721 TGCCCTGTGTTCTTTGATATACATCCATACAGCTTCTTCCCATCCGATCCGATCCG 780  
Db 742 TGCCCTGTGTTCTTTGATATACATCCATCCGCTTCTTCCCATCCGATCCGATCCG 801  
Qy 781 GTCCCTCACGGCGCTGGGCTCTCCACCTTGCATTTGATCTTGGCTGGCACTTAACCGT 840  
Db 802 GTCCCTCACGGCGCTGGGCTCTCCACCTTGCATTTGATCTTGGCTGGCACTTAACCGT 861  
Qy 841 GGTGATGCTTCTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTTCTCTGCAACCAAC 900  
Db 862 GGTGATGCTTCTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTTCTCTGCAACCAAC 921  
Qy 901 GTCATTACATCTGCACACACTATCCAGAGGTGCTCAGCGCGCGCGCGCTTTCAGAG 960  
Db 922 GTCATTGCACTTGACACACTATCCAGAGGTGCTCAGCGCGCGCGCTTTCAGAG 981  
Qy 961 ACCCGCAGTTACATCCAGCGCGCGCTTCCACCTGACAGATGAGAATCGGACGAGGGG 1020  
Db 982 ACCCGCAGTTACATCCAGCGCGCGCTTCCACCTGACAGATGAGAATCGGACGAGGGG 1041  
Qy 1021 CTGCTGCTGCGGTATTCGCCCGACGACGCTTGCCTGGAGATGAAGAAGACATCAACACA 1080



Db 1042 CTGCTGCTGTCGTAATGCCCCAGCAGTTGCCATGGAGATGAAGAAGACATCAACACA 1101  
QY AAAAAAGAGAC---ATGTTCCACAAGACTACATACAGAGCATGACAAATGTCAGCATC 1137  
Db 1102 AAAAAAGAGAGCATGATGTTCCACAAGATCTACATACAGAAGCATGACAAATGTCAGCATC 1161  
QY CTGTTTGCAGACATTTAGGGCTTTCACCCAGCTGGCATCCAGTGCATCTGCGCAGGAGCTG 1197  
Db 1162 CTGTTTGCAGACATTTAGGGCTTTCACCCAGCTGGCATCCAGTGCATCTGCGCAGGAGCTG 1221  
QY GTCATGACCTGTAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTGCGGAGAAATCACTGC 1257  
Db 1222 GTCATGACCTGTAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTGCGGAGAAATCACTGT 1281  
QY CTGAGATCAAGATCTTTGGGGGACTGTTACTACTGTGTGTCAGGGCTGCCGGAGGCCGG 1317  
Db 1282 CTGAGATCAAGATCTTTAGGAGACTGTTACTACTGCTGTCAGGGCTGCCCGAGGCCGG 1341  
QY GCCGACCATGCCACTGCTGTGTGGAGATGGGGGTAGACATGATGAGGCCATCTCGCTG 1377  
Db 1342 GCAGATCACGCCACCTGCTGTGTGGAGATGGGGGTAGACATGATCGAAGCCATCTCGCTG 1401  
QY GTACGTGAGGTGACAGTGTGAATGTGAACATCGCGGTGGGCATCCACAGCGGGCGCGTG 1437  
Db 1402 GTGCGTGAAGTAACAGGTGTGAACGTGAACATGCGTGTGGGCATCCACAGCGGACGTGTG 1461  
QY CACTGGGGCTGCTTGCGTTGGCGAATGCGAGTTCGATGTGTGGTCCCAATGATGTGACC 1497  
Db 1462 CATTGGCGGCTGCTTGCGCTACCGAATGGCAGTTTGTATGCTGTGGTCAACAGATGTGACC 1521  
QY CTGCCCCAACACATGGAAGCAGGAAGCCGGGCTGGCGCATCCACATCACTCGGGCAACA 1557  
Db 1522 CTGGCTAACACATGGAGGCCGGGGC---GGCCGGCGCATCCACATCACTCGGGCTACA 1578  
QY CTCGAGTACCTGAACGGGACTACGAAGTGGAGCCAGCGCGTGGTGGCAAGCCCAAGCG 1617  
Db 1579 CTGCATFACTGAACGGGGACTATAGGTGGAGCCAGCGCGTGGTGAACGCAATGCG 1638  
QY TACTCAAGGAGCAGCACATTTAGACTTTCCTCATCTGGCGGCCAGCCAGCAAGAACGAAA 1677  
Db 1639 TACTCAAGGAGCAGTGCAATTGAGACTTTCCTCATFACTTGGCGCCAGCCAAACGAAA 1698  
QY GAGGAGAAAGCATGTGCGCAAGCTGCAGCGGACTCGGGCCAACTCCATGGAAGGGCTG 1737  
Db 1699 GAGGAGAAAGCCATGCTGGCCAAGCTTCAGCGGACAGCGGCCAACTCCATGGAAGGACTG 1758  
QY ATGCCGGATGGTTCCTGATGTCGCTTCTCCGGACCAAGGACTCCAAAGGCTTCCCG 1797  
Db 1759 ATGCCCGCTGGGTTCTGACCGTGCCTTCTCCCGACCAAGGACTCTAAGGCAATTCCGC 1818  
QY CAGATGGGCATTGATGATTCACAAAGACAACCCGGGGCACCAAGATGCCCTGAACCCCT 1857  
Db 1819 CAGATGGGCATTGATGATTCACAAGACAACCCGGGGTCCCAAGATGCTCTGAACCCCT 1878  
QY GAGGATGAGTGGATGAGTTCTTGAGCCGTGCCATCGATCCCGCAGCATTTGATCAGCTG 1917  
Db 1879 GAAGATGAGTGGATGAGTTCTTGCGCGAGCCATCGATGCCCGCAGCAATTGATCAGCTG 1938  
QY CGAAGGACCATGTGGCGCGGTTTTTGCTCACCTTCAGAGAGAGGATTTTGAGAAGAG 1977  
Db 1939 CGAAGGACCATGTGGCGCGGTTTTGCTCACCTTCACCTTCACAGAGAGAGATCTTGAGAAGAG 1998  
QY TACTCCGGAGTGGATCCCCCTTCGGAGCCTAGTTCGCTGTCCTGTTGGTCTTC 2037  
Db 1999 TACTCCGGAGTGGATCCCCCTTCGGAGCCTAGTTCGCTGTCCTGTTGGTCTTC 2058  
QY TGCTTCATCTGCTTCATCCAGCTTCATAATTTTCCACACTCCACCTGATGCTTGGGATT 2097  
Db 2059 TGCTTCATCTGCTTCATCCAGCTTCATCTTCCCACTCCACCTGATGCTTGGGATC 2118  
QY TATGCCAGCATCTTCCTGCTGCTGCTTAATCACCGTGCATGCTGTGCTGTACTCCTGT 2157  
|||||

Db 2119 TATGCCAGCATCTTCCTGCTGCTGCTAAATCACCGTGCTGATGCTGTGCTACTCCTGT 2178  
QY GGTTCTCTGTTCCCTAAGGCCCTGCACAGCTCTGCCCGCAGCATGTCCTGCTCACGGCA 2217  
Db 2179 GGTTCTCTGTTCCCTAAGGCCCTGCACAGCTCTGCCCGCAGCATGTCCTGCTCACGGCA 2238  
QY CATAGCACCGCAGTTGGCATCTTTTCCGCTGCTGCTGTTTACTTCTGCAATTTGCCAAC 2277  
Db 2239 CATAGCACCGCAGTTGGCATCTTTTCCGCTGCTGCTGTTTACTTCTGCAATTTGCCAAC 2298  
QY ATGTTTCACTGTAAACACACACCCCATACGGAGCTGTGCAGCCGGATGCTGAATTTAAACA 2337  
Db 2299 ATGTTTCACTGTAAACACACACCCCATACGGAGCTGTGCAGCCGGATGCTGAATTTAAACA 2358  
QY CTTGCTGACATCACTGCTGCCACCTGCAGCAGCTCAATTACTCTCTGGGCCCTGGATGCT 2397  
Db 2359 CTTGCTGACATCACTGCTGCCACCTGCAGCAGCTCAATTACTCTCTGGGCCCTGGATGCT 2418  
QY CCCTGTGTGAGGCGACCATGTCACCTGCAGCTTTCCTGAGGTGTCCATCGGGAACATG 2457  
Db 2419 CCCTGTGTGAGGCGACCATGTCACCTGCAGCTTTCCTGAGTACTTTCATCGGGAACATG 2478  
QY CTGCTGAGTCTCTTGGCCAGCTCTGCTTCCCTGCACATCAGCAGCATCGGGAAGTTGGCC 2517  
Db 2479 CTGCTGAGTCTCTTGGCCAGCTCTGCTTCCCTGCACATCAGCAGCATCGGGAAGTTGGCC 2538  
QY ATGATCTTCTTCTTGGGGCTCATCTATTGCTGCTGCTTCTGCTGGGTCCCCAGCGGCC 2577  
Db 2539 ATGATCTTCTTCTTGGGGCTCATCTATTGCTGCTGCTTCTGCTGGGTCCCCAGCGACC 2598  
QY ATCTTTGACAACATGACCTTACTGCTTGGCTGCCATGGCTTGGCTTCTTCCAATGAGACC 2637  
Db 2599 ATCTTTGACAACATGACCTTACTGCTTGGCTGCCATGGCTTGGCTTCTTCCAATGAGACC 2658  
QY TTTGATGGGCTGAGCTGTCCAGCTGCAGGAGGGTGGCCCTCAAAATATATGACCCCTGTG 2697  
Db 2659 TTTGATGGGCTGAGCTGTCCAGCTGCAGGAGGGTGGCCCTCAAAATATATGACCCCTGTG 2718  
QY ATTCTGCTGCTGTTTGGCTGGCGCTGATCTGCTCAGCAGGTGGAATGACACTGCC 2757  
Db 2719 ATTCTGCTGCTGTTTGGCTGGCGCTGATCTGCTCAGCAGGTGGAATGACACTGCC 2778  
QY CGCTTAACTTCCTCTGGAACCTACAGGCAACAGGGGAAAAGAGAGATGGAAGAGCTA 2817  
Db 2779 CGCTTAGACTTCTCTGGAACCTACAGGCAACAGGGGAGAAGAGAGATGGAAGAGCTA 2838  
QY CAGGCATACAACCGGAGGCTGCTGCATAACATCTGCCCAAGGACGTGGCGGCCCACTTC 2877  
Db 2839 CAGGCATACAACCGGAGGCTGCTGCATAACATCTGCCCAAGGACGTGGCGGCCCACTTC 2898  
QY CTGGCCGGGAGCGCGCAATGATGAACCTACTACTCAGTCTGTGAGTGTGTGGCTGTT 2937  
Db 2899 CTGGCCGGGAGCGCGCAATGATGAACCTACTACTCAGTCTGTGAGTGTGTGGCTGTT 2958  
QY ATGTTTGCCTCCATTTGCCAACTTCTCTGAGTTCATGTGAGGCTGGAAGCAAAATGAG 2997  
Db 2959 ATGTTTGCCTCCATTTGCCAACTTCTCTGAGTTCATGTGAGGCTGGAAGCAAAATGAG 3018  
QY GGTGCCGAGTGCCTGCGGCTGCTCAGCAGATCATCCTGACTTTGATGAGATTTATCAGC 3057  
Db 3019 GGTGTCGAGTGCCTGCGGCTGCTCAGCAGATCATCCTGACTTTGATGAGATTTATCAGC 3078  
QY GAGGAGCGGTTCCGGAGCTGGAAGATCAAGACGATTTGTTAGCACCTACATGAGTGGCTGC 3117  
Db 3079 GAGGAGCGGTTCCGGAGCTGGAAGATCAAGACGATTTGTTAGCACCTACATGAGTGGCTGC 3138  
QY TCAGGGCTGAACGCCAGCACCTACGATCAGTGGCGGCTCCACACATCACTGCGCTGGCT 3177  
Db 3139 TCAGGGCTGAACGCCAGCACCTACGATCAGTGGCGGCTCCACACATCACTGCGCTGGCT 3198  
QY GACTACGCCATGCGGCTTCATGGAGCAGATGAAGCACATCAATGAGCAGCTCTCTTCAACAAT 3237  
Db 3199 GACTACGCCATGCGGCTTCATGGAGCAGATGAAGCACATCAATGAGCAGCTCTCTTCAACAAT 3258  
|||||

QY 3238 TTCCAGATGAAGATTGGGCTGAACATGGGCCAGTCGTGGCAGGTGTCATCGGGGCTCGG 3297  
|||||  
Db 3259 TTCCAGATGAAGATTGGGCTGAACATGGGCCAGTCGTGGCAGGTGTCATCGGGGCTCGG 3318  
|||||  
QY 3298 AAGCCACATATACATCTGCGGGGGAACACAGTGAATGCTCTAGTCGTATGACACAGCAG 3357  
|||||  
Db 3319 AAGCCACATATGACATCTGCGGGGAACACAGTGAATGCTCTAGTCGTATGACACAGCAG 3378  
|||||  
QY 3358 GGGGTCCCGACCGAATCCAGGTGACACCGGACCTGTACAGGTTCTAGCTGCCAAGGCG 3417  
|||||  
Db 3379 GGGGTCCCGACCGAATCCAGGTGACACCGGACCTGTACAGGTTCTAGCTGCCAAGGCG 3438  
|||||  
QY 3418 TACCAGCTGGAGTGTGAGGGGTGCTCAAGGTGAAGGCAAGGGGAGATGACCACTAC 3477  
|||||  
Db 3439 TACCAGCTGGAGTGTGAGGGGTGCTCAAGGTGAAGGCAAGGGGAGATGACCACTAC 3498  
|||||  
QY 3478 TTCCCTCAATGGGGGCCCCAGCAGTGAACAGGGCCCCAGCCACAATTCAGCTGAAGGGACC 3537  
|||||  
Db 3499 TTCCCTCAATGGGGGCCCCAGCAGTGAACAGGGCCCCAGCCACAATTCAGCTGAAGGGACC 3558  
|||||  
QY 3538 AAGGTGGGCAC 3549  
|||||  
Db 3559 AAGGTGGGCAC 3570  
|||||

## RESULT 5

AAQ42525

ID AAQ42525 standard; DNA; 4046 BP.

XX AC AAQ42525;

XX DT 14-SEP-1993 (first entry)

XX DE Cardiac adenylyl cyclase gene.

XX KW Regulation; cardiac function; heart; heart failure; ss.

XX OS Canis familiaris.

XX FH Key Location/Qualifiers

FT CDS 131..3627

FT /\*tag= a

XX EP543137-A.

XX PD 26-MAY-1993.

XX PF 12-OCT-1992; 92EP-0117374.

XX PR 18-NOV-1991; 91US-0793961.

XX PA (AMCY ) AMERICAN CYANAMID CO.

XX PI Ishikawa Y;

XX DR WPI; 1993-168873/21.

XX PS P-PSDB; AAR37309.

XX PT Purified DNA encoding cardiac adenylyl cyclase - useful to screen

XX PS for cpds. which stimulate activity of the cyclase

XX Claim 1; Fig 2; 34pp; English.

XX A canine heart cDNA library was constructed in lambda gt10 and was

XX screened with a 970 bp AatI-HincII fragment from type I adenylyl

XX cyclase cDNA probe (encodes the first cytoplasmic domain of adenylyl

XX cyclase, which has significant homology to other previously known

XX types of adenylyl cyclase). One positive clone, of 5.4 kb was obtd.

XX Positive colonies were subcloned into pUC18 and further subcloned

XX and sequenced bidirectionally. The 5.4 kb clone was used to

XX rescreen the library and on overlapping clone contg. the 5' end of

XX the gene was isolated. Together the two clones cover the complete

CC canine cardiac adenylyl cyclase gene. The gene is suspected of  
CC being involved in the regulation of cardiac function and it is thought  
CC that decreased activity of adenylyl cyclase in the heart may be a  
CC major factor in the development of heart failure. Thus the adenylyl  
CC cyclase gene is useful to screen cpds. which stimulate the activity  
CC of the cyclase.

XX  
SQ Sequence 4046 BP; 743 A; 1206 C; 1254 G; 843 T; 0 other;

Query Match 84.4%; Score 2996.8; DB 14; Length 4046;  
Best Local Similarity 91.0%; Pred. No. 0;  
Matches 3233; Conservative 0; Mismatches 307; Indels 12; Gaps 4;

QY 1 ATGTGTCATGTTTGTAGTGGCTCTGCTCCCTAAAGTGGATGAACGGAACACAGCCCTGGGGT 60  
|||||  
Db 131 ATGTGTCGTTTGTAGTGGCTCTGCTCCCAAGTGGATGAACGGAACACAGCCCTGGGGT 190  
|||||  
QY 61 GAACCAATGGCAGAAAGGTTTCGGGGCCCTGCGACTCGGGAGGTGCTTCATGTCACG 120  
|||||  
Db 191 GAACCAATGGCAGAAAGCGT---CCAGCCCGGGGACTCGGACCAAGTGGCTTCATGTCACG 247  
|||||  
QY 121 CCCCCTATATGAGCTGCTCCGGGATGCAGAGCCACCCAGCCACCCCTCGGGGCC 180  
|||||  
Db 248 CCCCCTATATGAGCTGCTCCGGGATGCAGAGCCACCCAGTCCACCCCTCGGGGCC 307  
|||||  
QY 181 CCTCGGTGCCCTGGCAGGATGACGCTTTCATCCGGAGGGGGCCCGCAGGCAAGGGCAAG 240  
|||||  
Db 308 CCTCGGTGCCCTGGCAGGATGAGGCTTTCATCCGGAGGGGGCCCGGCAAGGGCAAG 367  
|||||  
QY 241 GAGCTGGGGCTGCGGGCAGTGGCCCTTGGGCTTCGAGGATACCGAGGTGACACACAGCG 300  
|||||  
Db 368 GAGCTGGGGCTGCGGGCAGTGGCCCTTGGGCTTCGAGGACACTGAGG---CCATGTCAGCG 424  
|||||  
QY 301 GCGGGAGCGGTGAGGTGCGCCCGCAGCGGTGCCAGAGTGGCGATCTCTGCTGGCGC 360  
|||||  
Db 425 GTTGGGCGAGCTGGAGGTGGCCCTGACGTGACCCCGGAGTAGCGATCTCTGCTGGCGC 484  
|||||  
QY 361 GCTTTGGTGCAGGTGTTCCAGTGAAGCAGTTCCTTCGCGCAAGCTGAGAGCCCTGTAC 420  
|||||  
Db 485 CGTCTGGCCAGGTGTTCCAGTGAAGCAGTTCCTTCGCGCAAGCTGAGAGCCCTGTAC 544  
|||||  
QY 421 CAGCGGTACTTTTCCAGATGAACACAGAGCAGCTGAGCGTCTGCTGGCGGTGCTGGTG 480  
|||||  
Db 545 CAGCGGTACTTTTCCAGATGAACACAGAGCAGCTGAGCGTCTGCTGGCGGTGCTGGTG 604  
|||||  
QY 481 CTGCTCACAGGGTCTGCTGGCTTTTCAAGCCGACCCGCGCCCTCAGCTGCTGCTAT 540  
|||||  
Db 605 CTGCTGACAGCGGTGCTGCTAGCTTCCATGCTGACCTGCCCGCCCTCAGCTGCTGCTAC 664  
|||||  
QY 541 GTGGCAGTGTGGGCTGTGCGCCGCCCTGTGTTGTTGGGGCTCATGGTGTGTAAACCG 600  
|||||  
Db 665 GTGGCCCTGTGGCTGTGCGCCGCCCTCTTCTGTTGGGCTCATGGTGTGTAAACCG 724  
|||||  
QY 601 CATAGCTTCGCCCAGGACTCCATGTGGTGTGAGTACGTGCTGCTGGGCATCTGGCG 660  
|||||  
Db 725 CACAGCTTTTCGCCAGGACTCCATGTGGTGTGAGTACGTGCTGCTGGGCATCTGGCA 784  
|||||  
QY 661 GCAGTGCAGGTGCGGGGCGCTTTTCGACGACAGCCGCGAGCCCTCTCGGGGCTCTGG 720  
|||||  
Db 785 GCGGTTCAGTTGGGGGTGCGCTTGCACGACCAACCCCGCAGCCCTCTGTGGGCTCTGG 844  
|||||  
QY 721 TGCCCTGTGTTTGTATACATGCGATACAGCTTCTCCCATCCGATCCGATCGGGGCTGCC 780  
|||||  
Db 845 TGCCCTGTGTTTGTATACATGCGATACAGCTTCTCCCATCCGATCCGATCGGGGCTGCC 904  
|||||  
QY 781 GTCCTCAGCGGCTGGGCTCTCCACCTTGCATTTGATCTGGGCTGGCACTTAACCGT 840  
|||||  
Db 905 GTCCTCAGTGGGCTGGGCTGTCCACCTGCAATTTGATCTTGGGCTGGCACTTAACCGC 964  
|||||  
QY 841 GGTGATGCTTCTCTGGAAGCAGCTCGGTGCAATGTGCTGCTGCTCTCTGCAACCAAC 900  
|||||  
Db 965 GGTGAGGCTTCTCTGGAAGCAGCTCGGTGCAACATGCTGCTGCTTCTCTGCAACCAAC 1024  
|||||



[illegible]

Db 3182 GAGGAGCGGTTCCGCGACGCTGGAGAAAATCAAGACGATCGGTAGCACGCTACATGGCTGCG 3241  
Qy 3118 TCAGGCGCTGAACGCCAGCACCTACCATCAGGTGGCGCGCTCCACATCACTACCTGCTGCT 3177  
Db 3242 TCGGGGCTGAGCGCCAGCACCTACCATCAGGTGGCGCGCTCCACATCACTACCTGCTGCTG 3301  
Qy 3178 GACTACGCGCATCGGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCCCTTCAACAA 3237  
Db 3302 GACTATGCCATCGGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCCCTTCAACAA 3361  
Qy 3238 TTCCAGATGAGATTGGCTGAACATGGCGCCAGTCGTCGGCAGGTGTATCGGGGCTCGG 3297  
Db 3362 TTCCAGATGAGATTGGCTGAACATGGCGCCAGTCGTCGGCAGGTGTATCGGGGCTCGG 3421  
Qy 3298 AAGCCACAGTATGACATCTGGGGAACACACAGTGAATGTCTTAGTCGTATGGACAGCAG 3357  
Db 3422 AAGCCACAGTATGACATCTGGGGAACACAGTGAATGTCTTAGTCGTATGGACAGCAG 3481  
Qy 3358 GGGTCCCGACCGAATCCAGGTGACACGACCGACCTGTACCAAGTTCTAGCTGCCAAGGGC 3417  
Db 3482 GGGGTTCCTGACCGAATCCAGGTGACACGACCGACCTGTACCAAGTTCTAGCTGCCAAGGG 3541  
Qy 3418 TACCAGCTGGAGTGTGAGGGGTGCTCAAGGTGAAGGCAAGGGGAGATGACCACTTAC 3477  
Db 3542 TACCAGCTGGAGTGTGAGGGGTGCTCAAGGTGAAGGCAAGGGGAGATGACCACTTAC 3601  
Qy 3478 TTCTCAATGGGGGCGCCAGCAGTTAACAGGGGCCCGACCAAAATTCAGCTGAAGGGGACC 3537  
Db 3602 TTCTCAATGGGGGCGCCAGCAGTTAAGCAGCGCCAGCTACAAGTTCAAGTTGTCAGGACC 3661  
Qy 3538 AAGTGGGCACT 3549  
Db 3662 AAGTGGGCACT 3673

RESULT 6  
ABI99680  
ID ABI99680 standard; cDNA; 5841 BP.  
XX  
AC ABI99680;  
XX  
DT 07-MAR-2002 (first entry)  
XX  
DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:716.  
XX  
KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;  
KW vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.  
XX  
OS Mus musculus.  
XX  
PN W0200188188-A2.  
XX  
PD 22-NOV-2001.  
XX  
PF 18-MAY-2001; 2001WO-JP04192.  
XX  
PR 18-MAY-2000; 2000JP-0145977.  
XX  
PA (UYN1-) UNIV NIHON SCHOOL JURIDICAL PERSON.  
XX  
PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;  
XX  
DR WPI; 2002-034733/04.  
DR P-PSDB; ABB57257.  
XX  
PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring  
PT expression levels of particular genes defined in the specification or  
PT by determining the expression profile of a gene group comprising these  
PT genes -  
XX  
PS Claim 2; Page 1771-1780; 2690pp; English.  
XX  
CC The present invention describes a method for examining ischaemic

CC conditions, comprising measuring the expression levels of particular  
CC genes (I) in a test sample or determining the expression profile of a  
CC gene group in the sample comprising genes selected from (I). The method  
CC is useful for examining the ischaemic condition (e.g. compressive  
CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring  
CC expression levels of particular genes (ABI99202 to ABI99912), encoding  
CC the protein sequences in ABB57020 to ABB57374) or by determining the  
CC expression profile of a gene group comprising these genes. The  
CC expression levels or expression profiles produced by these genes are  
CC used as an indicator when screening for ischaemic condition-improving  
CC drugs or therapeutics for ischaemic diseases. ABI99913 and ABI99914  
CC represent PCR primers for a mouse ischaemic condition related sequence,  
CC which are used in the exemplification of the present invention.  
XX  
SQ Sequence 5841 BP; 1214 A; 1558 C; 1673 G; 1396 T; 0 other;  
  
Query Match 77.9%; Score 2765; DB 24; Length 5841;  
Best Local Similarity 87.1%; Pred. No. 0;  
Matches 3095; Conservative 0; Mismatches 445; Indels 13; Gaps 5;  
  
Qy 1 ATGTCATGTTAGTGGCTCTCTGCTCCCTAAAGTGGATGAACGGAACACAGCTTGGGGT 60  
Db 96 ATGTCATGTTAGTGGCTCTCTGCTCCCAAGTGGATGAACGGAACACAGCTTGGGGG 155  
Qy 61 GAACGCAATGGGCAAGACGTTGCGGCGCGCTGTCGCACTCGGGCAGGTGCTTTCGACG 120  
Db 156 GAACGCAATGGGCAAGACG--CCACGCGACGGAATCGAGCAGTGGCTTCTGCGCA 212  
Qy 121 CCCGCTATATGAGTGGCTCCGCGGATGAGGACGACGACCCACCCCTCGGGGCCCC 180  
Db 213 CTTGCTACATGAGTGGCTCAAGAAATCGGAGGACCCACGCTCTCTGCACTCAC 272  
Qy 181 CTTGCTGCTGCGCAGGATGAGCCTTCATCCGAGGCGGCGCCAGGCAAGGCAAG 240  
Db 273 ACTGCTGCTGCGCAGGATGAGCCTTCATCAGGAGGCGGCGCGGAGGGGTGTG 332  
Qy 241 GAGCTGGGGCTGCGGCGAGTGGCTTGGCTTCGAGGATACCGAGGTGACACGACAG 300  
Db 333 GAGCTGGGGCTGCGGCTAGTGGCTTGGGTTGACGACACTGAGGTGACACACCGATG 392  
Qy 301 GCGGGAGCGCTGAGTGGCGCGCGCGGTGCCAGAGTGGCGGATCTGCTGGCGCG 360  
Db 393 GCG---ACAGCTGAAGTGGCGACCGATACATCGCTCGAGCGGTCCCTCTGCTGGCAC 449  
Qy 361 CGTTGGTGCAGGTGTTCCAGTGAAGCAGTTCCTTCGCGCAAGCTGAGCGCTGTAC 420  
Db 450 CGGCTTGTGAGGTGTTCCAGTGAAGCAGTTCCTCTGCGCAAGCTGAGCGGCTGAC 509  
Qy 421 CAGCGTACTTTTCCAGATGAACAGACGACCTGAGCGCTGCTGGTGGCGGTGCTGTG 480  
Db 510 CAGCGTACTTTTCCAGATGAACAGACGACCTGAGCGCTGCTGCTGCTGCTGTG 569  
Qy 481 CTGCTCACAGCGGTGCTGCTGCTTCCAGCGCGCACCGCGCCCTCAGCTGACCTTAT 540  
Db 570 CTGCTCATGGCTGTACTGTTGACCTTCCAGCTGCGCTGCGCCCTCAGCTGCTTAC 629  
Qy 541 GTGCACTGTTGGGCTGTGCGCGCGCGCTGTTGCTGGGGCTCATGGTGTGTAAACGG 600  
Db 630 GTGGCCCTGCTGACCTGTGCGCTGCTCTCTTTTGTGGTACTATGTTGTGTAAACGA 689  
Qy 601 CATAGCTTCCGCGAGGACTCCATGTGGTGTGAGTACGAGTGGTGGTGGGATCTCGCG 660  
Db 690 CACAGCTTCCGCGAGGACTCCATGTGGTGGTGTGAGTATGTGGTCTCGGGGATCTCAG 749  
Qy 661 GCAGTGCAGGTCGGGGCGCTTCGACAGACGCGCGCGCGCTCTCGGGGCTCTGCG 720  
Db 750 GCGGTGAAGTGGGGGTGCGCTGGCAGCAATCCACAGCGCCCTCGCGGGGCTTTGG 809  
Qy 721 TGCCCTGTGTTCTTGTATACATGCAATACGCTTCCCTCCCATCCGATCGGGGCTGCC 780  
Db 810 TGCCCCGTGTTCTTCGTTACATACCTACACTCTTCTTCCATTCGATCGGACCGCA 869  
Qy 781 GTCCTACGCGGCTGGGCTCTCCACCTTGCATTTGATCTTGGGCTGGCAACTTAAACGT 840

Db 870 GTACTACGCGCCTGGCCCTCTACTCTGCATTTGATTTGGCCTGCAGCTCAACAGC 929  
QY 841 GGTGATCCCTTCCTCTGGAAGCAGCTCGGTGCCAATGTGCTGTGTTCCCTCTGCACCAAC 900  
Db 930 AGCAGCCCTTCCTTTTGGAGCAGCTCGGTGCTTAACGTGTGCTTCTTCCTCTGCACCAAT 989  
QY 901 GTCAATTAGCATCTGCACACACTATCCACGACAGAGGTGTCTCAGGGCCAGGCGTTTCAGGAG 960  
Db 990 GCCATCGGTCTCTGCACACACTACCCCTGCTGAAGTGTCTCAGCGCCAAAGCTTTTCAGGAG 1049  
QY 961 ACCCGCATTTACATCCAGGCCCGGCTCCACTCGAGCATGAGAAATCGGCAGCAGGAGCGG 1020  
Db 1050 ACCGAGGTTTACATCCAGGCGCGCTGCACCTGCAGCATGAGAACCCTCAGCAGGAACGG 1109  
QY 1021 CTGCTGTGTGCGTATTGCCCCAGCAGCTTGCCATGAGATGAAGAGATCAACACA 1080  
Db 1110 CTGCTGTATTCGGTGTGCCCCAGCAGCTTGCCATGAGATGAAGAGATCAACACA 1169  
QY 1081 AAAAAAGAAC --- ATGTTCCACAAGATCTACATACAGAAGCATGACAATGTCAGCATC 1137  
Db 1170 AAAAAAGACATGATGTTCCATAAGATCTACATCCAGAAGCATGATAATGTCAGCATC 1229  
QY 1138 CTGTTTCAGACATGAGGCGCTTACCAGCTTGSCATCCCACTGCCAGGAGCTG 1197  
Db 1230 CTGTTTCGGACATGAGGCGCTTACCAGCTTGSCCTCCCACTGCCAGGAACTG 1289  
QY 1198 GTCATGACCTGATGAGCTCTTTGCCCGTTTGACAACTGGCTGGGAGAAATCACTGC 1257  
Db 1290 GTCATGACCTTGAATGAGCTCTTTGCCCGTTTGACAAGCTGGCTGCCGGAATCACTGT 1349  
QY 1258 CTGAGGATCAAGATCTTTGGGGACTGTACTACTGTGTGTCAGGCTGCCGGAGGCCGG 1317  
Db 1350 CTGAGGATCAAGATCTTTAGGAGCTGTACTACTGCTGTCAGGCTGCCCGAGGCCGG 1409  
QY 1318 GCCGACCATGCCACTGCTGTGTGGAGATGGGGTAGACATGATGATGAGGCCATCTCGCTG 1377  
Db 1410 GCAGATCACGCCACTGCTGTGTGGAGATGGGGTAGACATGATCGAAGCCATCTCGCTG 1469  
QY 1378 GTACGTGAGGTGACAGGTGTAATGAACATGGCGTGGGCATCCACAGCGGCGGTG 1437  
Db 1470 GTGCGTAGGTACAGGTGTGACGTGAACATGCGTGTGGGCATCCACAGCGAGCTGTG 1529  
QY 1438 CACTGCGGCCTCTTGCTTGCAGAAATGCGAGTTGCATGTGTGGTCCAAATGATGTACC 1497  
Db 1530 CATTTGCGGCTCTTGSCCTACGMAATGCGAGTTGATGCTCTGGTCAACAGATGTACC 1589  
QY 1498 CTGGCCAAACACATGGAAGCAGGAAGCCGGGCTGGCGCATCCACATPCTCAGGGCAACA 1557  
Db 1590 CTGGCTAACACATGAGGCGCGGGGC --- GGC CGCGGCATCCACATPCTCAGGGCTACA 1646  
QY 1558 CTCAGTACCTGAACGGGACTACGAAGTGAAGCGCAGCGCGCTGGTGGCAAGCGCAAGCGG 1617  
Db 1647 CTGAGTACTTGAACGGGACTATGAGGTGGAGCGAGGCGCTGGTGTGAACCAATGCG 1706  
QY 1618 TACCTCAAGGAGCAGTCATTGAGACCTTCTCATCTACTTGGCGCCAGCCAAAACGGAAA 1677  
Db 1707 TACCTCAAGGAGCAGTCATTGAGACCTTCTCATCTACTTGGCGCCAGCCAAAACGGAAA 1766  
QY 1678 GAGGAGAAAGCATGTGCGCCAAGCTGACGCGGACTCGGGCCCAACTCCATGGAAGGCGTG 1737  
Db 1767 GAGGAGAAAGCCATGTGCGCCAAGCTTACGCGGACACGGGCCAACTCCATGGAAGGACTG 1826  
QY 1738 ATCCGCGGATGGGTCTCTGATCTGCTTCTCCCGACCAAGGACTCCCAAGGCTTCCCG 1797  
Db 1827 ATGCCCGCTGGGTCTCTGACCTGGCTTCTCCCGACCAAGGACTTAAGGCAATCCCG 1886  
QY 1798 CAGATGGGCATTGATGATTCAGCAAGACAACCGGGGACCCCAAGATGCGCTGAACCCCT 1857  
Db 1887 CAGATGGGCATTGATGATTCAGCAAGACAACCGGGGTCCCAAGATGCTCTGAACCCCT 1946  
QY 1858 GAGGATGAGGTGATGATTTCTGAGCCGTGCGCATCGATGCCCGCAGCATTTGATCAGCTG 1917  
Db 1917 GAGGATGAGGTGATGATTTCTGAGCCGTGCGCATCGATGCCCGCAGCATTTGATCAGCTG 1986

Db 1947 GAAGATGAGGTGATGAGTTCTCTGGCGCGACCATCGATGCCCGAGCATCGACCAACTG 2006  
QY 1918 CGAAGACACATGTGCGCGGTTTTCCTCACCTTCACAGAGAGAGATTTTGAAACAAG 1977  
Db 2007 CGTAAGACCATGTGCGCGGTTCCCTGCTCACCTTCAGAGAGAGAGATCTTGAAAGAAG 2066  
QY 1978 TACTCCGGAAGGTGGATCCCGCTTCGGAGCCCTACCTTTCGCTGTGCTGCTGCTGCTTC 2037  
Db 2067 TATTCAGGAAAGTAGATCCTCGCTTCGGAGCCCTACCTGCGCTGTGCTGCTGCTGCTT 2126  
QY 2038 TGCTTCATCTGCTTCATCCAGCTTCTAAATTTTCCACACATCCACCTGATGCTTGGGAT 2097  
Db 2127 TGCTTCATCTGCTTTATCCAGCTCTGTGTTCCTCATCTCCACCTGATACCTCGGAT 2186  
QY 2098 TATGCCAGCATCTTCCTGCTGCTAATCACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 2157  
Db 2187 TATGCCCTATCTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2246  
QY 2158 GGTTCCTGTTTCCCTAAGGCCCTGCAACGCTGTCCCGCAGCATTTGCCGCTCACGGCA 2217  
Db 2247 GGTTCCTTCCCGAAGGCCCTGCAACGCTGTCCCGCAATATTGTCGCTCACGGTG 2306  
QY 2218 CATAGCACCGAGTTGGCATCTTTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2277  
Db 2307 CACAGCACCGCGGTTGGAATCTTCTCGGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2366  
QY 2278 ATGTTACCTGTAAACACACACCCCATFACGAGCTGTCCAGCCCGGATGCTGAATTTAACA 2337  
Db 2367 ATGTTTACCTGTAAACACACCCCAATAAGAACCTTGCCGCGCGGATGCTGAACTTTAACA 2426  
QY 2338 CTTGCTGACATCTACTGCTGCCACTGACGAGCTCAATTTACTCTCTGGGCTGGATGCT 2397  
Db 2427 CCAGCGGATGTCACCGCTGCCACTACACAGCTCAATTTACTCTCTGGGACTGGATGCT 2486  
QY 2398 CCCCCTGTGAGGCGCACCATGCCCCACTGACGCTTTCCCTGAGGTGTCATCGGGAACATG 2457  
Db 2487 CCCCCTGTGAGGCGCACCGCACCCACTGACGCTTCCCTGAGTACTTCTGCTGGGAACGTG 2546  
QY 2458 CTGCTGAGTCTCTGGCCAGCTGTCTTCTGACATACAGCAGCATCGGMAAGTTGGCC 2517  
Db 2547 CTGCTGAGTCTCTAGCCAGCTGTCTTCTTCTACATACAGCAGCATCGGCAAGCTGGCC 2606  
QY 2518 ATGATCTTCTTGGGGCTCATCTATTGCTGCTGCTTCTGCTGGTCCCGCCAGCGCC 2577  
Db 2607 ATGACCTTCTATCTGGGGTTCACTTCTGCTGCTGCTTCTGCTGGTCCCGCCAGCGCC 2666  
QY 2578 ATCTTTGACAACTATGACCTACTGCTTGGCGTCCATGGCTTGGCTTCTTCAATGAGACC 2637  
Db 2667 ATCTTTGACAACTATGATCTACTGCTTGGCGTCCATGGCTTGGCTTCTTCAATGAGACC 2726  
QY 2638 TTTGATGGGCTGGACTCTCCAGCTGACGAGGAGGTGGCCCTCAAATATATGACCCCTGTG 2697  
Db 2727 TTTGATGGGCTGGACTCTCCAGCTGTGGGAGGAGTACGCTCAAATATATGACCCCTGTG 2786  
QY 2698 ATCTTCTGCTGTTTGGCTGGGCTGATCTGCTGCTCAGCAGGTGGAATGACCTGCC 2757  
Db 2787 ATCTTCTGCTGTTTGGCTGGGCTGATCTGCTGCTCAGCAGGTGGAATGACCTGCC 2846  
QY 2758 CGCCTAAACTTCTCTGGAACCTACAGGCAACAGGGGAAAAGAGGAGATGGAGGAGCTA 2817  
Db 2847 CGCCTGAGCTTCTGTGGAAGTTACAGGCAACAGGGGAGAGGAGGAGATGGAGGAGCTA 2906  
QY 2818 CAGGCATACAAACCGGAGCTGTGCAATAACTTCTGCCAAGGACGTGGCGGCCACTTC 2877  
Db 2907 CAGGCATACAAACCGGAGGTTGCTGCAATAACTTCTTCCCAAGGACGTGGCGGCCACTTC 2966  
QY 2878 CTGGCCCGGAGCGCCGAATGATGAACCTTACTATCAGTCTGCTGAGTGTGGCTGCTT 2937  
Db 2967 CTGGCCCGGAGCGCCGAATGATGAACCTTACTTACAGTCTGCTGAATGCTGCTGCTGCT 3026  
QY 2938 ATGTTTGGCTTCCATGTCGAACCTTCTCTGAGTCTTATGTGAGCTGGAGGCAACAATGAG 2997  
Db 3027 ATGTTTGGCTTCCATGTCGAACCTTCTCGGAGTCTTACGTGGAGTTCGAGGCAACAACGAG 3086



Qy	601	CATAGCTTCCGCCAGAGACTCCATGTGGGTGTGTAGTAACTGTGGTGCTCGGCAATCCTCGGC	660
Db	650	CATAGCTTCGCCCAGGACTCCATGTGGGTAGTACGTATGTGGTTCTCGGCATCCTACGA	709
Qy	661	GCAGTGCAGGTTCGGGGCGCTTTCGCAGCAGACCGCGCAGCCCTCTCGGGGCTCTCGG	720
Db	710	GCGTGCAGTTCGGGGTGGCTTGGCAGCCACCCACGACGCCCTCAGCAGGCTTTGG	769
Qy	721	TGCCCTGTGTTCTTTATACATCGCATACAGCTCTCCCCATCCGATCGCGGCTGCC	780
Db	770	TGCCCGTGTCTTCGTCTACATCACTTACACATTCCTCCCATTCGTATCGAGCGGCC	829
Qy	781	GTCTCTAGCGGCTGGGCTCTCCACTTGCATTTGATCTTGGCTTGGCACTTAAACGT	840
Db	830	GTGCTCAGTCGGCTGGGCTCTTCCACCCCTGCATTTGATTTTGGCTTGGCATCTCAACAAT	889
Qy	841	GGTGATGCCCTCTCTTGGGAAGCAGCTCGGTGCCAATGTGCTGTCTTCTCTGCACCAAC	900
Db	890	GGTGACCCCTCTCTTGGGAAGCAGCTCGGTGCTACGTGGTGTCTTCTCTGTGCACCAAT	949
Qy	901	GTCAATTAGCATCTGCACACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCGCTTTCAGGAG	960
Db	950	GCCATCGGTCTGCACGCACCTACCCGCTGAAGTGTCTCAGCGCCAAAGCCTTTCAGGAG	1009
Qy	961	ACCGCAGTTTACATCAGCGCGGCTCCACTTGCAGCATGAGAAATCGGCACAGGAGCGG	1020
Db	1010	ACCGTGGTTTACATCAGCGCGGCTGCACTTTCAGCATGAGAAATCGACAGCAGGAACGG	1069
Qy	1021	CTGCTGTCTGCGTATTGGCCCGCAGCAGTTCGCATGGAGATGAAAGAAGACATCAACACA	1080
Db	1070	CTGCTGTCTGCGTGTGGCCCGCAGCATGTTGCCATGGAAATGAAAGAGATATCAACACA	1129
Qy	1081	AAAAAAGAAC--ATGTTCCACAGATCTACATACAGAGCATGACAATGTGAGATC	1137
Db	1130	AAAAAGGAACATGATGTTTCCACAAGATTTACATCCAGAAGCATGACAATGTGAGATC	1189
Qy	1138	CTGTTTTCAGACATTCAGGGCTTCACCGCTGGCATCCCACTGCACGTGCGCAGGAGCTG	1197
Db	1190	CTGTTTCCGACATCGAGGCTTCACCGCTGGCTCCCACTGCAGTGCAGTGCAGGAACTG	1249
Qy	1198	GTCATGACCTGTAATGAGTCTTTGCCCGGTTTGACAAGCTTGGCTGGGAGAATCACTGC	1257
Db	1250	GTCAATGACCTTGAATGAGTCTTTGCCCGGTTTCGACAAGCTTGGCTGCGGAGAATCACTGT	1309
Qy	1258	CTGAGGATCAAGATCTTGGGGNACTGTACTACTGTGTGTAGGGCTCCCGGAGGCCCGG	1317
Db	1310	CTGAGGATCAAGATCTTAGGAGACTGTACTACTGTGTCTCGGGGCTCCCGGAGGCCCGG	1369
Qy	1318	GCCGACCATCCCACTCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTG	1377
Db	1370	GCAGACCATGCCACCTGCTGTGTGGAGATGGGGGTAGACATGATCGAGGCCATCTCGCTG	1429
Qy	1378	GTAGCTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGCATCCACAGCGGGCGGCTG	1437
Db	1430	GTGCGTGAAGTAAACGGGTGTAAATGTGAACATGCGCGTGGCATCCACAGCGGGCGTGA	1489
Qy	1438	CACGTGCGGCTCTTGGCTTGGCGGAATGGCAGTTTCGATGTGTGTCCAATGATGTGACC	1497
Db	1490	CACGTGCGGCTGTCTTGGCTTGGCGGAATGGCAGTTTGAATGTGTGTCCAACGATGTGACC	1549
Qy	1498	CTGCCCAACCATGGAAGCAGGAAGCCGGGCTGGCCGCATCCACATCACTCGGGCAACA	1557
Db	1550	CTGCCCAACCATGGAGCGGGGGCGCGGGCGGGCGGCGATCCACATCACTTCGGGCCACA	1609
Qy	1558	CTGCAGTACCTGAACGGGACTACGAAGTGGAGCCAGGCCGCTGTGTGCAAGCGCAACGCG	1617
Db	1610	CTGCAGTACCTGAACGGGACTATGAGGTGGAGCAGGCGCGTGGCGGTGAGCGCAACGCG	1669
Qy	1618	TACCTCAAGGAGCAGCACATTGAGACTTTCCTTCATCTTGGGGCCAGCCAGAACGGAAA	1677
Db	1670	TACCTCAAGGAGCAGTGCAATGAGACTTTCCTCATCTAGGCGCAGCAGCAACGGAAA	1729

QY	1678	GAGGAGAAAGCATGCTGCCAAGCTGACGCGACTCGGGCCAACTCCATGGAAGGCGTGG	17373
DB	1730	GAGGAGAAAGCCATGCTGTCTAAGCTTGACGCGACGCGGCCAACTCCATGGAAGACTGG	17899
QY	1738	ATGCGCGCATGGTTCCTCATCGTGCCTTCTCCCGACCAAGGACTCCAAGCGCTTCGCCG	17977
DB	1790	ATGCCCCGCTGGGTTCCTGACCGTGCCTTCTCCGGACCAAGGACTCTAAGGCATTTCCGA	18499
QY	1798	CAGATGGGCATTGATGATTTCCAGCAAAAGACAACCGGGGACCCAAAGATGCCCTGAAACCCCT	18577
DB	1850	CAGATGGGCATCGATGACTCTAGCAAAAGAAACCGGGTGCCCAAGATGCTCTGAACCCCT	19099
QY	1858	GAGGATGAGGTGGATGAGTTCTGAGCCGTGCGCATCGATGCGCGCAGACATTGATCAGCTGG	19177
DB	1910	GAGGATGAGTGGACGAGTTTCTGGGCCGAGCATCGATGCCGAAGACATCGACCAAGCTGG	19699
QY	1918	CGGAAGGACCATGTCGGCCGGTTTGTGCTCACTTCCAGAGAGAGATTTTCGAGAAGAAG	19777
DB	1970	CGTAAGGACCATGTGGCCGGTTCTGCTGCTCACTTCCAGAGGAGGATCTCGAGAAGAAG	20299
QY	1978	TACTCCCGGAAGGTGGATCCCGCTTCGGAGCCTACGTTGCCGTGTCCTGTGTGGTCTTTC	20377
DB	2030	TATTCACGGAAGTAGACCCCTGTTTCGGAGCCTAGTCGCCCTGTCCTCTGCTGTTTC	20899
QY	2038	TGCTTCATCTGCTTCATCCAGCTTCTAAATTTTCCACACTCCACCCCTGATGCTTGGGATTT	20977
DB	2090	TGCTTCATCTGTTTCATCCAGTTCTGCTATTTCCACACTCCGCCCTGATACTCGGGATTT	21499
QY	2098	TATGCCAGCATCTCCTGCTGCTGCTAATCACCGTGTCTGATCTGTGCTGTGTACTCTCTGT	21577
DB	2150	TATGCCGGGATCTTCTTTGTGCTGTGTACCGTGTCTCATCTGTGCTGTGTCTCTCTGT	22099
QY	2158	GGTTCTCTTCCCTTAAGSCCCTGCAACGCTCTGTCCCGAGGATGTTCCGCTCACGGGCA	22177
DB	2210	GGGTCTTTTCCCAACGCCCTGACGCGCCTGTGCCGAGTATCGTCCGCTCACGGGTG	22699
QY	2218	CATAGCACCGCAGTTGGCACTTTTCCGTCCTGTGTGTGTACTTCTCTGCCATTTGCCAAC	22777
DB	2270	CACAGCACGGCTGTGTGGAGCTTCTCTCGGTCTGTGTGTTCATCTCTGCCATTTGCCAAC	23299
QY	2278	ATGTTCACTGTAAACCACACACCCCATACGGAGCTGTGACGCGCGGATGCTGAATTTAACA	23377
DB	2330	ATGTTCACTGTGAGTTCACACCCCATGAGGACCTGTGCGGCCGGATGCTGAACTTTAACA	23899
QY	2338	CCTGCTGACATCACTGCTGCCACCTGCACAGCTCAATTACTCTCTGGGCCCTGGATGCT	23977
DB	2390	CCGTCCGATGTACCCGCTGCCACCTACGACAGCTCAATTACTCTCTGGACTTGGAGCT	24499
QY	2398	CCCCGTGTGAGGACACATGCCACCTGACAGCTTTCCTGAGGTGTCCATTCGGGAACATGG	24577
DB	2450	CCCCGTGTGTGAGGGACCCGACCCACCTGCAGCTTCCCTGAGTACTTGTGTGGGAGTGTG	25099
QY	2458	CTGCTGAGTCTCTGGCAGCTCTGTCTTCTGTGCATACAGACAGCATCGGAGTTGGCC	25177
DB	2510	CTGCTGAGTCTCTGGCCAGCTCCGCTTCTCCACATCAGCAGCATTTGGCAAGCTAGTT	25699
QY	2518	ATGATCTTTGCTTTGGGGCTCATCTATTTGGTGTCTTCTGCTGGGTCCCCCAGCCGCC	25777
DB	2570	ATGACCTTTGCTTTGGGGTTCATCTACTGTGCTTCTGCTTTTGTGGTCCCCCAGCCACC	26299
QY	2578	ATCTTTGACAACTATGACTACTGCTTGGCGTCCATGGCTTGGCTTCTTCCAATGAGACC	26377
DB	2630	ATCTTTGACAACTATGATCTAGTGTAGCGTTCAGCGTTCAGCGTTCCTCCAATGAGACC	26899
QY	2638	TTTGTATGGCTGGACTGTCCAGCTGCAGGGAGGGTGGCCCTCAAAATATATGACCCCTGTG	26977
DB	2690	TTTCGATGGGCTGGACTGTGCCACCGGTGAGGAGGGTAGCGCTCAAAATACATGACCCCTGTG	27499
QY	2698	ATTTCTGCTGGTGTGTCGCTGGCGTGTATCTGATGCTCACGAGGTGGAATCGACTGCC	27577
DB	2750	ATTTCTCTGCTGTTCGCCCTGGCACTGTATCTATACAGCAACAACAGGTGGAATCTACCGCC	28099
QY	2758	CGCCTAAACTTCTCTCTGGAACCTACAGCAACAACAGGGGAAAAAGAGAGAGATGAGGAGCTA	28177

Db 2810 CGCTGGACTTCTGTGGAACATGCGAGGCACAGGGGAGAAGGAGGATGGAGGATG 2869  
QY 2818 CAGGCATACAAACGGAGGTGCTGCATATACATCTCCCAAGGACGTGGCGCCACTTC 2877  
Db 2870 CAGGCTACAAACGGCGGTGCTGCATATACATCTCCCAAGGACGTGGCGCCACTTC 2929  
QY 2878 CTGGCCGGAGGCGCGCAATGATGAACCTCTACTATCATCTGCTGAGTGTGTGGCTGTT 2937  
Db 2930 CTGGCCGGAGGCGCGCAACGACGAGCTGTACTACCACTCTGCGAGTGGCTGTC 2989  
QY 2938 ATGTTTGCCTTCATTCGCCAACTTCTCTGAGTCTCTATGTTGAGCTGGAGGCAACAATGAG 2997  
Db 2990 ATGTTTGCCTTCATTCGCCAACTTCTCTGAGTCTCTATGTTGAGCTGGAGGCAACAATGAG 3049  
QY 2998 GTGCGGAGTGGCTGGCGTCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC 3057  
Db 3050 GCGTGGAGTGGCTGGCGTCTCAATGAGATCATCGCGGACTTTGATGAGATTATCAGT 3109  
QY 3058 GAGGAGCGGTTCGGCAGCTGGAAGAATCAAGACGATTGGTAGCACCTACATGGCTGCC 3117  
Db 3110 GAGGAGAGTTCGGCAGCTGGAGAGATCAAGACCATCGGTAGCACTTACATGGCGCC 3169  
QY 3118 TCAGGCTGAACGCCAGCAGCTACGATCAGTGGGCGCTCCACATCACTGCTGGCT 3177  
Db 3170 TCGGGCTAAATGCCAGCAGCTATGACAGTGGCGCTCGCACATCACCGCCCTGGCA 3229  
QY 3178 GACTACGCCATGGGCTCTGAGGAGATGAAGCAGATCAATGAGCAGCTCTTCAACAT 3237  
Db 3230 GACTACGCCATGGGCTTATGGAGCAATGAACACATCAAGCAACACTCTTCAACAC 3289  
QY 3238 TTCAGATGAAGATTGGGTGAACATGGCGCCAGTGGTGCAGGTGTCTATCGGGCTCGG 3297  
Db 3290 TTCAGATGAAGATCGGTTGAACATGGGTCCGGTTGTAGCAGGTGTCTATGGGCGCG 3349  
QY 3298 AAGCCACAGTATGACATCTGGGGGAACACAGTGAATGTCTTAGTCTGATGACAGCAG 3357  
Db 3350 AAGCCACAGTATGACATCTGGGGGAACACAGGTGAATGTCTTCCAGCGGTATGACAGCAG 3409  
QY 3358 GGGTCCCGACCGAATCCAGGTGACCGGACCTGTACAGGTCTTACGTGCTGACAGGCG 3417  
Db 3410 GAGTCTCTGACCGAATACAGGTGACCGGATCTTACAGGTCTTACGTGCTGACAGGCG 3469  
QY 3418 TACAGCTGGAGTGTGAGGGTGTGCAAGGTGAAGGCAAGGGGAGATGACCACTAC 3477  
Db 3470 TACCAACTGGAGTGTGAGGGTGTGCAAGGTGAAGGCAAGGGGAGATGACCACTAC 3529  
QY 3478 TTCTCAATGGGGCCCCAGCAGTTAACAGGGCCCA--GCCACAAATTCAGCTGAAGGA 3535  
Db 3530 TTCTCAATGGGGCCCCAGCAGTTAGCAGAGCGCACAGTGGAAATTCACCAAGAGGA 3589  
QY 3536 CCAAGTGGGCACT 3549  
Db 3590 CCAAGTGGGCACT 3603

RESULT 8  
ID AAD08562  
XX AAD08562 standard; cdna; 1812 BP.  
AC AAD08562;  
XX  
DT 04-SEP-2001 (first entry)  
DE Human partial cardiac adenylylase VI (ACVI) isoform #2 cdna.  
XX  
KW Human; cardiant; beta-adrenergic signalling protein; beta-ASP;  
KW myocardium; gene therapy; beta-adrenergic receptor; beta-AR;  
KW adenylylase; adenylylase; adenylylase; adenylylase; adenylylase;  
KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;  
KW cardiac adenylylase VI; ACVI isoform; beta-ASP transgene; ss.  
OS Homo sapiens.

XX Key Location/Qualifiers  
FH 1..1812  
FT /\*tag= a  
FT /product= "Human partial cardiac ACVI isoform #2"  
FT /note= "CDS does not include start and stop codon"  
FT /EC\_number= "4.6.1.1"  
XX WO200148164-A2.  
XX 05-JUL-2001.  
XX 26-DEC-2000; 2000WO-US35411.  
XX 27-DEC-1999; 99US-0472667.  
XX (REGC ) UNIV CALIFORNIA.  
XX Hammond HK, Gao M;  
XX WPI: 2001-418260/44.  
XX P-PSDB; AAE04309.  
XX Novel polynucleotide encoding a modified adenylylase polypeptide  
XX useful for enhancing cardiac function in mammalian hearts, and for  
XX treating heart disease, especially congestive heart failure -  
XX Example 5; Page 115-119; 153pp; English.  
XX The present invention relates to methods and compositions for enhancing  
XX cardiac function in mammalian hearts by inserting transgenes encoding  
XX beta-adrenergic signalling proteins (beta-ASP) which increase  
XX beta-adrenergic responsiveness within the myocardium using in vivo  
XX gene therapy. The beta-ASPs of the invention include beta-adrenergic  
XX receptors (beta-AR), adenylylases (also referred as adenylylase,  
XX adenylylase and cAMP synthetase) and G-protein receptor kinase  
XX (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function  
XX in mammalian hearts and for treating heart disease, especially  
XX congestive heart failure. The present cDNA sequence encodes human  
XX partial cardiac adenylylase VI (ACVI) isoform which is used for  
XX generating a third beta-ASP transgene, used in the exemplification  
XX of the invention.

SQ Sequence 1812 BP; 361 A; 539 C; 507 G; 405 T; 0 other;  
Query Match 51.0%; Score 1808.4; DB 22; Length 1812;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1809; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 636 TAACGTGTGTGGGCATCTGGCGCAGTGCAGGTGGGGCGCTTTCGACAGACCC 695  
Db 3 TAACGTGTGTGGGCATCTGGCGCAGTGCAGGTGGGGCGCTTTCGACAGACCC 62  
QY 696 GCGCAGCCCTCTGGGGCTCTGGTGCCTGTGTTCTTTGTATACATCGCATACGCT 755  
Db 63 GCGCAGCCCTCTGGGGCTCTGGTGCCTGTGTTCTTTGTATACATCGCATACGCT 122  
QY 756 CTCCCATCCGCGGCTGCGTCTCAGCGGCTGGGCTCTCCACCTTGCATTT 815  
Db 123 CTCCCATCCGCGGCTGCGTCTCAGCGGCTGGGCTCTCCACCTTGCATTT 182  
QY 816 GATCTTGGCTGGCAACTTAACCGTGGTGTGATGCTTCTCTGGAAGAGCTCGGTGCCAA 875  
Db 183 GATCTTGGCTGGCAACTTAACCGTGGTGTGATGCTTCTCTGGAAGAGCTCGGTGCCAA 242  
QY 876 TGTGCTGTGTTCTCTGCAACCAAGTCAATAGCATCTGCACACATATCCAGCAGGT 935  
Db 243 TGTGCTGTGTTCTCTGCAACCAAGTCAATAGCATCTGCACACATATCCAGCAGGT 302  
QY 936 GTCTCAGGCCAGGCTTTTCAGGAGACCGGAGTTACATCCAGGCCGCTCCACCTGCA 995  
Db 303 GTCTCAGGCCAGGCTTTTCAGGAGACCGGAGTTACATCCAGGCCGCTCCACCTGCA 362



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QY 996 GCATGAGAAATCGCAGCAGAGCGGCTGCTGCTGTGCTGATTGGCCCCAGCAGCTTGCCAT 1055
Db 363 GCATGAGAAATCGCAGCAGAGCGGCTGCTGCTGTGCTGATTGGCCCCAGCAGCTTGCCAT 422
QY 1056 GGAGATGAAGAAGACATCAACACAAAAAAGAACACATGTTCCACAAGATCTACATACA 1115
Db 423 GGAGATGAAGAAGACATCAACACAAAAAAGAACACATGTTCCACAAGATCTACATACA 482
QY 1116 GAAGCATGACAATGTCAAGCATCCTGTTTGCAGACATTTAGGGCTTCAACAGCCTGGCATC 1175
Db 483 GAAGCATGACAATGTCAAGCATCCTGTTTGCAGACATTTAGGGCTTCAACAGCCTGGCATC 542
QY 1176 CGAGTGCACTGCGAGAGAGCTGGTCATGACCTGTAATGAGCTTTTGGCCGGTTTGACAA 1235
Db 543 CCAGTGCACTGCGAGAGAGCTGGTCATGACCTGTAATGAGCTTTTGGCCGGTTTGACAA 602
QY 1236 GCTGGCTGGGAGAAATCACTGCTGAGGATCAAGATCTTTGGGGAGCTGTACTACTGTGT 1295
Db 603 GCTGGCTGGGAGAAATCACTGCTGAGGATCAAGATCTTTGGGGAGCTGTACTACTGTGT 662
QY 1296 GTCAAGGCTTGCAGAGGCGGCGGACCATGCCACTGCTGTGTGAGATGGGGTAGA 1355
Db 663 GTCAAGGCTTGCAGAGGCGGCGGACCATGCCACTGCTGTGTGAGATGGGGTAGA 722
QY 1356 CATGATTGAGGCATCTCCTGGTAGGTGAGGTGACAGGTGTAATGTGAACATGGCGGT 1415
Db 723 CATGATTGAGGCATCTCCTGGTAGGTGAGGTGACAGGTGTAATGTGAACATGGCGGT 782
QY 1416 GGGATCCACAGCGGCGGTCACTGCGCGCTGCTTGGCTTGGGAAATGGCAGTTCCA 1475
Db 783 GGGATCCACAGCGGCGGTCACTGCGCGCTGCTTGGCTTGGGAAATGGCAGTTCCA 842
QY 1476 TGTGTGTCATGATGTGACCTGCGCAACCAACATGGAAGCAGGAAGCGGCTGGCGG 1535
Db 843 TGTGTGTCATGATGTGACCTGCGCAACCAACATGGAAGCAGGAAGCGGCTGGCGG 902
QY 1536 CATCCACATCACTCGGCAACACTGAGTACCTGAACGGGGACTAGAAAGTGGAGCCAG 1595
Db 903 CATCCACATCACTCGGCAACACTGAGTACCTGAACGGGGACTAGAAAGTGGAGCCAG 962
QY 1596 CCGTGTGTCAGCAAGCGCTACTCTCAAGGAGCAGCATTGAGACTTTCTCATCT 1655
Db 963 CCGTGTGTCAGCAAGCGCTACTCTCAAGGAGCAGCATTGAGACTTTCTCATCT 1022
QY 1656 GGGCGCCAGCCAGAAAGAGAGAGAAAGGCATGCTGGCAAGCTCAGCGACTCG 1715
Db 1023 GGGCGCCAGCCAGAAAGAGAGAAAGGCATGCTGGCAAGCTCAGCGACTCG 1082
QY 1716 GGCCTCACTCCATGGAGGCTGATCGCGGATGGGTTCCTGATCGTTCCTCCGGAC 1775
Db 1083 GGCCTCACTCCATGGAGGCTGATCGCGGATGGGTTCCTGATCGTTCCTCCGGAC 1142
QY 1776 CAAGGACTCAAGGCTTCCGCCAGATGGCATTTGATGATTCAGCAAGAACACCGGG 1835
Db 1143 CAAGGACTCAAGGCTTCCGCCAGATGGCATTTGATGATTCAGCAAGAACACCGGG 1202
QY 1836 CACCAAGATGCCCTCAACCCCTGAGGATGAGGTGATGATGATTCAGCAAGAACACCGGG 1895
Db 1203 CACCAAGATGCCCTCAACCCCTGAGGATGAGGTGATGATGATTCAGCAAGAACACCGGG 1262
QY 1896 TGCCGCGCAGCATTTGATCAGCTCGGAAGGACCATGTGCGCGGTTTTTGTCTCACCTTCCA 1955
Db 1263 TGCCGCGCAGCATTTGATCAGCTCGGAAGGACCATGTGCGCGGTTTTTGTCTCACCTTCCA 1322
QY 1956 GAGAGAGGATTTGAGAGAAATCTCCCGGAGGTGGATCCCGCTTCGGAGCCCTACGT 2015
Db 1323 GAGAGAGGATTTGAGAGAAATCTCCCGGAGGTGGATCCCGCTTCGGAGCCCTACGT 1382
QY 2016 TGCCTGTGCGCTTGTGGTCTTCTGCTCATCTGCTTCATCCAGCTTCTAAATTTCCACCA 2075
Db 1383 TGCCTGTGCGCTTGTGGTCTTCTGCTCATCTGCTTCATCCAGCTTCTAAATTTCCACCA 1442
QY 2076 CTCCACCTGATGCTTGGGATTATGCCAGCATCTTCTGCTGCTTAATCACCGTGT 2135
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Db 1443 CTCCACCTGATGCTTGGGATTATGCCAGCATCTTCCCTGCTGCTTAATCACCGTGT 1502
QY 2136 GATCTGTGCTGTGTACTCTCTGTGGTTCTCTGTTCCTAAGGCCCTGCACAGCTGTCCCG 2195
Db 1503 GATCTGTGCTGTGTACTCTCTGTGGTTCTCTGTTCCTAAGGCCCTGCACAGCTGTCCCG 1562
QY 2196 CAGCATTTGCCGCTACAGGGCACATAGCACCGCAGTTGGCATCTTTTCCGTCTCTGTTGT 2255
Db 1563 CAGCATTTGCCGCTACAGGGCACATAGCACCGCAGTTGGCATCTTTTCCGTCTCTGTTGT 1622
QY 2256 GTTTACTTCTGCGCATTTGCCAACAATGTTACCTGTATAACACACCCCCCATACGAGCTGTGC 2315
Db 1623 GTTTACTTCTGCGCATTTGCCAACAATGTTACCTGTATAACACACCCCCCATACGAGCTGTGC 1682
QY 2316 AGCCCGGATGCTGAATTTAACACCTGCTGACATCACTGCTGCCACCTGCAGCAGCTCAA 2375
Db 1683 AGCCCGGATGCTGAATTTAACACCTGCTGACATCACTGCTGCCACCTGCAGCAGCTCAA 1742
QY 2376 TTACTCTCTGGCGCTGATGCTCCCTGTGTGTGAGGGCAGCATGCCACCTGCAGCTTTCC 2435
Db 1743 TTACTCTCTGGCGCTGATGCTCCCTGTGTGTGAGGGCAGCATGCCACCTGCAGCTTTCC 1802
QY 2436 TGAGGTGTCC 2445
Db 1803 TGAGGTGTTC 1812

RESULT 9
AAV23246
ID AAV23246 standard; cDNA; 2127 BP.
XX
AC AAV23246;
XX
DT 17-JUL-1998 (first entry)
XX
DE Human adenylyl cyclase isoform VI encoding cDNA.
KW Human; adenylyl cyclase VI; AC-VI; beta-adrenergic signalling protein;
KW transgene; gene therapy; congestive heart failure; cardiac function;
KW adenovirus; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 1..2127
FT /*tag= a
FT /product= "adenylyl cyclase isoform VI"
FT /transl_except= (pos:229..231,aa:Xaa)
FT /transl_except= (pos:315..317,aa:Xaa)
FT /note= "no stop codon given; Xaa = unknown"
FT misc_difference 315
FT /*tag= b
FT /note= "n indicates a gap of about 0.5 kb"
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PN W09810085-A2.
XX
PD 12-MAR-1998.
XX
PF 05-SEP-1997; 97WO-US15610.
XX
PR 16-JUN-1997; 97US-0048933.
PR 05-SEP-1996; 96US-0708661.
XX
XX (COLL-) COLLATERAL THERAPEUTICS.
PA (REGC ) UNIV CALIFORNIA.
PI Gao M, Hammond HK, Insel PA, Ping P, Post SR;
XX
XX WPI; 1998-193633/17.
DR P-PSDB; AAW53345.
XX
PT Vectors containing transgene(s) encoding beta-adrenergic signalling
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Db	1762	ATGGACATGATCAGGCGCATCTGCTTGGTCGGGAGGTGACAGGGGTGACAGCTGAACATG	1821
Qy	1411	CGGTGGGCATCACACGCGGGCGGTGCACTGCGCGCTCTTGGCTTGCAGAAATGGCAG	1470
Db	1822	CGTGTGGAAATTACACAGCGGGCGAGTACACTCGGTGTCTTGGTCTCAGGAAGTGGCAG	1881
Qy	1471	TTGATGTGTGTFCCAAATGATGTGACCTTGGCCACACATGGAGCAGGAAGCGCGGCT	1530
Db	1982	TTTGACGTCTGGTCTTAACGATGTCAAGCTAGCCACACCATGGAGGCTGGCGGCAAGGCA	1941
Qy	1531	GGCCGCATCCATCATCTCTGGGCAACACTGCACTAGTAGTACCTGAACGGGGACTACGAAGTGGAG	1590
Db	1942	GGACGCATCCACATCATCCAAGGCTACTACTAACTACCTGAATGGGACTACGAGGTGGAG	2001
Qy	1591	CCAGGCGGTGGTGGCAAGCGCAACCGGTACCTCAAGGAGCAGCACATTTAGACTTTTCCCT	1650
Db	2002	CCAGGCTGTGGGGCGAGCGCAACGCTACCTTCAAGGAGCACATGATCGGACACCTTCCCT	2061
Qy	1651	ATCCTGGGGCCAGCCAGCAAAACGGAAAGAGGAGAAGCATGCTGGCCAAAGCTCACACGG	1710
Db	2062	ATCCTGGCTGCAACCCAGAGCGGAAGAGAGAGAGGCCATGATCGCCAAAGTAGAACCGC	2121
Qy	1711	ACTGGGCCAACTCCATGGAAGGGCTGATGCGCGCATGGGTTCCTTGATGFGTCCCTTCTCC	1770
Db	2122	CAGAGAACCAACTCCATCGGGGCACAAACCCACCACTGGGGGGTGTAGCGCCCTTCTAC	2181
Qy	1771	-----CGGACCAAGCACTCCAAGGCTTCGCCAGATGGCGCATTGATGATTCC	1818
Db	2182	AACCACCTGGGTGGCAACCAAGGTGTCCAAGAGATGAAGCGGATGGGCTTTGAAGACCC	2241
Qy	1819	AGCAAGACAAACCGGGCCACCAAGATGCCCTGAAACCTGAGGATGAGGTGGATGAGTTC	1878
Db	2242	A-----AGCACAAAGAACCCAGAGAGAGTGCGAACCTGAGGATGAAGTGGATGAGTTT	2295
Qy	1879	CTGAGCGTGCCATCGATCCCGCAGCATTGATAGCTGCGGAAGGACCATGTCGCGCGG	1938
Db	2296	CTGGCGGTGCCATTGACGCCAGGACATTGATAGCTTCGGTCTGACACGCTCCGCAAG	2355
Qy	1939	TTTTTGTCACTTCCAGAGAGAGGATTTGAGAAAGATTACTCCCGAAGGTGGATCCC	1998
Db	2356	TTCTCTGTACCTTTCAGGAGGCTGACTTAGAGAAAGATTACTCCAAGCAGGTAGACGAC	2415
Qy	1999	CGTTCGGAGCCTACCTTGCTGCTGCGCTGTGGTCTCTGCTTCATCTGCTTCATCCAG	2058
Db	2416	CGATTTGGTGCCTATGTGGCGTGTGCTCGCTGCTTCTTCTTCATCTGCTTTGTCCAG	2475
Qy	2059	CTTCTAATTTCCACACTCCACCCTGATGCTTGGGATTTATGCCAGCATCTCCTGCTG	2118
Db	2476	ATCACCATCGTGCCCACTCCATATTATGCTCAGCTTCTACCTGACCTGTTCCCTGCTG	2535
Qy	2119	CTGCTAATCACCGTGTGATCTGTGTGTGTACTCCTCTGGTTCCTGTGTTCCCTAAGGCC	2178
Db	2536	CTGACCTTGGTGGTGTGTGTGTGTGATCTACTCCTCGCTAAAGCTCTTCCCTCCCCA	2595
Qy	2179	CTGCAAGCTCTGTCGGCAGCATTTGCGCTCACGGGCACATAGCACCGGATTTGGCATC	2238
Db	2596	CTGCAGACCTCTCCAGGAAGATGTGGGGTCCAAGATGAACACACCCCTGGTTGGGGTG	2655
Qy	2239	TTTTCCGTCTGTGTGTTTACTTCTGCCATTCGCCAACTGTTCACTGTTAACCACACC	2298
Db	2656	TTCAACATCAACCCTGTGTTCTCTGGCGGCTTTTGTCAACATGTTCAAGTGAACCTCAGG	2715
Qy	2299	CCCATACGGAGCTGTCCACCCCGGATGCTGAATTTAACACACCTGCTGACATCATGCTCGC	2358
Db	2716	GACCTGCTGGGCTGTGGCAGAGGACACACATFACGCGGACCGAGGTCAACGCGTGT	2775
Qy	2359	CACCTGCAGCAG-----CTCAATTACTCTCTGGGCTGGGATGCTCCCTGTGTGAGGGC	2412
Db	2776	CAGGTGGGGAGTGCGCCGTCAACTACAGCCTGGCGGATGAGCAGGGGTCTCTGTGGCAGC	2835
Qy	2413	ACCATGCCCACTGTGACGCTTTCCTGAGGTGTCCATFCGGGAACATGCTGCTGAGTCTCTTG	2472
Db	2836	CCCTGGCCAACTGCAACTTCCCGCAGTACTTCACTACAGCGTGTGCTCAGCCTGCTG	2895

Qy	2473	CCGAGCTCTGTCCTTCGTCACATCAGCAGCATCGGGAAGTTGGCCATGATCTTTGTCTTG	2535
Db	2896	GCCTTCCTCCGTGTCTCTGCAGATACAGCTGCATTCGGGAAGCTGGTCTCATCTCGCCATC	2955
Qy	2533	GGGCTCATCTATTGGTGTGCTTCCTGCTGGGTGCCCGCAGCGCCATCTTTTGACAACTAT	2592
Db	2956	GAGCTCACTA--CGTGCTCATCTGGAGGTGCCAGGTGCAGCTCTTCGACAACGCC	3012
Qy	2593	GACCTACTGCTTGGGCTCCATGGCTTGGCTTCTCCAAATGAGACCTTTGATGGGCTGGAC	2652
Db	3013	GACCTGTGCTCACCGCCAAACGCATPAGACTTCTTCA---ACAACGGGACCTCCACAGTGC	3069
Qy	2653	TGTCACCTCGAGGGAGGTGGCCCTCAATATATAGACCCCTGTGATTCTCTGCTGCTT	2712
Db	3070	CCTGAGCATGCAACCAAGTGGCATTTGAAGTGTGTGACGCCCATCATCATCTCAAGTCTTT	3129
Qy	2713	CGCTGGCGCTGTATCTGTCATGCTACGAGGTGGAAATCGACTGCCCGCTAAACTTCCTC	2772
Db	3130	GTGCTGGCCCTGTACCTGTCACGCCACGAGGTGGATCCACTTCCTGCCGCTCGACTTCTC	3189
Qy	2773	TGGAACCTACAGGCACAGGGGAAAAGAGGAGATGGAGGAGCTTACAGGCATACAAACGG	2832
Db	3190	TGGAACCTGACGCCACAGAGGAAGAAGAGAGATGGAGGAGCTGCAGGCCCTGCAACCGG	3249
Qy	2833	AGGCTGCTGCATATACATTTCTGCCCAAGGACGTGGCGGCCCACTTCTGGCCCGGAGGCGC	2892
Db	3250	CGGCTGCTGCACAACATCTCTGCCCAAGGACGTGGCGCTCACTTCTGGCCCGGAGGG	3309
Qy	2893	CGCAATGATGAATCTACTATCATAGTCGTGTAGTGTGTGGCTGTATTGTTTGGCTCCATT	2952
Db	3310	CGCAATGATGAGCTCTACTATCATGCTCTGTGTGTGTGGCGGTCAATGTTCCGCTCCATC	3369
Qy	2953	GCCAACTTCTGAGTCTATGTGGAGCTGGAGGCAACAATAGAGGTGCCAGTGCCTG	3012
Db	3370	GCCAACTTCTCCGAGTCTACGTTGAGCTGGAGGCCAACAGAGGTGTGAGTGCCTG	3429
Qy	3013	CGGCTGCTCAACGAGATCATCGCTGACTTTGTATGAGATTATCAGCGAGGAGCGTTCCGG	3072
Db	3430	CGGCTACTCAATGAGATCATCGCTGACTTTGTATGAGATCATCAGCGAGGATTCGGTTCCGG	3489
Qy	3073	CAGCTGGAAGAAGATCAAGACGATTGTGTAGCACTACATGGCTGCTCAGGGCTCAAGCGCC	3132
Db	3490	CAGCTGGAGAGATCAAGACCATCGGCACCACTACATGGGTGCTTCGGGCTCAACGAC	3549
Qy	3133	AGCACTACGATCAGGTGGCGCGCTCCACATCACTGCCCTGGGTGACTACGCCATCGGG	3192
Db	3550	TCTACTTACGACAAGGTGGSCAAGACCCACATCAAGGCACTGGCGGACTTTGGCCATGAAG	3609
Qy	3193	CTCATGAGCAGATGAAGCNACATCAATGAGCACTCCTTTCACAATTTCCAGATCAAAATT	3252
Db	3610	CTGATGACCAAGATGAAGTACATCAATGAGCACTCCTTTCACAACATTCAGATGAAGATC	3669
Qy	3253	GGGCTGAACATGGGCCAGTCGTTGGCAGGTGTCACTGGGGCTCGGAAGCCACAGTATGAC	3312
Db	3670	GGGCTCAACATCGGCCCTGTGTGGCCGGGTGATAGGGGCACGAAAGCCTCAGTAGCAC	3729
Qy	3313	ATCTGGGGAAACAGTGAATGTCTTAGTCTGTATGGACAGCAGGGGGTCCCGACCGGA	3372
Db	3730	ATCTGGGGCAATACCCTGMAACGTGGCCAGCCGACGTGGACAGCACCGGTGTACCCGACCGC	3789
Qy	3373	ATCAGGTGACCCAGCACTGTACCAAGTTCTTAGCTGCCAAGGGCTACCACTGGAGTGT	3432
Db	3790	ATCAGGTACCCACAGACATGTATACCAGTGTGGGTGGGTGCCAACACGTACCACTGGAGTGC	3849
Qy	3433	CGAGGGTGTCAAGGTGAAGGCAAGGGGAGATGACCACTACTTCTCAATGGGGGC	3492
Db	3850	CGGGGCTGTCAAGTCAAGGCAAGGCGGAGATGATGACCTACTTCTCAATGGAGGG	3909
Qy	3493	CCC 3495	
Db	3910	CCC 3912	

RESULT 11	
AAQ95540	
ID	AAQ95540 standard; DNA; 4356 BP.
XX	
AC	AAQ95540;
XX	
AC	31-JAN-1996 (first entry)
XX	
DT	Cardiac adenylyl cyclase gene.
XX	
DE	Cardiac adenylyl cyclase; effector enzyme; ss.
XX	
KW	Homo sapiens.
XX	
OS	
XX	
FH	Key Location/Qualifiers
FT	CDS 148..3702
FT	/*tag= a
XX	
PN	TW243453-A.
XX	
PD	21-MAR-1995.
XX	
PF	02-JUL-1992; 92TW-0105242.
XX	
PR	12-JUN-1992; 92US-0899068.
XX	
PA	(AMCY ) AMERICAN CYANAMID CO.
XX	
DR	WPI: 1995-214006/28.
XX	
DR	P-PSDB; AAR78519.
XX	
PT	Cardiac adenylyl cyclase and corresp. DNA - having specified sequences
PT	
PS	Claim 1; Fig 2; 45pp; Chinese.
XX	
CC	AAQ95540 encodes AAR78519, the novel effector enzyme cardiac adenylyl cyclase.
XX	
SQ	Sequence 4356 BP; 836 A; 1372 C; 1373 G; 775 T; 0 other;
	Query Match 47.68; Score 1690; DB 16; Length 4356;
	Best Local Similarity 70.1%; Pred. No. 0;
	Matches 2348; Conservative 0; Mismatches 980; Indels 20; Gaps 5;
QY	165 CACCCCTGCGGGCCCCCTCGGTGCCCCCTGGCAGGATGACGCCCTTCATCCGAGGGGGCGG 224
DB	
DB	.346 CGCCCTGCGGGCG 405
QY	225 CCCAGGCAAGGGCAAGGAGCTGGGCTCGGGCACTGGCCCTGGGCTTCGAGGATACCGA 284
DB	
DB	406 CTCGGTGAGCTGGGCCCTGGACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 465
QY	285 GGTGACACGACAGCGGGCGGACGGCTGAGTGGCGCCCGACGCGG--TGCCCAAGGAGT 342
DB	
DB	466 GCCGAGCCCGCCCCCGGGGGCGACCGGGGCGGGGACGGCGCGCGCGCGCGCGCGCGCG 525
QY	343 GGGCGATCCTCTGCGCGCGGTTTGGTGAGGTGTTTCCAGATGAACGACAGTTCGGTTGCGGC 402
DB	
DB	526 CCGCGGGCCTGCTGCGCGCGCTGCTGCAGATCTTCGCGTCCAAGAAGTTCCCGTCGGAC 585
QY	403 AAGCTGGAGCCCTGTACACGGGTACTCTTTTCCAGATGAACGACAGAGCCTGACGCTG 462
DB	
DB	586 AAGCTGGAGCGGCTGTACACGGGTACTCTTCGCCCTGAACGACAGAGCCTTCACCATG 645
QY	463 CTGCTGGCGGTGCTGCTGTCTACACGGGTGCTGCTGGCTTTCCAAAGCCGACCCGCG 522
DB	
DB	646 CTCATGCCGTGCTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 705
QY	523 CGCCCTCAGCCTGATGTGGCACTGTGTGGCCTGTGCGCGCGCCCTGTTCGTGGGGCTC 582
DB	
DB	706 CCGCTGGGGCTGCGCCACTGGCGTGTGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 765



PD 03-MAR-1993.  
XX  
PF 27-AUG-1992; 92EP-0114637.  
XX  
PR 29-AUG-1991; 91US-0751460.  
XX  
PA (AMCY ) AMERICAN CYANAMID CO.  
XX  
XX Ishikawa Y, Kanski AF;  
PI WPI; 1993-068888/09.  
DR P-PSDB; AAR32882.  
XX  
XX Isolated nucleic acid mol. encoding Cardiac adenyl cyclase type  
PT v - useful for determining and modifying cardiac function  
XX  
XX Claim 1; Page 15-27; 38pp; English.  
XX  
CC Left ventricular tissue of canine heart was used as a source of mRNA.  
CC A cDNA library was prep'd. in lambda gt10 phage. A 970 bp Aat-HincII  
CC fragment from type I adenyl cyclase cDNA was used as probe. The  
CC clones isolated were used to obtain cDNA encoding CACV. This probe  
CC may also be used to screen a human cardiac cDNA library to obtain  
CC the cDNA encoding human CACV. CACV, its analogues and antibodies  
CC are useful in therapy or diagnostic assays, e.g. in modifying and  
CC determining cardiac function. A decrease in CACV content of the  
CC heart contributes to impaired CAMP prodn. and in heart failure. The  
CC CACV can also be used to screen for cpds. which stimulate or inhibit  
CC the activity of the cyclase.  
XX  
SQ Sequence 4356 BP; 837 A; 1367 C; 1377 G; 775 T; 0 other;  
  
Query Match 47.6%; Score 1688.4; DB 14; Length 4356;  
Best Local Similarity 70.1%; Pred. No. 0;  
Matches 2347; Conservative 0; Mismatches 981; Indels 20; Gaps 5;  
  
QY 165 CACCCCTCGGGGGCCCCCTGCGTGGCCCTGGCAGAGTACGCTTCATCCGGAGGGCGCG 224  
DB 165 CACCCCTCGGG 224  
QY 225 CCAGGCAAGGCAAGAGCTGGGGCTGGGGGAGTGGGGCTGGGGCTTCGAGGATACCGA 284  
DB 225 CCAGGCAAGGCAAGAGCTGGGGCTGGGGGAGTGGGGCTGGGGCTTCGAGGATACCGA 284  
QY 285 GGTGACAACAGACAGCGGGGGGAGCGGTGAGGTGGGGGGGGGGGGGGGGGGGGGGGG 342  
DB 285 GGTGACAACAGACAGCGGGGGGAGCGGTGAGGTGGGGGGGGGGGGGGGGGGGGGGGG 342  
QY 343 GGGCGATCTGTCGG 402  
DB 343 GGGCGATCTGTCGG 402  
QY 526 CCGCGGG 585  
DB 526 CCGCGGG 585  
QY 403 AAGCTGAGCGCTGTACAGCGGGTACTTTTCCAGATGAACAGAGAGCGCTGAGCGTG 462  
DB 403 AAGCTGAGCGCTGTACAGCGGGTACTTTTCCAGATGAACAGAGAGCGCTGAGCGTG 462  
QY 463 CTGGTGGGGTGTGTTGCTGCTACAGAGGGTGTGCTGGCTTTTCCAGCGAGCGAGCGCG 522  
DB 463 CTGGTGGGGTGTGTTGCTGCTACAGAGGGTGTGCTGGCTTTTCCAGCGAGCGAGCGCG 522  
QY 646 CTATGCGCGTGTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 705  
DB 646 CTATGCGCGTGTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 705  
QY 523 CGCCCTCAGCGCTGCTATGTTGGGACATGTTGGGCTGTGGCGCGCGCGCTGTTGGGGGCTC 582  
DB 523 CGCCCTCAGCGCTGCTATGTTGGGACATGTTGGGCTGTGGCGCGCGCGCTGTTGGGGGCTC 582  
QY 706 CCGCTGCGGGTGTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 765  
DB 706 CCGCTGCGGGTGTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 765  
QY 583 ATGGTGTGTGTAACCGGATAGCTTCCCGCAGGACTCCATGTGGGTGTGAGTACGTTG 642  
DB 583 ATGGTGTGTGTAACCGGATAGCTTCCCGCAGGACTCCATGTGGGTGTGAGTACGTTG 642  
QY 766 GCGGTGCTGTGAACCGCGCGCGCTTCCACAGGACACATGGGCGCTGGCGCTGTACCGG 825  
DB 766 GCGGTGCTGTGAACCGCGCGCGCTTCCACAGGACACATGGGCGCTGGCGCTGTACCGG 825  
QY 643 GTGCTGGGCTGCTGGCGGAGTGCAGGTTCGGGGGGCTTTCGACGACAGCGCGCGCAGG 702  
DB 643 GTGCTGGGCTGCTGGCGGAGTGCAGGTTCGGGGGGCTTTCGACGACAGCGCGCGCAGG 702  
QY 826 CTCATCGCGCTGGTGTGCGCGCTGTCAGGTGTGGGGCTGCTGCTGCGCGCGCGCGCAGC 885  
DB 826 CTCATCGCGCTGGTGTGCGCGCTGTCAGGTGTGGGGCTGCTGCTGCGCGCGCGCGCAGC 885  
QY 703 CCGCTGCGGGGCTGCTGGTGGCGCTGTGTTTGTGATATGATATGATATGATATGATATG 942  
DB 703 CCGCTGCGGGGCTGCTGGTGGCGCTGTGTTTGTGATATGATATGATATGATATGATATG 942

DB 886 GCCTCCGAGGGCATCTGGTGGACCGTGTCTTTCATCTACACCATCTACACGCTGCTGCC 945  
QY 763 ATCCGATATGGGGCTGCGCTTCAGGGCTGGGGCTCTCCACCTTGATTTGATCTTG 822  
DB 946 GTGCGCATGCGGGCGCGCTCTCTCAGCGAGTGTCTCTGTCGGCCCTGACCTTGGCATC 1005  
QY 823 GCCTGGCAACTTAACCGTGGTGTCTCTCTGGAAGCAGCTCGGTGCGCAATGTGCTG 882  
DB 1006 GCCTGCGCGCAACGCCAGGACCGGTCTCTCAAGCAGCTGTCTCCAATGTCTC 1065  
QY 883 CTGTTCTCTGACCAACGCTCATTAGCATGTGACACACTATCCAGCAGAGGTGTCTCAG 942  
DB 1066 ATTTCTCTGTCACCAACATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1125  
QY 943 CGCCAGGCTTTCAGGAGAGCCCGAGTACATCCAGCCCGGCTCCACCTGCGAGCATGAG 1002  
DB 1126 AGACAGGCTTTCAGAGAGCCCGGAGTGCATCCAGGACCGGTCTCCACTGCAACCGGAG 1185  
QY 1003 AATCGGCAGCAGGAGCGGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1062  
DB 1186 AACCAGCAGCAGGAGCGGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1245  
QY 1063 AAGAAGACATCAACACAAACAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1119  
DB 1246 AAGCAGACATCAATGCAAGCAGGAGGATATGATGTTCATTAAGATTTACATCCAGAAA 1305  
QY 1120 CATGCAATGTACAGCATCTGTTTGGCAGACATTTAGGGCTTCCAGGCTGCGCATCCAG 1179  
DB 1306 CATGCAAGGTGAGCATCTGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1365  
QY 1180 TGCACTGCGCAGGAGCTGCTGATGACCTGATGAGCTCTTTCGCCGGTGTGACAGCTG 1239  
DB 1366 TGCACTGCGCAGGAGCTGCTGATGACCTGATGAGCTCTTTCGCCGGTGTGACAGCTG 1425  
QY 1240 GTCGCGAGAAATCACTGCTGTGAGGATCAAGATCTTGGGGGACTGTGTACTGTGTGTC 1299  
DB 1426 GCTGCGAGAAATCACTGCTGTGAGGATCAAGATCTTGGGGGACTGTGTACTGTGTGTC 1485  
QY 1300 GGCTCCGCGAGGCGCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1359  
DB 1486 GGCTCCGCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1345  
QY 1360 ATTGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1419  
DB 1546 ATTGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1605  
QY 1420 ATCCAGCGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1479  
DB 1606 ATTCAGCGGGCGGAGTACACTGCGGTGCTCTTGGTCTCAGGAAGTGGCAGTTCGAGTC 1665  
QY 1480 TGCTCCAAATGATGTGACCTTGGCCCAACACATGGAAGCAGAGCGGCTGGCGGCATC 1539  
DB 1666 TGCTCTAATGATGTGACCTTGGCCCAACACATGGAAGCAGAGCTGGCGGCGGCGGCG 1725  
QY 1540 CACATCACTCGGGCAACACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCA 1599  
DB 1726 CCAATCACCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1785  
QY 1600 GTTGGCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1659  
DB 1786 GGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1845  
QY 1660 GCAGCGCAAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1719  
DB 1846 TGACCCCAAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1905  
QY 1720 AACTCCATGGAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1779  
DB 1906 AACTCCATGGAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1965  
QY 1780 GACTCCAGGCGCTTCCGCGGAGATGGGCAATTTGATGATTTCCAGCAAGAGCAACCGGGCA 1837  
DB 1780 GACTCCAGGCGCTTCCGCGGAGATGGGCAATTTGATGATTTCCAGCAAGAGCAACCGGGCA 1837

Db 1956 GGAGGCAACAGGCTCCAGAGAGATGAAGCCATCGGCTTCGAAGAGACCCCAAGACAAAG 2025  
Qy 1838 -----CCCAAGATGCCCTGAACCCCTGAGGATGAGTGGATGAGTTCTCTGAGCGGTGCCATC 1893  
Db 2026 RACGCCAGGAAGTGCAGACCCCTGAGGATGAGTGGATGAATTTCTGGCGCGCCCAAT 2085  
Qy 1894 GATGCCCGAGCATTTGATCAGCTGCGGAAGAGCACATGTCGCGGGTTTTTGTCTACCTTC 1953  
Db 2086 GACGCCAGGAGCATGACAGAGTGGGTGCGGTCGAGACAGTCCGCAAGTTCTCTGACCTTC 2145  
Qy 1954 CAGAGAGAGGATTTGAGAAGAGTACTCCCGGAGGTGGATCCCGCTTCGGAGCCCTAC 2013  
Db 2146 AGGAGAGCTGACTTAGAAAAGAGTACTCCAGAGCAGTGGATGACCGATTCGGTGCCCTAC 2205  
Qy 2014 GTTGCTGTGCCCTGTGGTCTTCTGCTTCATCTCTCATCCACAGCTTCTAATTTCCCA 2073  
Db 2206 GTGGCATGTGCTCGTGTCTCTCTCTCTCATCTGCTTTGTCCAGATCACCATCGTACCC 2265  
Qy 2074 CACTCCACCCGTATGCTTTGGGATTTATGCCAGCATTTCTCTGCTGCTCTAATCACCCGTG 2133  
Db 2266 CACTCCGTGTTTCATGTTGAGTTTCTACTTGACCTGTTTCTCTGCTGCTGACGTTGGTGTA 2325  
Qy 2134 CTGATCTGTGCTGCTACTCTCTGTTGTTCTCTGTTCCCTAAGGCCCTGCAGAGTGTGCC 2193  
Db 2326 TTTGTGTCGTGATCTATTCTGCTGAGTCTTTCCCGGGCCCGCTCCAGAGCCCTTCG 2385  
Qy 2194 CCGACATTTGCCGTACGGGCACATAGCACCGAGTTGGATCTCTTTTCCGTCTGCTT 2253  
Db 2386 AGGAATCGTGGCTCCAGAACCAACAGACCCCTGGTTCGGGGTTCACCATCACCTG 2445  
Qy 2254 GTGTTTACTTCTGCAATTTGCCAATGTTACCTGTACCTTACCAACACCCCATACGGAGCTGT 2313  
Db 2446 GTGTTCTCTGCTGGCTTCTGCTCAACATGTTCTATGTTAACTCCGAGGACCTGTGGGGTGC 2505  
Qy 2314 GCAGCCGAGTCTGAATTTAACACCTCTGTCATCATCTGCTGCCACCT-----CGAG 2367  
Db 2506 CTGGCGGAGAGACAAACATCAGACACCGGGTCAACGGGTGCCACGCTGGCGGCGTGC 2565  
Qy 2368 CAGCTCAATTAATCTCTGCGGCTGGATCTCCCTCTGTGAGGGCACCATGCCACCTGC 2427  
Db 2566 GCGGCAACCTCAGCTGGCGAGCAGCAGGCTTCTCGGCACGCGCTTGCGCCAGCTGC 2625  
Qy 2428 AGCTTTCTGAGGTCTCATCGGGAACATGCTGCTGAGTCTCTTGGCCAGCTCTGTCTTC 2487  
Db 2626 AACTTTCCCGAGTACTTCACTACAGCTGCTGCTCAAGCTGCTGCGCTGCTGCTGCTGCTC 2685  
Qy 2488 CTGCATCAGCAGCATCGGGAAGTTGCCATGATCTTGTCTTGGGCTCATCTATTG 2547  
Db 2686 CTGCAGATCAGCTGCATCGGGAAGTGTGCTCATGCTGGCCATGAGCTCATATA---C 2742  
Qy 2548 GTGCTGCTTCTGCTGGGTCCCGGAGCCGCTCTTTGACAACTATGACTACTGCTTGGC 2607  
Db 2743 GTGCTCGCTGAGGTGCCCGGGTCACTGTTTGAACAGCTGACCTGCTGTCCACC 2802  
Qy 2608 GTCCATGCTTGGCTTCTTCAATGAGACCTTTGATGGCTGGAGCTGTCCAGCTGCAGGG 2667  
Db 2803 GCCAACGCCATAGACTTCAACAACAACAACGCGGACCTCGCAGTGTGCTGAGCACGCGACC 2862  
Qy 2668 AGGTGGCGCTCAATATATGACCCCTCTGATCTCTGCTGGTGTGGCTGCGCGCTGAT 2727  
Db 2863 AAGTGGCGCTGAGGTGCTGACGCCCATCATCTCCGCTCTGCTGCTGCGCTGTAC 2922  
Qy 2728 CTGCATGCTACAGAGTGGAAATGCACTCCCGCCCTAACTTCTCTGGAATACTACAGCA 2787  
Db 2923 CTGCATGCCAGCAAGTGGAGTCCACCGCCGCTCGACTTCTCTGGAATACTGAGGCC 2982  
Qy 2788 ACAGGGAAAGAGGAGATGGAGAGCTACAGCATACACCCGAGGCTGCTGCATAAC 2847  
Db 2983 ACAGGAGAGAGGAGATGGAGAGCTGACAGGCTTACACCCGCGCTGCTGCGACAAAC 3042  
Qy 2848 ATTCTGCCAAAGGAGCTGGCGGCCACTTCTGCGCGGAGCGCGCAATGTAACCTC 2907  
Db 3043 ATCTGTGCCAAGGAGCTGGCTGCCACTTCTTGGCCCTGAGCGACGCAAGCAGAGCTC 3102

Qy 2908 TACTATCAGTCTGTGAGTGTGTGCTGTTATGTTTGCCTCCATTTGCCCAACTTCTCTGAG 2967  
Db 3103 TACTACCAAGTCTGCGAGTGTGCTGTCATGTTGCGCTCCATGCGCAACTTCTCCGAG 3162  
Qy 2968 TTTATGTGGAGCTGGAGGCAACAATGAGGTTGCCGAGTGCCTGCGGCTGCTCAACAG 3027  
Db 3163 TTTACGTGGAGCTTTGAGGCCAACAATGAGGTTGCTCGAGTGCCTGCGGCTCTCAATGAG 3222  
Qy 3028 ATCATCGTCTGATTTGATGAGATATCAGCGAGGAGCGGTTCCGCGACGCTGGAAGAATC 3087  
Db 3223 ATCATCGTCTGATTTGATGAGATCATCAGCGAGGATCGGTTTCAAGCAGCTGGAGAATC 3282  
Qy 3088 AAGCAGTGTGTAGCACCTACATGGCTGCCTCAGGCTGGAACGCGCAGCACCTACGATCAG 3147  
Db 3283 AAGACCATTTGCGAGCACCTACATGGCGCTCAGGCTCAATGACTCTACATACGACAAG 3342  
Qy 3148 GTGGCGCTCTCCACATCACCTGGCTGGCTGACTACGCCATGGCGCTCATGAGCAGATG 3207  
Db 3343 GTGGCAAGACCCACATCAAAAGCCCTGGCTGACTTGGCATGAAGCTCATGGACCAATG 3402  
Qy 3208 AAGCACATCAATGAGCACTCTTCAACAATTTCCAGATGAAGATTGGGCTGAACATGGC 3267  
Db 3403 AAGTACATCAATGAGCACTCTTCAACAACCTTCCAGATGAAGATGGGCTCAACATCGC 3462  
Qy 3268 CCAGTCTGGCAGGTGTCTATCGGGCTCGAAGCCACACAGTATGACATCTGGGGGAACA 3327  
Db 3463 CCGCTGGTGGCGGGTGTATCGGGCTCGCAAGCTCAGTACGACATCTGGGGCAATAG 3522  
Qy 3328 GTGAATGCTCTAGTCTGATGAGACAGCAGGGGTGCCCGACCGAATCCAGGTGACACG 3387  
Db 3523 GTGAATGTGGCAGCGCATGGACAGCACCGCGCTGCGGACCGCATCCAGTCAACACG 3582  
Qy 3388 GACCTGTACAGGTCTAGCTGCCAAGGCTACCAAGCTGAGTGTGCGAGGGTGTCTCAAG 3447  
Db 3583 GACATGTACAGGTGTGGCTGCGCAACAGTACCAAGCTGAGTGTGAGGGTGTGTCTCAAG 3642  
Qy 3448 GTGAAGGCAAGGGGAGATGACCACTACTTCTCAATGGGGGCC 3495  
Db 3643 GTCAAGGCAAGGGAGATGATGACCTACTTCTCAACGGTGGGCC 3690

## RESULT 13

AAA53922

ID AAA53922 standard; cDNA; 3924 BP.

XX AC AAA53922;

XX DT 03-JAN-2001 (first entry)

XX DE Type V adenylyl cyclase coding sequence.

XX KW Adenylyl cyclase; type I; type II; recombinant; enzyme; CAMP;

XX KW cyclic AMP; adenosine monophosphate; screening; stimulation;

XX KW inhibition; treatment; cholera; pituitary tumour; heart failure;

XX KW ischaemia; endocrine disorder; cell necrosis;

XX KW pseudohypoparathyroidism; endocrine deficiency; human; ss.

XX OS Homo sapiens.

XX FH Key

XX FT CDS Location/Qualifiers

XX FT 3..3329

XX FT /\*tag= a

XX FT /product= Type V adenylyl cyclase

XX PN US6107076-A.

XX PD 22-AUG-2000.

XX PF 04-OCT-1996; 96US-0726214.

XX PR 04-OCT-1995; 95US-0005498.



(TEXA ) UNIV TEXAS SYSTEM.

Gilman AG, Tanq W;

WPI: 2000-578539/54.

P-PSDB; AAB02009.

Novel soluble mammalian polypeptide composition comprising adenylyl cyclase activity for screening stimulators and inhibitors of adenylyl cyclase, is activated by Gsalpha

Disclosure; Columns 65-70; 73pp; English.

A recombinant Adenylyl cyclase is described which lacks membrane bound domains. Separation and purification of the recombinant enzyme is much easier compared with wild type enzymes and the recombinant enzyme is more stable than the wild type enzyme which allows easier screening of compounds that stimulate and inhibit Adenylyl cyclase activity. The recombinant adenylyl cyclase comprises a chimera of adenylyl cyclase C<sub>1</sub> and C<sub>2</sub> domains linked covalently. The domains may be linked by a linker peptide. The recombinant adenylyl cyclase is useful for screening inhibitors and stimulators of adenylyl cyclase activity. Inhibitors of the enzyme are useful for treating cholera, pituitary tumors, heart failure, ischaemia, endocrine disorders and cell necrosis. Stimulators of adenylyl cyclase are useful for treating pseudohypoparathyroidism and other endocrine deficiencies.

Sequence 3924 BP; 860 A; 1103 C; 1110 G; 851 T; 0 other;

Query Match 46.4%; Score 1648.2; DB 21; Length 3924;  
Best Local Similarity 71.4%; Pred. No. 0;  
Matches 2265; Conservative 0; Mismatches 873; Indels 33; Gaps

345	QY	GCATCCTGCTGCGCGCGTTTGGTCAGAGTGTTCAGTGAAGCACTTCCGTTGTGGCCAA	404
128	Db	GGCGCGCTGCTGCTGCGCCCTTGGTCAGATATTCGCTTAAGAAGCTCCCGTCGACAA	187
405	QY	GCTGGAGCGCTGTACACGGGTACTTTTTCAGATGAACACAGACAGCCTGACGCTGT	464
188	Db	ACTGGAGCGTGTACACGGCTATTCTTCGCGCTGAACACAGACAGCCTACCAATGT	247
465	QY	GGTGGCGGTGCTGGTCTGCTACACGGCTGCTGCTGGCTTTCGAAGCGCACCCGCCG	524
248	Db	CATGGCGGTGCTGGTCTGCTGGCTGCTGCTCATGCTCGCTTTCACGCGCACGGCCCC	307
525	QY	CCCTCAGCCTGCCTATGTGGCACTGTGGCTGTGCGCGCGCCCTGTTGTGGGGCTCAT	584
308	Db	GTCCAAGTAGTCTACCTGGCCGTGTGGCAGCTGCTGTGGCGTGATCCTTATCATNGC	367
585	QY	GTTGGTGTGAACCGGCATAGCTTCCGCGCAGGACTCCATGTGGTGGTGGTGAATACTGT	644
368	Db	TGTCCTTGCACCGTGCAGCCTTCCACAGGACACATAGGGCCTGGCCGTGCTATGCGGT	427
645	QY	GCTGGGCATCTCGCGCGCAGTCAGGTGCGGGCGCTTTCGACGACAGACCCGCGACGCC	704
428	Db	CATTGCAGTGGTCTGCGCGTCAGGTAGTGGCCGTGTTGCTGCCACAGCCAGCAGCGC	487
705	QY	CTCTGGGGCCTCTGTTGCCCTGTGTTCTTTGTATACATCGCATACACGTCCTCCTCCCAT	764
488	Db	CTCGAGGGCATCTGTGGACCGCTTCTTCATCTATAGCATACACCTGCTGCTGT	547
765	QY	CCGCATGGCGGTGCGGTCTCCTCAGCGCCTGGGCGTCTCCACCTTGCAATTTGATCTGGC	824
548	Db	GCACATGAGGGCTGCGGTGCTCAGCGGGGTGCTTGTGCGGTCTCCATTTGGCCATCTC	607
825	QY	CTGGCAACTTAAACCGTGGTGATCGCTTCCTCTGGAAAGCAGCTCGGTGCCAATGTGCTGT	884
608	Db	TCTGCACACCAAGCGCCAGGACCATGTTCTGCTGAACAGCTGTCTCCACAGTCTCAT	667
885	QY	GTTCCTCTGCACAAGCTCATTTAGCATCTGACACACTATCCAGCAGAGGTGTCTCAGCG	944
668	Db	CTTCTCTGCACAACATGTTGGTGTGTCACCTACTACCCAGCGAGGTCTCCAGAG	727

QY 2010 CTACGTTGCCGTGGCCCTGTTGGTCTTCTGCTTTCATCGCTTCATCCAGCTTCTTAATTT 2069  
Db 1802 CTATGTGGCCGTGCGCTGCTGTTGTTTCTCTTCATCTGCTTGTGCCAGATCACCATGTT 1861  
QY 2070 CCCACATCCACCCTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGCTGCTTAATCAC 2129  
Db 1862 GCCCAGCTCCCTGTTTCATGCTGAGCTTCTACCTGTCGCTGTTTCTGCTGCTGCTGCTGCT 1921  
QY 2130 CGTGCTGATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2189  
Db 1922 GGTGTTTATATCTGTGATCTAGCGCTGTGTAAGCTCTTCCCTACTCCCTCCGCGACACT 1981  
QY 2190 GTCCCGCAGCATGTCCTGCTCACGGGCACATAGCACCCGAGTGTGGCATCTTTTCCGTCCT 2249  
Db 1982 CTCAGGAAGATAGTGCATCCAAAGAACAGACACCTGCTGCGGGTGTTCACCATCAC 2041  
QY 2250 GCTGTGTTTACTTCTGCCATGCCAATGTTACCTGTTAACACACCCCATACAGGAG 2309  
Db 2042 CTTGTGTTTCTCTCGGCTTTTGTCAACATGTTCTATGTCGAACCTCTAAGAACCTGCTGGG 2101  
QY 2310 CTGTCAGCCGGATGCTGAATTTAACACCTGCTGACATCACTGCTGCCACCTGCAGCA 2369  
Db 2102 TTGCTGCGAGGAGACACATCACCGTGAACAGGTGAACGATGTCATGTGATGA 2161  
QY 2370 G-----CTCAATTAATCTCTGGGCTGGATGCTCTCCCTGTGTGAGGCGACCATGCCAC 2423  
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Db 2576 GCGCACAGAGAGAGGAGATGAGGAGCTGAGGAGCTACACCGGCGCTGCTGCA 2635  
QY 2844 TAACATCTGCCAGGACGTGGGCGCCACTTCTGCGCGGAGCGCGCAATGATGA 2903  
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QY 3084 GATCAAGAGATTTGGTAGACCTTACATGGCTGCCTCAGGGCTGAACGCCAGCCTACGA 3143

Db 2876 GATCAAGACCATAGTAGTACCTACATGGCTGCTTGGCTCAACGACTCCACCTATGA 2935  
QY 3144 TCAGGTGGGCGCTCCACATCACTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3203  
Db 2936 CAAGCAGGCAAGACCCACATCAAGGCTTTCGACAGCTTCGCCATGAAGCTGATGGACCA 2995  
QY 3204 GATGAAGCACATCAATGAGCACTCTTCAACAATTTCCAGATGAAGATTGGCTCAACAT 3263  
Db 2996 AATGAAGTACATCAATGAGCACTCTTCAACAATTTCCAGATGAAGATCGGGCTTAACAT 3055  
QY 3264 GGGCCAGTCTGTCAGTGTATGCGGGCTCGGAAGCCACAGTATGATCATCTTGGGGAA 3323  
Db 3056 TGGACCTCTAGTGGCTGGGCTATTGGGCTCGCAAGCTCAGTATGATCATCTGCGGCAA 3115  
QY 3324 CACAGTGAATCTCTAGTGTATGAGCAGCAGCGGGGTCCCCACCAANTCCAGGTGAC 3383  
Db 3116 TACAGTAAATGTGGCCAGCCGATGAGCAGCAGTGGGTGCTGACCCGATCCAGGTTAC 3175  
QY 3384 CACGACCTGTACCAAGTCTTAGCTGCCAAGGGCTACCAGCTGGAGTGTGAGGGGTGGT 3443  
Db 3176 TACAGATATGTACCAAGTGTGCGGCCCAACACATACAGCTGGAGTGGCGGGTGGT 3235  
QY 3444 CAAGGTGAAGGCAAGGGGAGATGACCACTTACTTCTCAATGGGGGCC 3494  
Db 3236 CAAGGTCAAGGCAAGGGTGAGATGATGACCTACTTCTCAATGAGGGGCC 3286  
RESULT 14  
AAD28058  
ID AAD28058 standard; cdna; 3137 BP.  
XX  
AC AAD28058;  
XX  
DT 22-APR-2002 (first entry)  
XX  
DE Human adenyl and guanylyl cyclase (ADGUC)-2 cdna.  
XX  
KW Human; adenyl and guanylyl cyclase; ADGUC-2; cardiovascular disorder;  
KW angina pectoris; myocardial infarction; vision disorder; keratitis;  
KW iritis; cataract; neurological disorder; epilepsy; Alzheimer's disease;  
KW Pick's disease; stroke; mental disorder; mood and anxiety disorder;  
KW reproductive disorder; infertility; endometriosis; impotence; asthma;  
KW smooth muscle disorder; migraine; bacterial infection; gene therapy;  
KW transgenic animal; vaccine; enzyme; ss.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..2514  
FT FT /\*tag= a  
FT FT /product= "Human ADGUC-2 protein"  
XX  
PN WO200202757-A2.  
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PD 10-JAN-2002.  
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PF 26-JUN-2001; 2001WO-US20491.  
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PR 29-JUN-2000; 2000US-215476P.  
PR 04-AUG-2000; 2000US-223545P.  
PR 31-AUG-2000; 2000US-229876P.  
PR 22-SEP-2000; 2000US-234838P.  
PR 29-SEP-2000; 2000US-236483P.  
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PA (INCY-) INCYTE GENOMICS INC.  
XX  
PI Gandhi AR, Tribouley C, Ding L, Lu DAM, Lee EA, Yue H, Yang J;  
PI Baughn MR, Thornton M, Yao MG, Walia NK, Tang YT, Elliott VS;  
PI Lu Y;  
XX  
XX WPI; 2002-154740/20.  
DR P-PSDB; AAE17130.  
DR



xx Novel human adenylyl and guanylyl cyclases and polynucleotides encoding  
pt the cyclases, useful for treating, diagnosing or preventing  
pt cardiovascular, neurological, vision, reproduction and smooth muscle  
pt disorders - pt

PS Claim 5; Page 112-113; 116pp; English.

The invention relates to human adenyl and guanylyl cyclases (ADGUC) preferably ADGUC5 and nucleic acid molecules encoding such polypeptides. ADGUC sequences are useful in the diagnosis, prevention and treatment of cardiovascular disorders (e.g. angina pectoris, myocardial infarction, ischaemic heart disease, hypertension and atherosclerosis), vision disorders (e.g. keratoconjunctivitis sicca, keratitis, iritis, cataract), neurological disorders (e.g. epilepsy, Alzheimer's disease, Pick's disease, Huntington's disease, dementia, Parkinson's disease, Creutzfeldt-Jakob disease, stroke, schizophrenia, mental disorders including mood and anxiety and prion diseases including kuru), reproductive disorders (e.g. infertility, endometriosis, impotence, uterine fibroid and gynaecomastia), smooth muscle disorders (e.g. arrhythmias, asthma and migraine) and bacterial infections. ADGUC polynucleotides are useful for creating knock-in humanised animals or transgenic animals to model human diseases. They are useful in somatic or germline gene therapy. ADGUC polynucleotides are also useful for detecting differences in the chromosomal location due to translocation, inversion, etc. among normal, carrier or affected individuals. ADGUC polypeptides are useful in a number of drug screening techniques and in vaccines. The present sequence is human ADGUC-2 CDNA.

Sequence 3137 BP: 553 A: 973 C: 1044 G: 567 T: 0 other:

Query Match 23.8%; Score 843; DB 24; Length 3137;  
Best Local Similarity 68.4%; Pred. NO. 7.6e-195;  
Matches 1286; Conservative 0; Mismatches 500; Indels 93; Gaps 5;

QY 214 CGAGGGCGGCCAGGCAAGGCAAGGAGCTGGGGCTGCGGGCAGTGGCCCTGGGCTTC 273

db 712 CGCGGGCAAGGGCGCGCGCGCGCTGGAGGCCGCCGCTCGAGGGCGGCGAG 771

QY 274 GAGGATACCGAGGTGACAACGACAGCGGGCGGGCTGAGGTGGCGCCGACGCGGTG 333

Db 772 GGGTCCGGGGATGGCGGGCAGCTCGGGGCACTCGGGGCTCGGGGCGCGGGCGCGGTG 831

OV 334 CCCAGGAGTGGGGCGATCCTGCTGGCGCCGTTTGGTGCAGGTGTCCAGTCCGAGCAGTTC 393

db 832 C--TGTCCCTGGGGGGCTGCTGGCTGGCGTTGCTGCAGATATTCCGTCACAAGAGTTC 888

394 CGTTGGGCCAAGCTGGAGGGCCTGTACCAAGCGTACTTTTCCAGATGAACCAAGCAGCACC 453

db 889 CCGTCGGACAAACTGGGAGCGCGCTCTACACCGCTACTTCTTCCCGCTCCACCGCTCC 948

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Db	1180	CTGCTGCGCGTGCGCATGTCGGGCGCGAGTGCATCAGCGGGGTGCTCTCTGTCGGCCCTCCAC	1233
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QY	934	GTGTCACGCGCCAGSCCTTTTCAGGAGACCCGCAGTATACATCCAGGCCCGGCTCCACCTG	993
Db	1360	GTCTCCAGAGACAGCTTTTCAGGAGACCCGAGAGTGCATCCAGGCGGGCTCCACTCG	1419
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Db	1420	CAGGGGAGAACGACGACGAGNACGGCTCTGCTGTCTGTCCTTCCCGTCATGTTGCC	1479
QY	1054	ATGGAGATGAAGAAGACATATCAACACAAAAAAGAAGA--CATGTTCACAAGATCTAC	1110
Db	1480	ATGGAGATGAAGAAGACATATCAACGCAAGCAGGAGGATATGATGTTCATTAAGATTAC	1539
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Db	1540	ATCCAGAAACATGACAACTGAGCATCTCTGTTGCTGACATCGAGGGCTTCACCAAGCTG	1599
QY	1171	GCATCCAGTGCACCTCGCAGGAGCTGTCATGACCTGAAATGAGCTCTTTTGCCCGGTTT	1230
Db	1600	CGTCCCATGTGCACTGCACAGNACTGTTCATGACCTCAAGAGCTCTTCGCCCGCTTT	1659
QY	1231	GACAAGCTGGCTGCGGGAATCACTGCTTGAGGATCAAGATCTTTGGGGACTGTTACTAC	1290
Db	1660	GACAAGCTGGCCGACAGAATCACTGTTTACGTATTAAGATCTTTGGGGAATGTTATTAC	1719
QY	1291	TGTGTGTCAAGGCTGCCGAGGCCGGCCGACCATGCCCCACTGCTGTGTGGAATGGGG	1350
Db	1720	TGGGTCTCGGGGCTGCTCGAAGCAAGGGCTGACACGCCCCACTGCTGTGTGGAGATGGC	1779
QY	1351	GTAGACATGATTGAGGCCATCTCGCTGGTACGTGAGGTGACAGGTGTCAATGTCAACATG	1410
Db	1780	ATGGACATGATGAGGCCATCTGTTGTTCCGGGAGGTGACAGGGGTGAACGTGAACATG	1839
QY	1411	CGCGTGGGCATCCACAGCGCGGCGCTGCACTCGCGCGCTCTTGCTTCCGGAATGGCAG	1470
Db	1840	CGTGTGGAAATTCACAGCGGCGAGTACACTCGCGTGTCTTGGTCTCAGGAAGTGGCAG	1899
QY	1471	TTGATGTGTGTTCCAAATGATGTACCTTGGCCACACCATGGAAGCAGGAAGCGGGCT	1530
Db	1900	TTCCAGCTGTGGTCTAACGATGTCAGCTTAGCCACCAACACATGAGGGCTTGGCGCAAGCA	1959
QY	1531	GGCGGATCCACATCACTCGGCACACATGCACTAGTACCTGAACGGGACTACGAAGTGGAG	1590
Db	1960	GGAGCATCCACATCAACAAAGGCTACATCAACTCACTGAATGGGACTACGAGGTGGAG	2019
QY	1591	CCAGCGCGTGTGGCAAGCGCACCGGTACCTCAAGGAGCAGCACATTTGACACTTTCCTC	1650
Db	2020	CCAGGCTGTGGGGCGAGCGCAACGCCATCTCAAGGACACAGTATCGACACCTTCCCTC	2079
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Db	2080	ATCCTCGGCTGCAACCAGAAAGGGGAAGAAGAGAGAGGCCATGATCGCCAAGATGAACCGC	2139
QY	1711	ACTCGGGCCAACTCCATGAAAGGGTGTATGCCCGCATGGGTTCCTGTGATGTCCTCTCC	1770
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QY	1771	-----CGGACCAAGGACTCCAAGGCTTTCCGCCAGATGGGCATTTGATGATTC	1818
Db	2200	AACCACCTGGGTGCAACCAAGTGTCCAGAGAGATGAAGCGGATGGGCTTTGAAGACCCC	2259
QY	1819	AGCAAGACACACCGGGGCAACCAAGATGCCCTGAAACCTTGAGATGAGGTGGATGATTC	1878
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QY 1096 TTCCACAAGATCTACATACAGAAGCATGACAATGTGAGCATCTGTTTGGCAGACATTGAG 1155  
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QY 1156 GGCTTCAACAGCCTGGCATCCCATGTCGACTGCGCAGGAGTGTCATGACCCCTGAATGAG 1215  
Db 1039 GGCTTCAACAGCCTGGCGTCACAGTGCACGGCCAGGAGTGTGAAACTCCTCAATGAG 1098  
QY 1216 CTCTTTGCCGGTTTACAGAGCTGGCTGGGAGAAATCACTGCTGAGGATCAGATCTTG 1275  
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QY 1336 TGTGTGGAGATGGGGTAGACATGATTGAGGCCATCTCGGTGGTAGCTGAGGTGACAGGT 1395  
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QY 1636 ATTGAGACTTTCCTCATCTCGGGCGCCAGCCAGAAACGGAAGAGGAAAGGCATGCTG 1695  
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QY 1756 GATCGTGCCTCTCCCGGACCAAGGACTCCAAGGCCCTTCGCGCAGATGGCATGTATGAT 1815  
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QY 1816 TCCAGAAAGACAAACCGGGGCACCCAAAGATGCCCTGAACCTGAGGATGAGTGGATGAG 1875  
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QY 1876 TTCTGAGCGGTGCCATCGATGCCCGCAGATTTGATCAGTGGGGAAGACCATGTGGCG 1935  
Db 1743 ACTCAGAAAACCGCTGCTCTTCTCTACA----- 1770  
QY 1936 CGGTTTTTGTCACTTCCAGAGAGGATTTTGAGAAGTACTCCCGGAAGTGGAT 1995  
Db 1771 AAGGTTGTCAAACCAACCCCGCAGACAGTGTCAACAGGTACATCGGCGCCCTCCGGA 1830  
QY 1996 CCGCGCTCGGAGCCTACGTTGCGCTGCGCTGTGGCTTCTGCTTTCATCTCTCTTCATC 2055  
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QY 2056 CAGCTTCTAATTTTCCACACATCCACCTGATGCTTTGGGATTTATGCCAGCATCTTCCTG 2115  
Db 1888 CAAGCTGAGCGAGAGGCAAGTACCACAGCTTCAGGACGAGTATTTTACCAGCGCGGTG 1947  
QY 2116 CTGCTCTAATCACCGTGTGATCTGCTGTGTGATCTCTCTGTGGTGTCTGTGTCCTTAAG 2175  
Db 1948 GTTCTGGCTCTCATTTCTGGCCGCTTATTTCCGGCCTTGTCTACCTTCTAATAATCCACAG 2007

QY 2176 GCCTGCAACGTCGTCTCCCGCAGCATTTGCTCGCTCAAGGCGCATAGCACCCGAGTTGGC 2235  
Db 2008 AGTGTGGCTGCTCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2067  
QY 2236 ATCTTTTCOGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2295  
Db 2068 TACCTACACATCACCCGGT-----CCAGTGTGTTTCCAGGGTGTGCTGACCATCC 2116  
QY 2296 ACCCCATACGAGAGCTGTGCGAGCCCGGATGCTGAATTTAACACCTGCTGACATCACTGCC 2355  
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QY 2356 TGCCACCTGCAGCAGCTCAATTAATCTCTGCGGCTGGATGCTCCCTGCTGAGAGCACC 2415  
Db 2176 -----TGTGTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2227  
QY 2416 ATGCCACCTGACGCTTTCCTGAGGTGTCATCGGAACATGCTGCTGCTGCTGCTGCTGCTG 2475  
Db 2228 TGTGTGCTGCTGCTTCTGCGGGCGGAGCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2286  
QY 2476 AGCTCTGCTTCTCTGCACATCAGCAGCATCGGGAAGTTGGCCATGATCTTTGCTTGGGG 2535  
Db 2287 GCGCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2346  
QY 2536 CTCACTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2595  
Db 2347 GTCTCTCTTTCGCAAAATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2406  
QY 2596 CTACTGCTGGCGTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2655  
Db 2407 CTGGAGCTCAGCG-----GGTACACGAAGGCGCATG 2436  
QY 2656 CAGCTGCGAGGAGGGTGGCCCTCAAAATATATGACCCCTGTGATTTGCTGGTGTGCTG 2715  
Db 2437 GGGCGGCTGCCATCTCAGGGCGCAGCTGCGAGCGGATGATGCCATCTCTGCTATTCTCG 2496  
QY 2716 CTGGCGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2775  
Db 2497 TGCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2556  
QY 2776 AAATACAGCAACAGGGGAAAAGAGAGATGAGGAGCTACAGGCATACACCGGAGG 2835  
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QY 2836 CTGCTCATTAACATTTGCCCAGGAGCTGGCGGCCACTTCTGCGCCGGAGCGCGC 2895  
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QY 2896 AATGATGAACCTCTACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2955  
Db 2677 AACATGACCTGTATTACCACTCATCTCGCAGTGGGGTCTGCTGCTGCTGCTGCTGCTG 2736  
QY 2956 AACTTCTCTGAGTCTATGCTGAGCTGGAGGCAACAAATGAGGGTGGCGGAGTGGCTGCGG 3015  
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QY 3076 CTGGAAGAGATCAAGAGATTTGGTAGCCCTACATGCTGCTGCTGCTGCTGCTGCTGCTG 3132  
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QY 3133 -----AGCACCTTACGATCAGGTGGCGCGCTCCACATCACTGCTGCTGCTGCTGCTG 3186  
Db 2917 GCTGGGCAAGGCTAAGAAGTGCATCTCTCCACCTCAGCAGCTTGGCAGATTTTGGC 2976  
QY 3187 ATCGGCTCATGAGCAGATGAAGCAGATCAATGAGCAGCTCTTCAACATTTCCAGATG 3246  
Db 2977 ATCGAGATGTTGATGCTGCTGATGAGATCACTACAGCTCTTATAACGACTTTTGTGCTC 3036



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2003, 22:03:11 ; Search time 86,927 Seconds  
(without alignments)  
12520.796 Million cell updates/sec

Title: US-09-750-240-5

Perfect score: 3549

Sequence: 1 atgtcatgttttagtgccct.....aagggaaccaagtgggcact 3549

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA.\*

- 1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*
- 2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3549	100.0	3549	4 US-09-008-097-5	Sequence 5, Appli
2	3478.4	98.0	4942	4 US-09-474-076-1	Sequence 1, Appli
3	2990.4	84.3	4046	1 US-07-793-961A-1	Sequence 1, Appli
4	2990.4	84.3	4046	1 US-08-240-357-1	Sequence 1, Appli
5	2751.2	77.5	4131	3 US-08-726-214-11	Sequence 11, Appli
6	1808.4	51.0	1812	4 US-09-008-097-3	Sequence 3, Appli
7	1703.4	48.0	4523	4 US-09-473-716-1	Sequence 1, Appli
8	1648.2	46.4	3924	3 US-08-726-214-9	Sequence 9, Appli
9	595	16.8	3978	3 US-08-726-214-1	Sequence 1, Appli
10	505.2	14.2	3518	4 US-09-412-210-2	Sequence 2, Appli
11	463.6	13.1	4601	3 US-08-726-214-15	Sequence 15, Appli
12	459	12.9	4008	3 US-08-307-896-5	Sequence 5, Appli
13	459	12.9	4008	3 US-08-726-214-3	Sequence 3, Appli
14	459	12.9	4008	5 PCT-US95-11808-5	Sequence 5, Appli
15	441.6	12.4	4533	3 US-08-726-214-5	Sequence 5, Appli
16	433	12.2	5199	3 US-08-726-214-13	Sequence 13, Appli
17	428	12.1	3357	3 US-08-726-214-7	Sequence 7, Appli
18	393.2	11.1	1652	3 US-08-726-214-17	Sequence 17, Appli
19	295.2	8.3	314	4 US-09-008-097-1	Sequence 1, Appli
20	288.2	8.1	2092	3 US-08-307-896-6	Sequence 6, Appli
21	288.2	8.1	2092	5 PCT-US95-11808-6	Sequence 6, Appli
22	216.8	6.1	4473	3 US-08-894-173-1	Sequence 1, Appli
23	216.8	6.1	4473	4 US-09-398-193-1	Sequence 1, Appli
24	209.4	5.9	4985	4 US-09-473-717-1	Sequence 1, Appli
25	207.8	5.9	5515	4 US-09-398-193-98	Sequence 98, Appli
26	73	2.1	7218	1 US-08-232-463-14	Sequence 14, Appli
27	64.4	1.8	1259	2 US-08-997-080-123	Sequence 123, App

28	64.4	1.8	1259	2 US-08-997-362-123	Sequence 123, App
29	64.4	1.8	1259	4 US-09-095-855-123	Sequence 123, App
30	64.4	1.8	1259	4 US-09-324-542-123	Sequence 123, App
31	64.4	1.8	1259	4 US-09-205-426-123	Sequence 123, App
32	64.4	1.8	2013	2 US-08-997-362-176	Sequence 176, App
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42	54.4	1.5	3243	2 US-08-331-193A-44	Sequence 44, Appli
43	54.4	1.5	3243	2 US-08-486-273A-44	Sequence 44, Appli
44	54.4	1.5	3243	3 US-08-480-474-44	Sequence 44, Appli
45	54.4	1.5	3243	3 US-08-940-086A-44	Sequence 44, Appli

ALIGNMENTS

RESULT 1  
US-09-008-097-5  
; Sequence 5, Application US/09008097  
; Patent No. 6306830  
; GENERAL INFORMATION:  
; APPLICANT: Hammond, H. Kirk  
; APPLICANT: Insel, Paul A.  
; APPLICANT: Ping, Peipei  
; APPLICANT: Post, Steven R.  
; APPLICANT: Gao, Meihua  
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE  
; TITLE OF INVENTION: HEART FAILURE  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/008,097  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dylan, Tyler M  
; REGISTRATION NUMBER: 37,612  
; REFERENCE/DOCKET NUMBER: 22000-20567.21  
; TELEPHONE: 650-813-5600  
; TELEFAX: 650-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3549 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Coding Sequence  
; LOCATION: 1...3501  
; OTHER INFORMATION:

US-09-008-097-5

Query Match		100.0%;	Score 3549;	DB 4;	Length 3549;		
Best Local Similarity		100.0%;	Pred. No. 0;				
Matches 3549;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
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QY	61	GAACGCAATGGCAGAAAGCGTTCGGCGCGCTGGCACTCGGGCAGGTGGCTTCGACG	120				
DB	61	GAACGCAATGGCAGAAAGCGTTCGGCGCGCTGGCACTCGGGCAGGTGGCTTCGACG	120				
QY	121	CCCCGCTATATAGCTGCCCTCCGGGATGACAGACCCACGCCCCCCTGCGGGGCC	180				
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QY	181	CTCGGTCGCCCTGGCAGGATGAGCCCTTCATCCGAGGGCGGCCAGGCAAGGCAAG	240				
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QY	241	GAGCTGGGGCTCGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACAAACGACG	300				
DB	241	GAGCTGGGGCTCGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACAAACGACG	300				
QY	301	GCGGGACGGCTGAGTGGCGCGCCGACGCGGTGCCAGGAGTGGCGATCCTGCTGGCG	360				
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QY	841	GGTGATGCCCTTCTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTCTCTGCACCAAC	900				
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Db	1201	ATGACCTCTGAATGAGCTCTTGGCCCGGTTTGACAAAGCTGGCTGCGAGAAATCACTGCCTG	1260
Qy	1261	AGGATCAAGATCTTGGGGGACTGTTACTACTGTGTGTCAGGGCTGCCGAGGCCCGGCC	1320
Db	1261	AGGATCAAGATCTTGGGGGACTGTTACTACTGTGTGTCAGGGCTGCCGAGGCCCGGCC	1320
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RESULT 2

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US-09-474-076-1
; Sequence 1, Application US/09474076
; Patent No. 6465237
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, James E.
; APPLICANT: COR Therapeutics, Inc.
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
; FILE REFERENCE: 44481-5028-01-US
; CURRENT APPLICATION NUMBER: US/09/474,076
; CURRENT FILING DATE: 1999-12-12
; PRIOR APPLICATION NUMBER: PCT/US98/13694
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/070,904
; PRIOR FILING DATE: 1997-07-01
; PRIOR APPLICATION NUMBER: 08/886,550
; PRIOR FILING DATE: 1997-07-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4942
; TYPE: DNA
; ORGANISM: human type VI adenylyl cyclase
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (145)..(3648)
US-09-474-076-1
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Query Match 98.0%; Score 3478.4; DB 4; Length 4942;  
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Db 2365 C A T A G C A C C G A G T T G G C A T C T T T T C C G T C C T G C T T G T T A C T T C T C C C A T T G C C A C 2424  
Qy 2278 A T G T T C A C C T G T A A C A C A C C C C A T A C G A G C T G T G C A G C C C G A T G C T G A A T T T A C A 2337  
Db 2425 A T G T T C A C C T G T A A C A C A C C C C A T A C G A G C T G T G C A G C C C G A T G C T G A A T T T A C A 2484  
Qy 2338 C C T G C T G A C A T C A C T G C C T G C C A C C T G C A G C A G C A A T T A C T C T C T G G C C T G G A T G C T 2397



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Db 2605 CTGCTGAGTCTCTTGGGCCAGCTCTGTCTTCTGTCACATCAGCAGCATCGGGAAGTTGGCC 2664  
QY 2518 ATGATCTTTCTTGTGGGCTCACTATTGTTGCTGCTTCTGCTGGTCCGCCAGCCGCC 2577  
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QY 2638 TTTGATGGGCTGAGCTTCCAGCTGACGAGGAGGTGGCCCTCAAAATATATGACCCCTGTG 2697  
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QY 2758 CGCTAAACTTCTCTGGAACCTACAGGCAACAGGGGAAAGAGGAGATGGAGGAGCTA 2817  
Db 2905 CGCTAGACTTCTCTGGAACCTACAGGCAACAGGGGAAAGAGGAGATGGAGGAGCTA 2964  
QY 2818 CAGCATACACCGGAGGCTGTGCTATACATTAACATTTGCCCCAAGGACGTTGGGCCCTTC 2877  
Db 2965 CAGCATACACCGGAGGCTGTGCTATACATTAACATTTGCCCCAAGGACGTTGGGCCCTTC 3024  
QY 2878 CTGGCCCGGAGGCGCCCATGATGATGAATCTACTATCAGTCGTGTGAGTGTGGCTGTT 2937  
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QY 3058 GAGGAGCGGTTCCGGCAGCTGGAAAGATCAAGACGATTCGTAGCAGCTACATGGCTGCC 3117  
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QY 3418 TACCAGTGGAGTGTGAGGGGTGTCAAGGTGAAGGGCAAGGGGAGATGACCACTAC 3477  
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RESULT 3  
US-07-793-961A-1  
; Sequence 1, Application US/07793961A  
; Patent No. 5334521  
; GENERAL INFORMATION:  
; APPLICANT: Yoshihiro Ishikawa  
; TITLE OF INVENTION: Cloning and Character-  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Alan M. Gordon  
; ADDRESS: American Cyanamid Company  
; STREET: 1937 West Main Street,  
; STREET: P.O. Box 60  
; CITY: Stamford  
; STATE: Connecticut  
; COUNTRY: USA  
; ZIP: 06904  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM PC AT  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: ASCII from DM4  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07793,961A  
; FILING DATE: 19911118  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gordon, Alan M.  
; REGISTRATION NUMBER: 30,637  
; REFERENCE/DOCKET NUMBER: 31,705  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 203 321 2719  
; TELEFAX: 203 321 2971  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4046 base pairs listed  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-07-793-961A-1

Query Match 84.3%; Score 2990.4; DB 1; Length 4046;  
Best Local Similarity 90.9%; Pred. No. 0;  
Matches 3229; Conservative 0; Mismatches 311; Indels 12; Gaps 4;

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Db 131 ATGTGCTGTTAGTGGCTTCTGCTCCCTAAAGTGATGAACGAAACAGCCTGGGT 190  
QY 61 GAACGCAATGGCAGAGCGTTCGCGCGCTGGGACTCGGGCAGGTGGCTTCTGCACG 120  
Db 191 GAACGCAATGGCAGAGCGTTCGCGCGCTGGGACTCGGACCAAGTGGCTTCTGCACG 247  
QY 121 CCGCGCTATATGAGTGCCTCCGGGATGCAGAGCCACCCAGCCCTGCGGGGCC 180  
Db 248 CCGCGCTATATGAGTGCCTCCGGGATGCAGAGCCACCCAGTCCACCCCTGCGGCTCC 307

QY 181 CTTGGTGGCCCTGGCAGGATGACGCTTTCATCCCGAGGGCGGCCAGGCAAGGGCAAG 240  
Db 308 CTTGGTGGCCCTGGCAGGATGAGGCTTTCATCCCGAGAGGGCGGCCGCAAGGGCAAG 367  
QY 241 GAGCTGGGGCTGGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGTGACACGACAGCG 300  
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QY 301 GCGGGCAGGCTGAGTGGCGGCCGAGCGGTGCCAGAGTGGGGCATCTGCTGGCGC 360  
Db 425 GTTGGGCGAGCTGAGGTGGCCCTGACGTGACCCCGGAGTAGCGATCTGCTGGCGC 484  
QY 361 CGTTTGGTCCAGGTGTTCCAGTGAAGCAGTTCGCTGGCGCAAGCTGAGCGCCGTGTAC 420  
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QY 721 TGGCTGTGCTTTTGTATACATCGATACAGCTCCTCCCATCCGATGGGGGTGCC 780  
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Db 1085 ACCCGCGTTACATTCAGCGCGGCTGCACTTGCAGATGAGAACCGCGCAGGAGCGG 1144  
QY 1021 CTGCTGCTCTGCTGATTTGCCCGCAGCAGTGGCATGGAGATGAAAGAGACATCAACACA 1080  
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QY 1678 GAGGAAAGGACTGCTGGCCAAAGTTCGAGCGACTTCGGGCAACCTCCATGGAAGGGCTG 1737  
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QY 1738 ATGCGCGGATGGGTTCCTGATCGTCCCTTCTCCCGACCAAGAGCTTCCAGGCTTCCGC 1797  
Db 1862 ATGCGCGGATGGGTTCCTGATCGTCCCTTCTCCCGACCAAGAGCTTCCAGGCTTCCGC 1921  
QY 1798 CAGATGGGCAATTTGATGATTTCCAGCAAGAACACACCGGGGCGCCAGATGCCCTGAACCT 1857  
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QY 2158 GGTCTCTGTTCCCTAAGGCCCTTGAACGCTGTCCCCGAGCATTTCTCCGCTCACCGGCA 2217  
Db 2282 GGTCTCTGTTCCCTAAGGCCCTTGAACGCTGTCCCCGAGCATTTCTCCGCTCACCGGCA 2341  
QY 2218 CATAGCAGCGAGTTGGGCACTTTTCCGCTGCTGCTGCTTACTTCTGCCATTTGCCAAC 2277  
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QY 2278 ATGTTTACCTGTAACACACACCCCTTACGAGCTGTGAGCGCGGATGCTGAATTTAACA 2337  
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Db 293 GAGCTGGGGCTCGGCTCAGTGGCCCTTGGGTTTGTATGACACTGAGGTG---ACCACCG 349  
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QY 421 CAGCGGTACTTTTCCAGATGAACACAGACAGCCCTGACGCTGCTGGTGGCGGTGCTGGTG 480  
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QY 2458 CTGCTGAGTCTCTGTGGCCAGCTCTGTCTTCTGCACATCAGCAGCATCGGGAAGTTGGCC 2517  
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QY 3058 GAGGAGCGGTTCGGCAGCTGGAAGAATCAAGACGATTGGTAGCAGCTACATGGCTGCC 3117  
Db 3110 GAGGAGAGTTCGGCAGCTGGAAGAAGATCAAGACCATCGGTAGCAGTTACATGGCGGCC 3169  
QY 3118 TCAGGCTGAACGCAGCACTACGATCAGTGGCGCGCTCCACATCATCTGCTCGCTGGCT 3177  
Db 3170 TCCGGCTAATGCCAGCACTATGACCAGGTGGCGGCTCGCACATCACCGCTGGCA 3229  
QY 3178 GACTAGCCATGGCGCTCATGGAGAGATGAAGCACATCAATGAGCACTCCTTCAACAAT 3237  
Db 3230 GACTAGCCATGGCGCTTATGGAGCAAAATGAAACACATCAACGAACACTCTTCAACAAC 3289  
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Db 3290 TTCAGATGAAGATTGGGTTGAACATGGGTTCCGCTTGTAGCAGGTGTCTATGGGGCCCGG 3349  
QY 3298 AAGCCACAGTATGACATCTCGGGGAAACACAGTGAATCTCTAGTCGTATGAGCAGACG 3357  
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Db 3410 GGAGTTCTGACCGAATACAGGTGACCAAGATCTTACAGGTTTCTAGCTGCAAGGGC 3469  
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QY 3478 TTTCTCAATGGGGGCCCCAGCACTTAAACAGGGCCCA - GCCACAAATCTAGCTGAAGGGA 3535  
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RESULT 6  
US-09-008-097-3  
; Sequence 3, Application US/09008097  
; Patent No. 6306830  
; GENERAL INFORMATION:  
; APPLICANT: Hammond, H. Kirk  
; APPLICANT: Insel, Paul A.  
; APPLICANT: Ping, Peipei  
; APPLICANT: Post, Steven R.  
; APPLICANT: Gao, Meihua  
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE  
; TITLE OF INVENTION: HEART FAILURE  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/008,097  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dylan, Tyler M  
; REGISTRATION NUMBER: 37,612  
; REFERENCE/DOCKET NUMBER: 22000-20567.21  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-813-5600  
; TELEFAX: 650-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1812 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Coding Sequence  
; LOCATION: 1...1812  
; OTHER INFORMATION:  
; US-09-008-097-3

Query Match 51.0%; Score 1808.4; DB 4; Length 1812;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1809; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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Db 63 GCGCAGCCCTCTCGGGGCTCTGGTCCCTGTGTTCTTTGTATACATCGCATACAGCT 122  
QY 756 CTCCCCCATCCGATCGGGGCTGCCGTCTCAGGGGCTGGGCTCTCCACCTTGCATTT 815  
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QY 816 GATCTTGGCTGGCAACTTAAACCGTGTGATGCTTCTCTGGNAGCAGCTCGGTGCCAA 875







Qy	2413	ACCATGCCCACTTGCAGCTTTCTCTGAGGTGTCATCAGGGAACATGCTGCTGAGTCTCTTTG	2472
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Qy	2533	GGGCTCATCTATTGGTGTGCTTCTGCTGGGTCCGCCAGCGCCATCTTTTGACAACTAT	2592
Db	2956	GAGCTCATCTA---CGTGTCTATCGTGGAGGTGCCAGGTGTCAAGCTTCTCGACAACGCC	3012
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Qy	2773	TGGAACCTACAGCAACAGGGGAAGAGAGATGGAGGAGCTACAGGCATACAACCGG	2832
Db	3190	TGGAACCTCAGGCCACAGAGGAAAGAGAGATGGAGGAGCTGCAGGCCATCAACCGG	3249
Qy	2833	AGGCTGTGCTATACATTTCTGCCAAGGACGTGGCGGGCCACTTCTTGGCCCGGGAGCGC	2892
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Qy	2953	GCCAACCTTCTCAGTCTTATGTGAGCTGGAGGCAACAATGAGGTCGCGAGTGCCTG	3012
Db	3370	GCCAACCTTCTCCAGTCTTACGTTGACCTGGAGGCCAACAGAGGGTGTGAGTGGCTG	3429
Qy	3013	CGGCTGCTCAACGAGATCATCGCTCACTTTGATGAGATTATCAGCAGGAGCGGTTCCGG	3072
Db	3430	CGGCTACTCAATGAGATCATCGTCACTTTGATGAGATCATCAGCAGGAGTCTGTTCCGG	3489
Qy	3073	CAGCTGGAAGAAGATCAAGACGATTGGTAGCCCTACATGGGTGCGCTCAGGGCTGAACGC	3132
Db	3490	CAGCTGGAGAAGATCAAGACCATCGGCACGACTACATGGTGCCTCCGGCTCAACGAC	3549
Qy	3133	AGCACTTACCATCAGTGGGCGCTCCCACTACCTGCCCTGGCTGACTACGCCATCGG	3192
Db	3550	TCCTACCTACGCAAGGTGGGCAAGACCCACATCAGGCACCTGGCCGACCTTGGCCATGAAG	3609
Qy	3193	CTCATGGAGAGATGAAGCACATCAATGAGCACTCCTTCAACAATTTCCAGATGAAGATT	3252
Db	3610	CTGATGGACCATGAAGTACATCAATGAGCACTCCTTCAACAACCTTCCAGATGAAGATC	3669
Qy	3253	GGGCTGAACATGGGCCAGCTGCTGGCAGGTGTATCGGGGTCTGGAGCCACAGATATGAC	3312
Db	3670	GGGCTCAACATCGGCCCGGTGGTGGCGGGGTGATAGGGGACGAAAGCCCTCAGTACGAC	3729
Qy	3313	ATCTGGGGAAACAGTGAATGTCTTAGTCTGATGGACACAGGGGTCCCGACCGA	3372
Db	3730	ATCTGGGGCAATACGTTGAACGTGGCCAGCCGATGGAGAGCCCGGTGTATCCCGACCGC	3789
Qy	3373	ATCCAGGTGACCAACGACCTGTACCAAGTCTTAGCTGCGCAAGGGCTACCAAGCTCGAGTGT	3432
Db	3790	ATCCAGGTTCACCAAGACATGTACCAAGTGTGCTGCTGCCAACAGCTACCAAGTGGATGC	3849
Qy	3433	CGAGGGTGTCAAGGTGAAGGCAAGGGGAGATGACCACTTCTTCTCAATGGGGC	3492
Db	3850	CGGGGGTGTCAAGGTCAAGGCAAGGCGAGATGATGACTTCTTCTCAATGGAGGG	3909

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Qy 3493 CCC 3495
   III
Db 3910 CCC 3912

RESULT 8
US-08-726-214-9
; Sequence 9, Application US/08726214
; Patent No. 6107076
; GENERAL INFORMATION:
; APPLICANT: Tang, Wei-Jen
; APPLICANT: Gilman, Alfred G.
; TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLIC CYCLASE
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726,214
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/005,498
; FILING DATE: 04-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: UTSD:450
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3924 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-726-214-9

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Db 428 CATTGCAAGTGGTGGTGGCCGTCCAGGTAGTGGCCCTGTTGCTGCCACAGCCAGCGC 487  
QY 705 CTCTGCGGGCTCTGGTGCCCTGTGTCTTGTGTATACATCGCATACAGGCTCTCCCCAT 764  
Db 488 CTCGAGGGCATCTGGTGGACCGTGTCTTCTCATCTATACCATCTACACCCCTGCTGCCTGT 547  
QY 765 CCGCATCGGGCTGCGCGCTCTAGCGCCTGCGGCTCTCCACCTTGCATTTGTATCTTTGGC 824  
Db 548 CGCGATGAGGGCTGCGGTGCTACGCGGGTGTCTCTGCGGCTCTCCACTTGGGCATCTC 607  
QY 825 CTGGCAACTTAAACGTGGTGATGCTTCCCTCTGGAAGCACTCGGTGCCAATGTGCTGCT 884  
Db 608 TCTGCACACCAACGCCAGACCAAGTTTCTGCTGAACAGCTTGTCTCCAACTCCCTCAT 667  
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QY 945 CCAGGCGCTTTCAGGACAGCCGAGTTACATCCAGGCCGCGCTCCACCTGCAGCATGAGAA 1004  
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QY 2130 CGTGTGATCTGTGCTGTGTACTCTCTGTGTCTGTTCTGTTCCCTAAGGCCCTGCAACGTCT 2189  
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QY 2664 AGGAGGTTGGCCCTCAATATATGACCCCTGTGATTCCTGCTGTGTTGGGCTGGCGCT 2723  
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QY 2724 GTATCTCATGCTCAGCAGGTGGAATCAGCTGCGCGCTAAACTTCTCTGGAACATACA 2783  
Db 2516 GTATCTCATGCTCAGCAGGTGGATCCACTGCTGCGCTTGACTTCTCTGGAACATGCA 2575  
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Db	2636	CAACATTCTGCCAAGGAGCTGGCTGCCACATTCCTGGCCCGGAGCGCGCAATGATGA	2695
Qy	2904	ACTCTACTATCAGTCGTGTGAGTGTGGCTGTATTATGTTTGCCCTCCATTGCCAACTTCTC	2963
Db	2696	ACTGTACTACCAATCTCGGAGTGGCTGGCTGTCAATGTTTGCCCTCCATCGCCAACTTCTC	2755
Qy	2964	TGAGTTCTATTGGAGCTCGAGGCAAAACAATGAGGGTSCCGAGTGCCTGGCGTGCTCAA	3023
Db	2756	CGAATTCACGTGGAGCTAGAGCCACAANTGAGGGCGTTGAATGCCATCGGCTGCTCAA	2815
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Qy	3324	CACAGTGAATGTCTTAGTGTGATGGACAGACGCGGGGTCCCCGACCGAATCCAGGTGAC	3383
Db	3116	TACAGTAAATGTGGCCAGCCGTATGGACAGCACTGGGGTGCTGACCGCATCCAGGTATC	3175
Qy	3384	CACGACCATGTACCAAGTTCTAGCTGCCAAGGGCTACCAGCTGAGGTGTCGAGGGGGT	3443
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Db	3236	CAAGGTCAAGGGCAAGGGGTGACATGATCACTTCTCTCAATGGAGGGC	3286

## RESULT. 9

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RESOLUT. 3
US-08-726-214-1
; Sequence 1, Application US/08726214
; Patent No. 6107076
; GENERAL INFORMATION:
; APPLICANT: Tang, Wei-Jen
; APPLICANT: Gilman, Alfred G.
; TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726,214
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 435

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QY 1576 GACTACGAAGTGGAGCAGGCGCTGGTGGCAAGCGCAAGCGGTACCTCAAGGAGCAGCAC 1635  
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QY 1756 GATCGTGCCTTCTCCGGAACCAAGGACTTCCAAGGCTTCCGCCAGATGGGCAATTGATGAT 1815  
Db 1633 GTGAGCTCATGCACTGCCGAAGATGTTCAAGCGCCGAGATCCCTTTCTTCAACGTCATG 1692  
QY 1816 TCCAGCAAGAACACCGGGGACCCAAAGATGCCCTGAACCCCTGAGGATGAGGTGGATGAG 1875  
Db 1693 ACCTGTGAGGATGA-----CGACAAGCGGAGGCACTGAGAACAGCCTCGGAAA 1742  
QY 1876 TTCCTGAGCGGTGCCATCGATGCGCGGAGCATTTGATCAGTGCAGGAGGACCATGTGCGC 1935  
Db 1743 ACTCAGAAACCGCTCGCTTCTCTACA----- 1770  
QY 1936 CGGTTTTTGTCTACCTTCCAGAGAGAGGATTTTGAGAAGAGTACTCCCGGAGGCTGGAT 1995  
Db 1771 AACGTTGTCCAAACCCCGGCACACAGTGTCAACAGGTACATCGCGCGCGCTCTCTGGAA 1830

QY 1996 CCCGCTTCGGAGCCTAGTTGGCTGTCGCCCTGTGGCTTCTGCTTCACTGCTGCTTATC 2055  
Db 1831 GCCCGCCAGATGG---AGCTGGAGATGGCAGACCTGAACCTTCTTACCCCTGAAGTACAA 1887  
QY 2056 CAGCTTCTTAATTTTCCACACATCCACCCCTGATGCTTGGGATTTATGCGAGCATCTTCTG 2115  
Db 1888 CAAGCTGAGCAGAGCGAAAGTACACAGCTTCAGGACGAGATATTTCCACGAGCGCGCTG 1947  
QY 2116 CTGCTGTCTAATCAACGCTGCTGATCTGTGCTGTACTCTCTGCTGGTCTCTGTTCCCTAAG 2175  
Db 1948 GTTCTGCTCTCATCTTTCGCGCGCTTATTCGCGCTTGTCTACCTTCTAATAATCCACAG 2007  
QY 2176 GCCGTGAACGTCTGCCCGCAGCATTGTCCGCTCAACGGGCACATAGCACCGCAGTTGGC 2235  
Db 2008 AGTGTGGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2067  
QY 2236 ATCTTTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2295  
Db 2068 TACCTACACATCACCCGGT-----CCAGTGTTCAGGGTGCCTGACCATCC 2116  
QY 2296 ACCCCCATACCGAGCTGTGCAGCGCGGATGCTGAATTTAAACCTGCTGACATCACTGCC 2355  
Db 2117 AGATCCGACCGCTGTTGTCATCTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2175  
QY 2356 TGCCACCTGACAGAGCTCAATTAATCTCTGCTGGCTGGATGCTGCCCTGTGAGGGCACC 2415  
Db 2176 -----TGTGTGTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2227  
QY 2416 ATGCCCACTGCAGCTTTCCTGAGGTGTCATCGGGAAACATGCTGCTGCTGCTGCTGCTG 2475  
Db 2228 TGTGTGCTCTGCTTCTGCGGCGCGGACCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 2286  
QY 2476 AGCTGTGCTCTTCACATCAGCAGCATCGGAGGTTGGCCATGATCTTGTCTTGGG 2535  
Db 2287 GCGCCCATGCCCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2346  
QY 2536 CTCTATCTATTTGGTGTCTTCTGCTGGGTCCCCAGCGCCCATCTTTTGACAACATATGAC 2595  
Db 2347 GTCTCTCTCTGCGCAAAAATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2406  
QY 2596 CTACTGCTTGGCTCCATGGCTTGGCTTCTTCCAAATGAGACCTTTTGATGGGCTGGACTGT 2655  
Db 2407 CTGGAGCTCAGCG-----GGTACACGAAGGCCCATG 2436  
QY 2656 CCAGCTCAGGAGGGTGGCCCTCAATATATGACCCCTGTGATCTCTGCTGCTGCTGCTGCTG 2715  
Db 2437 GGGCGCGGTGCCATCTCAGGCGCGAGCTTCAGGCGGATCATGGCCATCTCTGCTATCTCG 2496  
QY 2716 CTGCGCTGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2775  
Db 2497 TGCAGCTGGCGCTGCGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2556  
QY 2776 AAATACAGGCAACAGGGGAAAAAGAGAGATGAGGAGCTACAGGCTACAGGATCAACCGGAG 2835  
Db 2557 GCGGCCAGGCGAGGAGGAGCGGGATGACATGGAGAAAGTGAAGCTGGACAAACAAGAG 2616  
QY 2836 CTGCTGCATAAATCTTCCCAAGAGCTGGCGGCCCACTTCTGCTGGCGCGGAGCGCGC 2895  
Db 2617 ATTCTCTTCAACCTCTGCGGACCCAGCTTCCAGGACTTCTTAATGCTCAACCCCTGCG 2676  
QY 2896 AATGATGAACCTCTACTATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2955  
Db 2677 AACATGAGCTGTATTACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2736  
QY 2956 AACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3015  
Db 2737 AACTTCAATGACTTCTACATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2796  
QY 3016 CTGCTCAACGAGATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3075  
Db 2797 CTTCTGAATGAGATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2856  
QY 3076 CTGGAAGAAGATCAAGAGGATTGGTAGACCTTACATGGCTGCTGCTGCTGCTGCTGCTGCTG 3132

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Db 2857 CTAGAGAAGATCAAGACCAATTTGGGACAGCTACATGGCTGCTGTGGGGTGGCGCCCACT 2916
QY 3133 -----AGCACCTTACGATCAGTGGCGCTCCACACACTCCTCCCTGGCTGACTACGCC 3186
Db 2917 GCTGGGACCAAGCTAAGAGTGCATCTCTCCACCTCAGACGCTTGGCAGATTTTGCC 2976
QY 3187 ATGCGGCTCATGGAGCAGATGAAGCACATCAATAGCACTCCTTCAACAATTTCCAGATG 3246
Db 2977 ATCAGATGTTGATGCTCTCGATGAGATCAACTACCACTCTTATAACGACTTTTGCTC 3036
QY 3247 AAGATTGGCTGNACATGGCCCGCAGCTGGGAGGTGATCGGGCTCGGAAGCCACAG 3306
Db 3037 CGTGTGGCATCAATGTTGGCCCGCTGGTGGTGGAGTATCGGGCTCGCAGCGCGCAG 3096
QY 3307 TATGACATCTGGGGAAACAGTGAATGCTCTTAGTCGTATGACAGCAGCGGGGTCCCC 3366
Db 3097 TATGACATTTGGGGAAACAGTGAATGCTCGGATGCGGATGACAGTACCGCGTCCAG 3156
QY 3367 GACCGAATCCAGGTGACCCAGCACTGTATCCAGGTTCTAGCTGCCAAGGGCTACCACTG 3426
Db 3157 GCGAGATCCAGGTCAAGAGGAAGTTACCGGCTGCTGGCGGGGTTCTTACCGCTTC 3216
QY 3427 GAGTCTCAGGGGTGTCAGGTGAAGGCAAGGGGAGATGACCACTACTTCTCAAT 3486
Db 3217 GTGTGCCGAGCAAGTCAAGTGTCAAGGCAAGGGTGAGATGCTGACATCTTCTGGAA 3276
QY 3487 GGGGGGCC 3495
Db 3277 GCGAGACC 3285

RESULT 10
US-09-412-210-2
; Sequence 2, Application US/09412210
; Patent No. 6403358
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: 21529, A NOVEL ADENYLATE CYCLASE
; FILE REFERENCE: 5800-47
; CURRENT APPLICATION NUMBER: US/09/412,210
; CURRENT FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 3518
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: 21529 adenylate cyclase
; NAME/KEY: CDS
; LOCATION: (247)...(3480)
US-09-412-210-2

Query Match 14.2%; Score 505.2; DB 4; Length 3518;
Best Local Similarity 50.0%; Pred. No. 1.6e-115;
Matches 1560; Conservative 0; Mismatches 1488; Indels 72; Gaps 9;

QY 435 CCAGATGAACAGAGCAGCTGACGCTGCTGGTGGCGGTGCTGCTGCTCACAGCGCT 494
Db 318 CCAGAGTACCCGCTGCTGCTGCTGGGATGCTGCTGCTGGCTCGCGCT 377
QY 495 GCT----GCTGGCTTTCCAAAGCCGACCCCGCCGCTCAG--CCTGCCATATGTGGCACT 548
Db 378 GCTCGCAGTGGCTGGGCCAGCGGAGGAGCTGACCTCAGACCCGAGCTTCTGACCAAC 437
QY 549 GTTGGCTGTGGCGGCCCTGTGCTGGGGTCAATGGTGGTGTGTGTAACCGGCATAGCTT 608
Db 438 TGTGCTGTGCGGGGCTTCTCGCTGCTGCTGGGCTCGCTTCCCGGGAGCAGCG 497
QY 609 CCGCCAGGACTCCATGTGGTGGTGAAGTAACTGGTGGCTGGGCATCTTGGCGGCGATGCA 668
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Db 498 ACTGCAGCCTGGACGCTCCCTGCTTCCGCTTGGTATGGTGCCTGCTAGCGCTAGG 557
QY 669 GGTGCGGGCGCTTTTCGACGACAGACCCGCGACGCCCTCTGCGGGCTCTGTGGTGCCTGT 728
Db 558 CCACGCTTCCCTGTTTACCAGGGGCTGGTGGCGCTGGGACCAAGTGTCTATTTCCT 617
QY 729 GTTCTTTTATACATCGCATACACGCTCCTCCCATCCGATCCGCGGCTGCGCTCCTCAG 788
Db 618 CTTGCTCATCTTCAAGCGCTATGCCATGCTGCCCTTGGGATCGCGGACGCGCGCTCGC 677
QY 789 CGGCTTGGGCTCTCCACCTTGCATTTGATTTGGCTGGCA-----CTTAACC 838
Db 678 GGGCTTCGCTCCTCACTCTCGCATCTGCTGGTCTCTCGGCTGTATCTTGGGACACAGCC 737
QY 839 GTGGTGCATCCCTTCCCTG--GAAGCAGCTCGGTGCGCAATGCTGCTCTCTCTCTGAC 896
Db 738 GGACTCACGGCTGCACTGCTGCCGAGTTGGCAGAAACGAGTCTGTTCCTGTGCGG 797
QY 897 CAACGTCTATAGCATCTGCACACACTATCCAGCAGAGGTCTCTCAGCGCACGCGCTTCA 956
Db 798 GAACGTGGCAGAGTGTACCACAAGCGCTGATGAGCGCGCTCGGGCCACGTTCCG 857
QY 957 GGAGACCCGAGTTACATCCAGGCCGCTCCACCTGACAGCATGAGAAATCGGCGACGGA 1016
Db 858 GGAGGCACCTCAGCTCCTGCACTACCGCGGCGCTGGACCGAGAAGAACCAAGA 917
QY 1017 GGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1076
Db 918 ACACCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 977
QY 1077 CACAA-----AAAAAGAGACATGTTCCACAAGAT 1106
Db 978 GGCACGGCTGACGAGGAGGAGGCTACGCGCAGAGACACTAACTTCCACAGCCT 1037
QY 1107 CTACATACAGAGCATGACAATGTACAGATCTGCTGTTTGGCAGCATTTAGGGCTTACCAG 1166
Db 1038 CTATGTCAAGAGGACACAGGAGTACGCTGCTGATGCTGACATGCTGGGCTTCCAGCG 1097
QY 1167 CTTGGCATCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1226
Db 1098 GCTGGCCAGGAGTGTCCCTTAAGAGTGGTCTCATGCTCATGAGCTCTTTGGCAA 1157
QY 1227 GTTGCACAGCTGGCTGCGGAGAACTACCTGCTGAGGATCAAGATCTTGGGGACTGTTA 1286
Db 1158 GTTCGACCAAGATTGCCAAGAGCATGAATGCTGCGATCAAGATCTCGGGGACTGTTA 1217
QY 1287 CTACTGTGTGTCAGGGCTCGCGGAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1346
Db 1218 CTACTGTGTGTCAGGGCTCGCGGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1277
QY 1347 GGGGGTAGACATGATTGAGGCCATCTCGCTGGTACGTCAGGTGACAGGTGTGAATGTGAA 1406
Db 1278 GGGCTTGGACATGTCCCGGCCATCAGAAACTGCGGGCAGCAGCTGCGGCTGGACATCAA 1337
QY 1407 CATGCGGTGGGATCCACAGCGGGCGCTGACCTGCGGGGCTTGGCTTGGGGAATG 1466
Db 1338 CATGCTGTGGGCTGCTCAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1397
QY 1467 GCAGTTCGATGTGTGCTCAATGATGACCTGGCCGACCAACCATGGAAGCAGGAGCGG 1526
Db 1398 GCAGTACGAGCTTGTGTCATGATGTCACATGGCTAACCACATGGAGCGAGCGGTGT 1457
QY 1527 GGCTGGCCGCATCCACATCCTCGGCAACACTGCACTGCACTGCACTGCACTGCACTGCACTGCACT 1586
Db 1458 ACCAGGCGAGTGCACATCACAGGGCTACCTGCGGCTGCTGGCAGGGCTTATGCTGT 1517
QY 1587 GGAGCAGCGGCTGGTGGCAAGCGCAACCGGTACCTCAAGAGGAGCAGCATTTGAGACTTT 1646
Db 1518 GGAGCAGCAGGATGAGCATCGGACCGCTTACCTTCGGGAGCTAGGGGAGCGCTACCTA 1577
QY 1647 CCTCATCTTGGGCGGCGCAGCAGAAAGGAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1706
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Db 1578 TCTGGTCAATCGATCCACGGGACAGGAGGAGGATGAGAGGGCACTGACAGAGGCTTGCT 1637  
QY 1707 GCGGACTCGGCGCACTCCCATGAAAGGCTGATGCGCGATGGTCCCTGATCGTCCCTT 1766  
Db 1638 GTCTCTGCTTGGGGCTCAAGATGGCTCATCATCTGCTGATGACCGGTACCTGGAGTC 1697  
QY 1767 CTCCCGACCAAGGACTCCAAAGCCCTTCGCGCCAGATGGGCAATTCATGATTCAGCAAGA 1826  
Db 1698 CTGGGGGACGCAAGCCCTTTTCCCACTAGCCAGGACAGCCCTGTGTGCCACCTC 1757  
QY 1827 CAACCGGGGACCCAGATGCCCTG--AACCTGAGAGTGAAGTGA--TGAGTTCCTGAG 1883  
Db 1758 CACCCCTCTCCCGGAGAAGACCTGCTTCCCTTCAGCACCCAGTGGAGCCTGTGATCGGAG 1817  
QY 1884 CCGTGCCATCGATGCCCGACGATTCATCAGCTGCGGAAGGACCATGTCGCGCGGTTTTT 1943  
Db 1818 CCGTACCCCGGGGACTAGATGATGAACCTGGACACCGGGGATGCCAAGTTCCTCCAGGT 1877  
QY 1944 GCTCAGCTTCCAGAGAGAGATTTTGAAGAAGTACTCCCGGAAGGTGGATCCCGCTT 2003  
Db 1878 CATTGACAGCTCAACTCGCAGAAACAGTGGAAAGCAGTGAAGGACTTCAACCCACTGAC 1937  
QY 2004 CGGAGCCTAGTTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2063  
Db 1938 ACTGTACTTCAGAGAGAGAGATGGAGAAAGATACCGGACTCTCTGCAATCCCGCCCTT 1997  
QY 2064 AATTTTCCCACTCCACCCCTGATGCTTGGGATTTATGCGAGCATCTCTCTGCTGCTGCT 2123  
Db 1998 CAATACTATGAGCCCTGACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2057  
QY 2124 AATCAGGTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2183  
Db 2058 AGTGACAAACAGGCCCCGACCTGCGCCATCAG--TATAGCATCACTTTCTGCTGCTT 2114  
QY 2184 ACCTGCTCCCGCAGCATGCTCGCTCAGGCGACATAGACCCGAGTGGCATCTTTTC 2243  
Db 2115 CTCTCTCATCTTTTGTGCTTCTCAGAGGACCTGATGAGTGTGCTGAAAGGCC 2174  
QY 2244 CGTCTGCTGCTGCTTACTTCTGCCATTTGCCAATGTTTCACTGTAACACACACCCCCAT 2303  
Db 2175 CAAGATGCTGCATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2234  
QY 2304 ACGGAGCTGTGACCGCGGATGTAATTAACACCTGTGATCATCACTGCTGCTGCTGCTGCT 2363  
Db 2235 AATAGCCTTGGGACCGCCACCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2294  
QY 2364 GCAGCAGCTCAATTAATCTCTGCGGCTGGATGCTCCCTGCTGAGGGGACCATGCCAC 2423  
Db 2295 CTCTTCCCAACATCATCAGACTGCCCCCTTTCCAAAGTCCCAATGCTGCTCCATGATTC 2354  
QY 2424 CTGAGCTTCTCGAGGTGTCATCGGGAACATGCTGCTGAGTCTCTTGGCCAGCTCTGT 2483  
Db 2355 CAACCTCTCTGGGAGCTCCCTGGGTCTGCTGCTCTCATCAGTGTCCCATCTCCATGCA 2414  
QY 2484 CTCTCTGCATCAGCAGCATCGGAAGTGGCCATGATCTTGTCTTGGGGCTCATCTA 2543  
Db 2415 CTGCTGCAGCTGGGCTTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2474  
QY 2544 TTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2603  
Db 2475 GCT 2534  
QY 2604 TGGCGTCCATGGCTGCTGCTTCTTCCAAATGAGACCTTTGATGGGCTGAGTGTCCAGCTGC 2663  
Db 2535 CTGGCTGCTGGAAATGCTCATGCTGCGCTCTATCTGGGCCCCCTTGGACTCCAGGCCCGG 2594  
QY 2664 AGGAGGGTGGCCCTCAATATATACCCCTGTGATCTGCTGGTGTGCTGCTGCTGCTGCTGCT 2723  
Db 2595 AGTGTGAAGAGGCCCAACTGATGGTGTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2654  
QY 2724 GTATCTGATGCTCAGCAGGTGAATCAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2783  
Db 2655 CTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2714

QY 2784 GGCAACAGGGGAAAAAGAGAGATGGAGGAGCTACAGGCATACAAACCGAGGCTGTGCA 2843  
Db 2715 GCTGAGGAGGAGGAGGAGAGACAGAGACCATGAGAGACCTGACTCGGCTGTCTTGA 2774  
QY 2844 TAAATTTCTGCCAAGACAGTGGCGCCCACTTCTTGGCCCGGAGCGCCGAATGATGA 2903  
Db 2775 GAACGTGCTCCCTGCACACGTCGCCCCCAAGTTTCATTGGCGAGAACCGGCGCAACGAGGA 2834  
QY 2904 ACTCTACTATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2963  
Db 2835 TCTCTACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2894  
QY 2964 TGAGTCTTATGTGGAGTGGAGCAACAAATGAGGTTGCCAGTGGCTGAGTGGCTGCTGCTGCT 3023  
Db 2895 GGAGTCTTACTCTGATCCCAACATCAATCATGAGGGCTAGAGTGTCTGAGGCTGCTGCTGCT 2954  
QY 3024 CGAGATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3083  
Db 2955 TGAGATAAATGCTGATTTTGTGAGTGTCTTCCAAAGCCCAAGTTTCAGTGGGTGGAGAA 3014  
QY 3084 GATCAAGACGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3137  
Db 3015 GATCAAGACCATCGGCGACCTTACATGCGCAGCCACAGGCTTAAATGCCACCTCTGAGCA 3074  
QY 3138 -----CTAGCATCAGGTGGCGCTCTCCACATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3185  
Db 3075 GGATGCACACAGGATGCTGAACGGAGTGCAGCCACTTGGCAGCTATGCTGGAAATTTGC 3134  
QY 3186 CATGCGGCTCATGGAGAGATGAAGCACATCAATGAGCACTCTTCAACAAATTTCCAGAT 3245  
Db 3135 CGTGGCCCTGGGTCTAAGCTGGACGCTCATCAACAGCATTCATTCAACAACTTCCGCT 3194  
QY 3246 GAAGATTGGCTCAACATGGCCAGTCGTCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3305  
Db 3195 GCAGTGGGTTGAACCATGGACCCGCTAGTGGAGTTATTGGGGCCCAAGAGCCGCA 3254  
QY 3306 GTATGATCTGGGGGAACACAGTGAATGCTCTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3365  
Db 3255 ATATGATCTTGGGGCAACACAGTGAACGTCGCGCCGATGAGAGTACAGAGTCTCT 3314  
QY 3366 CGACCAATCCAGGTGACCAAGCACTGTTACAGGTTCTAGCTGCCAAGGCTGCTGCTGCTGCTGCT 3425  
Db 3315 TGCAAAATCCAACTGCTGAGGAGACAGCATGGCCCTACAGTCCCTGGGCTACACCTG 3374  
QY 3426 GGAGTCTGAGGCTGCTCAAGTGAAGGCAAGGCGGAGATGACCACTACTTCTCTCA 3485  
Db 3375 CTACAGCCGGGTGCTCATCAAGGTGAAGGCAAGGCGAGCTCTGCACTACTTCTCTGAA 3434

RESULT 11  
US-08-726-214-15  
; Sequence 15, Application US/08726214  
; Patent No. 6107076  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Wei-Jen  
; APPLICANT: Gilman, Alfred G.  
; TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYL CYCLASE  
; TITLE OF INVENTION: AND USES THEREFOR  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States of America  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:



:	APPLICATION NUMBER:	US/08/726,214
:	FILING DATE:	Concurrently Herewith
:	CLASSIFICATION:	435
:	PRIOR APPLICATION DATA:	
:	APPLICATION NUMBER:	US 60/005,498
:	FILING DATE:	04-OCT-1995
:	ATTORNEY/AGENT INFORMATION:	
:	NAME:	Highlander, Steven L.
:	REGISTRATION NUMBER:	37,642
:	REFERENCE/DOCKET NUMBER:	UTSD:450
:	TELECOMMUNICATION INFORMATION:	
:	TELEPHONE:	(512) 418-3000
:	TELEFAX:	(512) 474-7577
:	INFORMATION FOR SEQ ID NO:	15:
:	SEQUENCE CHARACTERISTICS:	
:	LENGTH:	4601 base pairs
:	TYPE:	nucleic acid
:	STRANDEDNESS:	single
:	TOPOLOGY:	linear
:	US-08-726-214-15	

  

Query Match	13.1%;	Score 463.6;	DB 3;	Length 4601;
Best Local Similarity	51.5%;	Pred. No. 3.8e+105;		
Matches 1439;	Conservative	0; Mismatches 1194;	Indels 159;	Gaps

  

QY	712	GGCCTCTGGTGCCTGTGTTCTTTGTATACATCGCATACAGCTCTCCGCCATCCGCAATG	771
Db	1575	GGCATAGGTAAGTGCTGTTTTTACACTCTTCGCCACCTACAGCATGCTTCGCTCGCTCTC	1634
QY	772	CGGGCTTCCTCTACAGCGCTCGGGCTCTCCACCCTTGCATTGTGATCTTGGCTGGCAA	831
Db	1635	ACCTGGGCATCTTGGCCGGCTGGGCACATCCTTGTGTGAAGTCACACTTCAAGTGCTC	1694
QY	832	CTTAACCGTGGTAGNCCCTTCCTCTTGAAGCAGCTCGGTGCCAATGTGCTGTCTTCTC	891
Db	1695	ATACCCAGACATAGCGGTCTTTTCCATCAACCAGGTCTCTGGCCAGGTGCTCTTCTCATG	1754
QY	892	TGCACCAACGTCAATTAGCATCTGCACACACATATCAGCAGAGGTGTCTCAGCGCCAGGCC	951
Db	1755	TGCATGAATACAGAGGCATCTTCATCATAGTTACCTTTTCAGACC CGCC CAGCGCAGGCC	1814
QY	952	TTTCAGGAGACCCGCGAGTTTACATCCAGGCCCGCGCTCCACCTTGCAGCATGAGAATCGGCAG	1011
Db	1815	TTCTTGAGACCCGGAGGTGTGTGGAGGCCAGGCTCCGCCCTGGAGACAGAACAAAGA	1874
QY	1012	CAGGAGCGGTGCTGTGTGCGGTATTGCCCAGCACAGTTCGCCATGGAGATGAAGAAAGAC	1071
Db	1875	CAGGAGCGCTGTGTGCTCTGTCTGTCTCCCGAGTTGTGTCTCTAGAAAATGATCAATGAC	1934
QY	1072	ATCAACACAAAAAAGAAG-----ACATGTTCCACAAGATCTACATACAGAAG	1119
Db	1935	ATGACCANTGTGGAGGACGAGCACCTTGCAGCATCAGTTTCCACCGCATCTACATCCATCGC	1994
QY	1120	CATGACAATGTCAGCATCTGTTTTCAGACATTTGAGGCTTTCACCAGCCTGGCATCCCGAG	1179
Db	1995	TACGAGACGTCAGTATTCTTTTTCAGATGTCAAGAGATTACCAACCTCTCTACGACC	2054
QY	1180	TGCACHTGGCAGAGAGCTGGTCAATGACCCCTGAAATAGCTCTTTTCCCGGTTTGACAAGCTG	1239
Db	2055	TTGTCTGTCTCAGGAGGTTGTCTAGGATGTCTAACGAGCTCTTTTGGCAGATTGATCGGCTG	2114
QY	1240	GCTGCGGAGAACTACATGCTCTGAGGATCAAGATCTTTGGGGAGCTGTACTACTGTGTCTCA	1299
Db	2115	GCCCCATGAGCATCACTGTCTTCGCATTTAAATTCCTTGGGGAGCTGCTACTACTGTGTGTCA	2174
QY	1300	GGGCTCCGGAGGCCCCGGCCGACCATCGCCACTGCTGTGTGGAGATGGGGGTAGACATG	1359
Db	2175	GGACTGCCGTGAGCCCGCCAGGACCATGCTCATTTGCTGTGTGAATGGGCCCTCAGCATG	2234
QY	1360	ATTGAGGCCATCTCCGCTGGTACTGCTGAGGTGACAGAGGTGTGAATGTGAACATGCGCGTGGCG	1419
Db	2235	ATCAAAACTATCAGGTTGTGTAGGTTCCAGAACGAAGCATGATGTTGACATCCGAATTTGGA	2294



QY 1662 CAGCCAGAAACGAAAGAGGAGAAAGGATGCTGGCCCAAGCTGCAGCGGACTTCGGGCCAA 1721  
Db 1458 -----CAATCCCAAGGAGAGCGAGGAGTCTCTCAGCATCTCTTCAGACCTCGACACAC 1511  
QY 1722 CTCCTAGGAGGCTGTATGCTCCCGATGGGTTCCTGATCGTGGCTTCTCCGCGACCAAGA 1781  
Db 1512 TCTGACGAGGACCAAGATGAGAGCATCTGTCCG-----CATGACCGGTACTTGA 1562  
QY 1782 CTCCTAAGGCTTCCGCCAGATGGGATGATGATTCCAGCAAGAACACCGGGGACCCA 1841  
Db 1563 GTCTCTGGGAGCAGCCAGCCATTCCGACATCTGCACACAGATAGATGACCACAGA 1622  
QY 1842 AGATGCCCTGAACCTGAGGATGAGGTGGATGAGTTCCTGAGCCGTCATCGATCCCGC 1901  
Db 1623 GAATGGGAAGATTAGTACCACGGATGTCCTAATGGGTCAACATAATTTTCAAAATCGCAC 1682  
QY 1902 CAGCATGATGATGCTGCGGAAGGACCATGTGCGCCGGTTTGTGTCACCTTCCAGAGA 1961  
Db 1683 CTTAAGAACTAAGTCACAGAAGAAGAGATTGTGAAGAAGAACTGAATGAAGGATGATCCA 1742  
QY 1962 GGATTTTGAGAAAGTACTCCCGGAAGGTGGATCCCGCTTCGGAGCTACGTTGCGCTG 2021  
Db 1743 AGCAATTGATGGATCAATGCACAGACGAATGGCTCAAGTCAGAGACATTCGAAGAT 1802  
QY 2022 TCCCTGTGTGCTTCTGCTTCATCTGCTTCATCCAGCTTCTTAATTTTCCACACTCCAC 2081  
Db 1803 CTCCTGCTTTTCTATAACAAGAAATATAGAGAAAGAAATACCGAGCTACTGCACTGCCAGC 1862  
QY 2082 CCTGATG---CTTGGGATTTATGCCAGCATCTCTGCTGCTGCTTAATCACCGTGTGAT 2138  
Db 1863 ATTCAAGTACTACGTGACCTGTGCGTGCCTCACTTTCTGTCATCTTCAATGTACAGAT 1922  
QY 2139 CTGTGCTGTG-----TACTCCTGTGTTCTCTGTGTC--CTAAGGCCCTGCAACG 2186  
Db 1923 ACTTGATTTGCCAANAACGTCCATCCTTGGCTTCTCTTGGAGCTGCAATTTCTCCTCT 1982  
QY 2187 TCTGTCCCGACATATGCTCGGTACGGGCACATAGCAGCGCAGTTGGGATCTTTTCGGT 2246  
Db 1983 CATCTTCATCTCTTGTCTGTCTGCTGGTGGACAGCTTTTGCAATGACGCAAAAGGCTC 2042  
QY 2247 CCGTCTGTGTTTACTTCTGCCATTTGCCAATGTTCACTGTACCTTAACCAACACCCCATAGC 2306  
Db 2043 CACCTCTCTCATGTGGCTTTTGAATCATCAGGCAATCATGCGCAACCGGCCATGGCCAG 2102  
QY 2307 GAGCTGTGAGCCCGGATGCTGAATTTAACAACCTGCTGACATCACTGCTGCACCTGCA 2366  
Db 2103 GATCTCCCTCAACATGCTCACACCGCTATCATATACTAACCATGGCTGTGTTCAACATGTT 2162  
QY 2367 GCAGCTCAATTAATCTCTGGGCTGGATGCTCCCTGTGTGAGGGACCATGCCACCTG 2426  
Db 2163 TTTCTGTAGCAACTCTGAGGAGACAACCTTCCCACTGCAATATACATCAAAATGCAAGGT 2222  
QY 2427 CAGCTTTCTGAGGTGCTCATCGGAACATGCTGCTGAGTCTCTTGGCCAGCTCTGCTT 2486  
Db 2223 TTTCTGTCGGGATACACAGCGCTCATCTTCTGCTCGAATCTGTGTTTCTCCCTCCCGTA 2282  
QY 2487 CCTGCACATCAGCAGCATCGGGAAGTTGGCCATGATCTTTGTCTTGGGCTCATCTATT 2546  
Db 2283 CTTCATATACACTGCAUCCTGGGTGATCTCTGCTGCTCCGTTTCTGAGGGTGAACATA 2342  
QY 2547 GGTGCTGCTTCTGCTGGTCCCGCCCGCCCATCTTTTGACAACTATGACCTACTGCTGG 2606  
Db 2343 TGAGTTAAAAATGTTAATCATGATGTTGSCACTCGTGGCTACACACATTTCTACTCCA 2402  
QY 2607 CTTCCATGCTGCTGCTTCTTCAATGAGACCTTTGATGGGCTGGAGTGTCCAGCTGACG 2666  
Db 2403 CACCCATGCC---CATGTTCTGCTGCTGCTGATTTCTGCTGTTTGGCTGGCGCTGTA 2459  
QY 2667 GAGGTGGCCCTCAATATATACCCCTGTGATTTCTGCTGTTTGGCTGGCGCTGTA 2726  
Db 2460 TTGGAAGACCTGAAGACCATGGCTCGCTGTCACTCTCCCATATTCTTCATCAGCTGCT 2519

QY 2727 TCTGCATGCTCAGCAGGTGGATCGACTCCCGCCTAAACTTCTCTTGTGAAACTACAGGC 2786  
Db 2520 GGTTCCTGGCAGACAGAGTGAATATTACTGTAGGTTAGACTTCTTGTGGAACAAGTT 2579  
QY 2787 AACAGGGGAAAAGAGGAGATGGAGGAGCTACAGCATACACCGGAGGCTGCTCATAA 2846  
Db 2580 CAAAAAAGAGGGGAGGAGATAGAAACCATGGAGAACCTAAATCGAGTGTCTGTGGAAA 2639  
QY 2847 CATTCCTGCCAAGGAGCTGGGGGCCACTTCTGCGCCGGAGCGCCCAATGATGAAT 2906  
Db 2640 GGTGCTTCTGCACACAGTGGCTGAACACTTCTGCGCAGGAGCTGAAAATGAGAGCT 2699  
QY 2907 CTACTATCAGTGTGTGAGTGTGTGCTGTATGTTTGCCTCAATGCAACTTCTCTGA 2966  
Db 2700 GTACCACCACTCTACGACTGTGTGTCTGTATGTTTGCCTCAATCGGACTTCAAGGA 2759  
QY 2967 GTTCTATGAGGCTGGAGGCAACAATGAGGTGCCAGTGCCTGCGGCTGCTCAACGA 3026  
Db 2760 GTTCTACACAGATCAGATGTGAACAAGAGGCTTGAATGCCCTGCGCTCCTGAATGA 2819  
QY 3027 GATCATCTGCTGACTTTGATGATTATCAGGAGGAGCGGTTCCGGCAGCTGGAAAAAGAT 3086  
Db 2820 GATCATCTGCTGACTTTGATGATCTGCTTCTAAGCCAAAGTTCACTGGTGTGAAAAGAT 2879  
QY 3087 CAAGACGATTGGTAGCCTACATGCTGCTGAGGTGAGTGAACGACGACCTACGATCA 3146  
Db 2880 CAAGACCATTTGGAGCACATACATGCGACGACGAGGACTGAGTGCATACCCAGCCAGCA 2939  
QY 3147 GGTGGGCC-----GCTCCACATCACTGCCCTGGCTGACTACGCCAT 3188  
Db 2940 GCACGCCCAGGAACCTGAGCGTCACTATGACATAGCCACCATGGTGGAGTTTGCATA 2999  
QY 3189 GCGGCTCATGAGCAGATGAAGCACATCAATGAGCAGCTCTTCAACAATTTTCCAGATGAA 3248  
Db 3000 TGCCCTGTGTGGGAAACTGGATGCCATCAATAAGCACCTTCAACAGCTTCAAACTGCG 3059  
QY 3249 GATTGGGCTGAACATGCGGCCAGTCTGCGAGGTGTCTATCGGGGCTCGGAAGCCACAGTA 3308  
Db 3060 AGTGGGTATCAACCATGGGCTGTAAATAGTGGCTCATAGGGGCTCAAAAGCCACAGTA 3119  
QY 3309 TGACATCTGGGGAACACAGATGAATGCTCTAGTCTGATGACAGACGCGGGGTCCCGCA 3368  
Db 3120 TGACATCTGGGGAACACATGTCACGTGGCCAGCAGATGAGACAGCAGCGGGGTCTGGA 3179  
QY 3369 CGAATCCAGGTGACCGGACCTGTACAGGTCTTAGCTGCCAAGGCTACCACTGGA 3428  
Db 3180 CAAAATACAGTGTGACTGAGGAGACAAGCTCATCTTGCAGACGCTTGGCTACACGTGAC 3239  
QY 3429 GTGTCAGGGTGTGTCAGGTGAAGGCAAGGGGAGATGACCACCTACTTCTCAA 3485  
Db 3240 ATGTCAGGTATCATCAATGTGAAGGGGAAAGGGGACCTGAAAGACATATTTTGTAAA 3296

## RESULT 13

US-08-726-214-3

; Sequence 3, Application US/08726214

; Patent No. 610706

; GENERAL INFORMATION:

; APPLICANT: Tang, Wei-Jen

; APPLICANT: Gilman, Alfred G.

; TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYL CYCLASE

; TITLE OF INVENTION: AND USES THEREOF

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White &amp; Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: Texas

; COUNTRY: United States of America

; ZIP: 77210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/726,214  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/005,498  
FILING DATE: 04-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L.  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: UTSD:450  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4008 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-726-214-3

Query Match 12.9%; Score 459; DB 3; Length 4008;  
Best Local Similarity 50.8%; Pred. No. 4.9e-104;  
Matches 1370; Conservative 0; Mismatches 1240; Indels 87; Gaps 8;

QY 852 CCTCTGGAAGCAGCTCGGTGCCAATGCTGCTGCTTCTCTGACCAACGTCATTAGCAT 911  
DB 624 CCGTCTTCTGCAGATATGCGCAATGTGATCAATTTTCAATTTGGGAACATTGGCGGAGC 683  
QY 912 CTGCACACATATCCAGCAGAGTGTCTCAGCGCCAGGCGCTTTCAGGAGACCGCGAGTTA 971  
DB 684 CTACCACAAGCACCCTCATGAGCTTGCCTTGCACCAACCTATCGGACACGTTGTAATG 743  
QY 972 CATCCAGGCCGGCTCCACCTGCAGCATGAGAAATCGGCAGCAGGCGGCTGCTGTGTC 1031  
DB 744 CATCAAGTCCCGATCAAGCTGGAATTTGAAAAACGCGCAGCAGCGGCTCTGCTCTC 803  
QY 1032 GGTATTGCCCCAGCAGTTCCTGATGGAGTGAAGAGACATCA----- 1075  
DB 804 CTGCTGCCAGCTCACATCGCCATGGAGATGAAGCTGAAATCATTCAGAGGCTGCAGGG 863  
QY 1076 -----ACACAAAAAAGAGACATGTTTCCACAAGATCTACATACAGAAGCA 1121  
DB 864 CCCAAAGCAGGACAGATGAAACACAAACAATCTCCACAATCTGTATGTCAAACGACA 923  
QY 1122 TGACATGTGAGCATCTGTTTGCAGACATGAGGGCTTCCACAGCTGCGATCCCAAGTG 1181  
DB 924 CACCAAGCTGAGCATATTATACGCTGACATTTGTTGGCTTCCACCGCGCTTGAAGCGATTG 983  
QY 1182 CACTGCGCAGAGCTGGTCTATGACCTGATGAGCTCTTTGCCGGTTTCACAAGCTGGC 1241  
DB 984 CTCCCTGGCGAATGGTCCACATGCTGAATGAACCTTTTGGGAAGTTTGATCAATAGC 1043  
QY 1242 TGGCGAGAATCACTGCTGAGGATCAAGATCTTTGGGGAGCTGTACTACTGTGTGTCAGG 1301  
DB 1044 AAAGGAGAATGAATGATGAGAAATTAATTTTAGGAGACTGCTATTACTGTGTGTTCCGG 1103  
QY 1302 GCTGCGGAGCGCGCGGCCACCATGCCCACTGCTGTGTGGAGATGGGGGTAGACATGAT 1361  
DB 1104 GCCTCCCTATATCACTCCCTTAACCATGCCAAGAACTGTGTGAAATGGGATTTGATATG 1163  
QY 1362 TGAGGCCATCTCGCTGGTACGTGACAGGTGTGAATGTGAACATGCGCGTGGSCAT 1421  
DB 1164 CGAAGCCATAAAGAGTGAAGGATGCTACCGGAGTTGATCAACATGGCTGAGAGT 1223  
QY 1422 CCACAGCGGCGCGCTGACCTGCGGCGCTTCTTGGCTTTCGCGAAATGGCAGTTTCGATGTG 1481  
DB 1224 GCATTCTGGGAAGCTTCTCTGTGTGTGATTTGCTCCAGAAAGTGGCAGTATGATGTG 1283  
QY 1482 GTCCAAATGATGTGACCTGCGCCCAACCATATGGAAGCAGGAAGCCGGGCTGGCGCATCCA 1541

DB 1284 GTCTCATGATGTTACTCTGGCAAAACCATGGAAAGCTGGAGGAGTCCCTGGCGGTGTCA 1343  
QY 1542 CATCACTCGGCAACACTGCAGTACCTGAACGGGAGTACGAAGTGGAGCGAGCCCTGG 1601  
DB 1344 CATTTCTTCAGTCACTCTGGAGCACTTGAATGGGGCTTATAAGTGGAGGAAGAGATGT 1403  
QY 1602 TGGCAAGCGCAAGCGGTACCTCAAGAGCAGACATTTGAGACTTTCTCATCTCTGGGCGC 1661  
DB 1404 TGAGATAAGAGACCCATATTTAAGCAGACACTTGGTGAAAACCTACTTTGTAAT----- 1457  
QY 1662 CAGCCAGAAAACGGAAGAGGAAAGCATGCTGGCCAAAGTGCAGCGGACTTCGGGCCAA 1721  
DB 1458 -----CAATCCCAAGGAGAGCGAGCTCTCTCAGCATCTCTTCAGACCTCGACAC 1511  
QY 1722 CTCCATGGAAGGGCTGATCGCGCATGGGTTCCTGTATCGTCCCTCTCCCGGACCAAGGA 1781  
DB 1512 TCTGGACGGAGCCAAAGATGAGAGCATCTGTCG-----CATGACCGGTACTTTGGA 1562  
QY 1782 CTCGAAGGCTTCGCGCAGATGGGCATTTGATTTCCAGCAAAAGACAAACCGGGGCACCCA 1841  
DB 1563 GTCCTGGGAGCAGCCAAAGCCATTCGCACATCTGCACCACAGATAGCATGACCACAGA 1622  
QY 1842 AGATGCCCTGAACCTGAGGATGAGGTGGATGATTCCTGAGCCGTGCCATCGATGCCCCG 1901  
DB 1623 GAATGGGAAGATTAGTACCACGGATGTGCCAATGGGTCAACATAAATTTCAAAATCGCAC 1682  
QY 1902 CAGCATTTGATCAGCTCGGGAAGGACCATGTGCGCCGGTTTTTGCTCACCTTCCAGAGAGA 1961  
DB 1683 CTTAAGAACCTAAGTTCACAGAAGAAGAGATTTGAAGAAGAACTGAATGAAAGGATGTCCA 1742  
QY 1962 GGATTTTGAAGAAGTACTCCCGGAAGGTGGATCCCGCTTCGGAGCGCTACGTTGCGCTG 2021  
DB 1743 AGCAATTTGATGGGATCAATGCACAGAAGCAATGGCTCAAGTCAGAAGACATTTCAAAGAT 1802  
QY 2022 TGCCCTGTTGGTCTTCTGCTTCATCTGCTTCAATCCAGCTTCTAATTTTCCOCACACTCCAC 2081  
DB 1803 CTCCTCTCTTTCTATAAACAAGATATAGAGAAAGAAATACCGAGCTACTGCACTGCCAGC 1862  
QY 2082 CCTGATG---CTTGGGATTTATGCCAGCATCTTCTCTGCTGCTGCTATACCGTGCAT 2138  
DB 1863 ATTCAAGTACTAGTGACCTGTGCTGCTGCTCTCATCTTCTCTGCACTCTTCATTTGACAGAT 1922  
QY 2139 CTGTGCTGTG-----TACTCCTGTGTTCTCTGTTTCC---CTAAGGCCCTGCAACG 2186  
DB 1923 ACTTGATTTGCCAAAACGCTCCATCTTGGCTTCTCTCTCTTGGAGCTGCAITTTCTCCCT 1982  
QY 2187 TCTGTCCCGCAGCATTTGTCGCTCAGCGGCACATAGCACCGCAGTTGGCATCTTTTCCGT 2246  
DB 1983 CATCTTTCATCTCTTGTCTGCTTGGCTGGACAGCTTTTGCAATGCGACAAAAGGCTC 2042  
QY 2247 CTTGCTTGTGTTTACTTCTGCCATTGGCAACATGTTCCACCTGTAACACACACCCCATACG 2306  
DB 2043 CACCTCTCATGTGGCTTTTGAATCATCAGGACATCATGCCAACCGCCCATGGCCACG 2102  
QY 2307 GAGCTGTGACGCGGATGCTGAATTTAACAACCTGTGTGACATCACTGCCCTGCCACTGCA 2366  
DB 2103 GATCTCCCTCACAATCTCACACAGCGGTATCATACTAACCATGGCTGTGTTCACACATGTT 2162  
QY 2367 GCAGCTCAATTAATCTCTGGCCCTGGATGCTCCCTGTGTGAGGGGACCATGCCCCACTG 2426  
DB 2163 TTTCTTGAGCAACTCTGAGGAGACAAACCTTCCCACTGCCAATACATCAATGCAACAGT 2222  
QY 2427 CAGCTTTCTCTGAGGTGCTCATCGGAACATGCTGCTGAGTCTCTTGGCCAGCTCTGTCTT 2486  
DB 2223 TTTGTCGCCGATTAACACGCGTCGATTTCTCATGCTCGAAACTTTGTTTCTCCCGTA 2282  
QY 2487 CCTGCACATCAGCAGCATCGGGAAGTTGGCCATGATCTTTGCTTGGGGCTCATCTATTT 2546  
DB 2283 CTTTCAATATACAGTGCATCTCGGCTTGTATCTCTGCTCGCTTTTCTGAGGGTGAACATA 2342  
QY 2547 GGTGCTGCTTCTGCTGGGTCCCCCAGCGCCCATCTTTTGACAACTATGACCTACTGCTGG 2606

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Db 2343 TGAGTTAAATGTTAATCATGATGTCGACCTCGTGGGCTACAAACACATCTTACTCCA 2402
QY 2607 CPTCCATGGCTGGCTTCTTCCAAATGAGACAGCTTTTGATGGCTGGACTGCCAGCTCAGG 2666
Db 2403 CACCCATGCC---CATGTTCTGGATCGGTACAGCCAGGTCCTGTTTCAGAGACCAGCAT 2459
QY 2667 GAGGTGGCCCTCAATATATATGACCCTGTGATCTGCTGCTGGTGTTCGCTGGCGCTGTA 2726
Db 2460 TTGGAAGACCTGAAGACCATGGCTCCGCTGCTCACTCTCATATCTTCAACGCTGCT 2519
QY 2727 TCTGCACTCTCAGCAGGTGAAATCGACTGCCGSCCTAACTTCCCTGCTGAAACTACAGC 2786
Db 2520 GGTTCGGGCAGACAGAGTAAATTAATCTAGGTAGACTTCTTGTGGAAGAACAAAGTT 2579
QY 2787 AACAGGGGAAAAGAGAGATGAGGAGCTACAGGCATACACCGGAGGCTGCTGATAA 2846
Db 2580 CAAAAGAGCGGAGAGATAGAACCATGGAGACCTAATCGAGTCTGCTGGAGAA 2639
QY 2847 CATTCGCCAAGGAGCTGGCGCCACATTCCTGGCCCGGAGCGCCGCAATGATGAAT 2906
Db 2640 CGTCTTCCTGACACAGCTGGCTGAACACTTCCTGGCCAGGAGCTGAAAAATGAGGAGCT 2699
QY 2907 CTACTATCACTCTGCTGAGCTGTGGCTGTATGTTGCTTCCATTCGCAACTTCTCTGA 2966
Db 2700 GTACCACTGCTCTAGCACTGTCTGTGTCATGTTGCTTCCATTCGCGACTTCAAGGA 2759
QY 2967 GTTCTATGAGCTGGAGGCAACAAATGAGGCTGCCAGTGCCTGCGCTGCTCAAGCA 3026
Db 2760 GTTCTACAGAGTCAAGTGTGNACAGGAAGCTTGGATGCTGCTGCGCTCTGATGA 2819
QY 3027 GATCATCGCTGACTTTGATGAGATTATCAGCAGGAGCGGTTCCGSCAGCTGGAAGAAT 3086
Db 2820 GATCATTCGCTGACTTTGATGATCTGCTTCTTAAGCCAAAAGTTCAGTGGTGTGAAAAGAT 2879
QY 3087 CAAGCAGATTGTGATGACCTACATGCTGCTCAGGCTGAAGCCAGCAGCACTACGATCA 3146
Db 2880 CAGACCAATTGGGAGCACATACATGCGACCGCAGGAGTGAAGTGCATACCCAGCCAGGA 2939
QY 3147 GGTGGGCC-----GCTCCACATCACTGCGCTGGCTGACTACGCCAT 3188
Db 2940 GCAGCGCCAGGAACCTGACGCTCAGTACATGCATAGCAGCACCATGGTGGATTGCATA 2999
QY 3189 GCGGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCTTCAACAATTTCCAGATGAA 3248
Db 3000 TGCCCTGTGGGAAAACCTGGATGCCATCAATAAGCACTCTTCAACGACTTCAAACTGG 3059
QY 3249 GATTGGCTGAACATGGGCCCACTCGTGGCAGGTGTCTATCGGGGCTCGGAAGCCACAGTA 3308
Db 3060 AGTGGGTATCAACCATGGGCGCTGTAATAGCTGGCGTATAGGGGCTCAAAAGCCACAGTA 3119
QY 3309 TGACATCTGGGGAAACACAGTGAATGCTCTAGTGTATGACAGCAGCGGGGTCCCGCA 3368
Db 3120 TGACATCTGGGCAACACTGTCAAGTGGCCAGCAGATGGACAGCCGCGGTCTCTGA 3179
QY 3369 CCGAATCCAGGTGACACCGGACTGTACAGGTTCTAGTGTGCAAGGGGTACAGCTGGA 3428
Db 3180 CAAAATACAGGTGACTGAGGAGCAACAGCCTCATCTTGCAGAGCGCTGGCTACAGGTGAC 3239
QY 3429 GTGTCGAGGGTGGTCAAGGTGAAGGGCAAGGGGAGGATGACCACCTACTTCTCTAA 3485
Db 3240 ATGTCGAGGTATCATCAATGTGAAGGGGAAAGGGGACCTGAAAGACATATTTTGTAAA 3296
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## RESULT 14

PCT-US95-11808-5

; Sequence 5, Application PC/TUS9511808

; GENERAL INFORMATION:

; APPLICANT: Iyengar, Srinivas Ravi V.

; TITLE OF INVENTION: MUTANT ACTIVATED GSALPHA AND

; TITLE OF INVENTION: ADENYL

; TITLE OF INVENTION: CYCLASE 2 FOR USE AS THERAPEUTIC AGENTS

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

```
; ADDRESSEE: Brumbaugh, Graves, Donohue and
; ADDRESSEE: Raymond
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.
; ZIP: 10112-0228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/11808
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,896
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Richard S.
; REGISTRATION NUMBER: 26,154
; REFERENCE/DOCKET NUMBER: 29970 165/28755
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 408-2500
; TELEFAX: (212) 765-2519
; TELEX: 650 6111063
; INFORMATION FOR SEQ ID NO: 5:
; LENGTH: 4008 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
PCT-US95-11808-5
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Query Match 12.9%; Score 459; DB 5; Length 4008;

Best Local Similarity 50.8%; Pred. No. 4.9e-104;

Matches 1370; Conservative 0; Mismatches 1240; Indels 87; Gaps 8;

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QY 852 CTTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTGCTCTCTGCACCAACGTCTATAGCAT 911
Db 624 CCGTCTCTGGCAGACTCGGCCAATGTGATCATTTTCATTTGTGGGAACCTTGGCGGAGC 683
QY 912 CTGCACACACTATCCAGCAGAGGTGCTCAGCGCCAGGCGTTTCAGGACACCGCAGTTA 971
Db 684 CTACCAACAGCACCCTCATGGAGCTTGCCCTTGAGCAGCAACCTATCGGGACACGTGTATTG 743
QY 972 CATCCAGGCCCGGCTCCACCTGCAGCATGAGAAATCGGCAGAGGAGCGGCTGCTGCTGC 1031
Db 744 CATCAAGTCCCGGATCAAGCTGGAATTTGAAAAAGGCGCAGGAGGAGGCTCTCTGCTCTC 803
QY 1032 GGTATTTGCCAGCAGGTTGCCATGGAGATGAAAGAAAGACATCA----- 1075
Db 804 CTTGTGTCAGCTCATCGCCATGGAGATGAAAGCTGAAATCATTTACAGAGGCTGCAGGG 863
QY 1076 -----ACACAAAAAAGACACATGTTCCACAGATCTACATACAGAACA 1121
Db 864 CCCCAGAGCAGACAGATGGAAGAACACAAACACTTCCACAACTCTGTATGTCAAGACACA 923
QY 1122 TGACAATGTGACATCCTGTTTTCAGACATTTGAGGCGCTTCCAGCAGCTGGCATCCAGTG 1181
Db 924 CACCAAGCTGACATATTATACGCTGACATTTGTGCTTCCACCGCTTTCGAAGCGATTG 983
QY 1182 CACTGCGGAGGAGCTGGTCATGACCTGACCTGATGAGCTCTTTGCGCGGTTTGGACAAGTGG 1241
Db 984 CTCCCTCGGCGAATGCTCCACATGCTGAATGAACCTTTTGGGAAGTTTGTATCAATATGC 1043
QY 1242 TCGCGAGAACTACTGCTGAGGATCAAGATCTTTGGGGAGCTGTACTACTGTGTGTCAGG 1301
Db 1044 AAGAGAGATGAATGCATGAGAAATTAATAATTTAGGAGACTGCTATTACTGTGTTCCGG 1103
QY 1302 GCTGCCGAGGCGCGGCGGACCATGCCCACTGCTGTGTGGAGATGGGGGTAGACATGAT 1361
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RESULT 15
US-08-726-214-5
; Sequence 5, Application US/08726214
; Patent No. 6107076
; GENERAL INFORMATION:
; APPLICANT: Tang, Wei-Jen
; APPLICANT: Gilman, Alfred G.
; TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726.214
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/005.498
; FILING DATE: 04-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: UIUSD:450
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4533 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-726-214-5

Query Match 12.4%; Score 441.6; DB 3; Length 4533;
Best Local Similarity 50.1%; Pred. No. 1.1e-99;
Matches 1359; Conservative 0; Mismatches 1284; Indels 67; Gaps

QY 853 CTCGTGAAGCAGCTCGGTGCCAATGTGCTGTGTTCTCTGCACCAAGCTCATTAGCATC 912
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1030 CTGCTGAGGAGATCTCGGCTAACGCTCTCTCTACCTGTGCGCATCATCGTGGGCATC 1089
QY 913 TGCACACATATCCACGACAGAGGTGTCTAGCGCCAGGCGCTTTCAGGAGACCCGACGTAC 972
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1090 ATGCTCTACTACATGGCAGACCGCTGAAGCACCGAAAGGCGCTTCTCGGAGCCCGCAGTCG 1149
QY 973 ATCCAGGCCCGGCTCCACCTGCAGCATGAGAAATCGGACGAGGAGCGGCTGCTGCTGTCG 1032
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1150 CTGGAGCTGAAGATGAATCTGAGGAGCAGACGCCACGACGAGGAACCTTATGCTTCC 1209
QY 1033 GTATTGCCCCAGCAGTTGCCATGGAGATGAAGAAGACATCAACACA ----- 1080
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1210 ATCCTCCCAAAGCATGTGGCTGACGAGATGTTGAAGGACATGAAGAAGATGAGAGTCAG 1269
QY 1081 AAAAAAGAAGACATGTTCCACAAAGATCTACATACAGAAAGCATGCAATGTCAGATCCTG 1140
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1270 AAGGACCACGACGATGTTCAACACCATGATCATGTACCCCATGAGAATGTCAGCATCCTG 1329
QY 1141 TTFTGACACATTTGAGGGCTTCCACCGCTGGCATCCCACTGCCTGCGCAGGAGCTGGTC 1200
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1330 TTFTGACATATTGTGGGCTTTTACCAGCTGTCTCTGCTTGCAGTGCACGAGAGCTGCTG 1389

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QY 2280 GTTCACTGTAAACACACACCCCATACGGAGC-----TGTGAGCCCGGATGCTGA 2329
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2469 GGCCAGAAATACCTGGGCCATGTTAGCCCATTTCACTTCTGGTTATGGCCAAATGTTGTGGA 2528
QY 2330 ATTTACACCTGCTGACATCACTGCTGCCACTGCAGCAGCTCAATTTACTCTCTGGGCC 2389
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2529 CATGCTGAGCTGTCTCCAGTACTACATGATGGACCT-TACACGCTGACCAACCGGATAGAGC 2587
QY 2390 TGGATGCTCCCTGTGTGAGGGCACCATGCCACCTGCAAGCTTTCTGAGGTGTCCATCG 2449
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2588 TGGACGGTGGCTGATGGAGAACCCCAAGTACTACAACATATGTTGCTGTCTCTCA 2647
QY 2450 GGAACATGCTGTGAGTCTCTTGGCAGCTCTGTCTTTCGTGACATFAGCA-GCATCGGG 2508
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2648 TCGCCACCATCATGCTGGTGCAGGTGAGCATGATGGAAGCTGACACTCATGCTGCTCG 2707
QY 2509 AAGTTGGCCATGATCTTTGCTTGGGGCTCATCTATTGTTGGTGTCTTCTGCTGGGTCCC 2568
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2708 TCACAGGCGGTGATGCGCATCAACCTGTATGCCCTGGTGTCTCTTGTGATGAATACG 2767
QY 2569 CGAGCGCCATCTTTGACAACTATGACCTACTGCTTGGGGTCCATGGCTTGGCTTCTTCC 2628
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2768 ACCACAAACGTTTCAGGAAGGACTCTCCTATGTTGGCTTAGAGAGATCAGGTAC 2827
QY 2629 AATGAGACCTTTGATGGGTGGACTGTCCAGCTGCAAG--GAGGGTGGCCCTCAAAATATA 2686
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2828 TTTCCACCCCTGGGCTCAATGGCACTGACAGCAGGCTGCCCTGGTGCCTTCCAAGTACT 2887
QY 2687 TGACCCCTGTGATCTGCTGGTGTGTTGGCTGGCGTGTATCTGCACTGTCAGCAGGTGG 2746
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2888 CGATGACTGTGATGATGTTTCGTTATGATGCTGAGCTTTTACTACTTCTCACGCCACGTGG 2947
QY 2747 AATCGACTGCCGCCCTAAATCTCTCTGGAACCTACAGCTCAACAGGGGAAAGAGGAGA 2806
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2948 AGAACTGGCCCGGACACTGTCTTGTGGAAGTTGAGGTCCATGACCAGAAAGACGTG 3007
QY 2807 TGAGAGGCTACAGGCATACAACGGAGGCTGCTGCATACAATCTGCCCAAGGACGTGG 2866
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3008 TGTACGAGATGCGCGGTGGAACGAGGCTTGGTCAACCAATGTTGCCAGAGCATGTTG 3067
QY 2867 CGGCCCATCTCTGGCCCGGAGCGCGCAATGATCAACTCTACTATCATGCTGTGTGAGT 2926
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3068 CAGGCCATTTCTGGGCTCCAAGAGAGAGATGAGGAGCTGTACAGCCAGTCTTATGACG 3127
QY 2927 GTGTGCTGTATTGTTTGTCTTCCAACTTCTCTGAGTTCTATGTGGAGCTGSAGG 2986
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3128 AGATTGGAGTCAATGTTTGCCTCTGCCCCAACTTTGCCGACTTCTACACTGAGGAGCA 3187
QY 2987 CAAACAATGAGGTTGCCGCTGCTCGGCTGCTCAACGAGATCATCGCTGACTTTGTATG 3046
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3188 TCAATAATGGTGCATCGAGTGTCTAGCTTCTCAATGAGATCATCTCTGATTTTGACT 3247
QY 3047 AGATTATCAGCAGGAGCGGTTCCGGCAGCTGGAAAAGATCAAGACGATTTGGTAGCACCT 3106
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QY 3107 ACATGGCTGCTCAGGCTGAACGCCAGCACCTAC----- 3141
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3488 GCATAGGCATGAACAAGAGGAGTGTCTGGCTGGAGTCAATTGGAGCCCGGAAGCCACACT 3547
QY 3308 ATGACATCTGGGGAAACACAGTGAATGCTCTAGTGTGAGACACGCGGGGTCCCCG 3367
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QY 3428 AGTGTGAGGGGTGGTCAAGGTGAAGGGCAAGGGGAGATGACCACTACTTCTCAATG 3487
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Job time : 136.927 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: March 1, 2003, 02:24:48 ; Search time 145.712 Seconds  
(without alignments)  
15188.998 Million cell updates/sec

Title: US-09-750-240-5

Perfect score: 3549

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 460893 seqs, 311809382 residues

Total number of hits satisfying chosen parameters: 921786

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	3478.4	98.0	4942	9	US-10-201-000-1
4	3379.2	95.2	3582	10	US-09-750-240-12
5	1808.4	51.0	1812	10	US-09-750-240-3
6	1703.4	48.0	4523	9	US-10-175-158-1
7	586	16.5	837	9	US-09-989-442-23
8	529.6	14.9	915	9	US-09-764-868-181
9	529.6	14.9	915	9	US-09-989-442-69
10	505.2	14.2	3518	9	US-10-121-911-2
11	395.8	11.2	2601	10	US-09-925-297-352
12	295.2	8.3	314	10	US-09-750-240-1
13	284.4	8.0	1180	10	US-09-915-582-11
14	265.6	7.5	1140	10	US-09-925-297-56
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17	216.8	6.1	4473	10	US-09-751-100B-1
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19	207.8	5.9	5515	10	US-09-751-100B-98

20	164.4	4.6	358	9	US-09-933-797-165	Sequence 165, App
21	145.8	4.1	449	10	US-09-960-352-13136	Sequence 13136, A
c 22	127.6	3.6	455	9	US-09-954-531-848	Sequence 848, App
23	127.4	3.6	630	9	US-09-764-868-180	Sequence 180, App
24	127.4	3.6	630	9	US-09-989-442-66	Sequence 66, Appl
25	124.4	3.5	330	9	US-09-764-868-182	Sequence 182, App
26	124.4	3.5	330	9	US-09-989-442-71	Sequence 71, Appl
27	124.4	3.5	330	10	US-09-764-869-445	Sequence 445, App
28	94.6	2.7	220	10	US-09-728-445-487	Sequence 487, App
29	79.2	2.2	11881	9	US-09-764-868-1351	Sequence 1351, Ap
30	79.2	2.2	11881	9	US-09-764-868-1353	Sequence 1353, Ap
c 31	79.2	2.2	11881	10	US-09-764-869-2124	Sequence 2124, Ap
32	78.8	2.2	237	9	US-09-796-692-5599	Sequence 5599, Ap
33	75.2	2.1	2335	10	US-09-917-800A-1569	Sequence 1569, Ap
34	64.4	1.8	1259	9	US-10-051-643-123	Sequence 123, App
35	64.4	1.8	1259	9	US-09-880-505-123	Sequence 123, App
36	64.4	1.8	2013	9	US-10-051-643-176	Sequence 176, App
37	64.4	1.8	2013	9	US-09-880-505-176	Sequence 176, App
38	64.4	1.8	2172	9	US-10-051-643-173	Sequence 173, App
39	64.4	1.8	2172	9	US-09-880-505-173	Sequence 173, App
c 40	54.4	1.5	3243	9	US-09-945-901-44	Sequence 44, Appl
c 41	54.4	1.5	3243	9	US-10-007-747-44	Sequence 44, Appl
c 42	54.4	1.5	3243	9	US-10-038-937-44	Sequence 44, Appl
c 43	54.4	1.5	3698	9	US-09-945-901-43	Sequence 43, Appl
c 44	54.4	1.5	3698	9	US-10-007-747-43	Sequence 43, Appl
c 45	54.4	1.5	3698	9	US-10-038-937-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1  
US-09-750-240-5  
; Sequence 5, Application US/09750240  
; Patent No. US20020103147A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammon, H. K.  
; APPLICANT: Insel, P. A.  
; APPLICANT: Ping, P. A.  
; APPLICANT: Post, S. R.  
; APPLICANT: Gao, M.  
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART FAILURE  
; FILE REFERENCE: 220002056723  
; CURRENT APPLICATION NUMBER: US/09/750,240  
; PRIOR FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 09/472,667  
; PRIOR FILING DATE: 1999-12-27  
; PRIOR APPLICATION NUMBER: US 09/008,097  
; PRIOR FILING DATE: 1998-01-16  
; PRIOR APPLICATION NUMBER: US 08/924,757  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: US 60/048,933  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: US 08/708,661  
; PRIOR FILING DATE: 1996-09-05  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 3549  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-750-240-5

Query Match	100.0%;	Score 3549;	DB 10;	Length 3549;
Best Local Similarity	100.0%;	Pred. No. 0;		
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QY	1	ATGTCATGTTTACTGGCTCTGGTCCCTAACTGGATGAACGAAACAGCTGGGGT	60	
Db	1	ATGTCATGTTTACTGGCTCTGGTCCCTAACTGGATGAACGAAACAGCTGGGGT	60	
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Qy	2281	TTGACCTGTAAACACACACCCCACTATGCGAGCTGTGCAGCCCGGATGTCTGAATTTAAACACCT	2340
Db	2281	TTGACCTGTAAACACACACCCCACTATGCGAGCTGTGCAGCCCGGATGTCTGAATTTAAACACCT	2340
Qy	2341	GCTGACATCACTGCCCTGCCACCTGCAGCAGCTCAATTACTCTCTGGCCTGGATGCTCCC	2400
Db	2341	GCTGACATCACTGCCCTGCCACCTGCAGCAGCTCAATTACTCTCTGGCCTGGATGCTCCC	2400
Qy	2401	CTGTGTGAGGGACCAATGCCACCTGCAGCTTTCCTGAGGTGTCCATCGGGAACATGCTG	2460
Db	2401	CTGTGTGAGGGACCAATGCCACCTGCAGCTTTCCTGAGGTGTCCATCGGGAACATGCTG	2460
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Db	2461	CTGAGTCTCTTGGCCAGCTCTCTTCTGTCACATCAAGCAGCATCGGGAATTTGGCCATG	2520
Qy	2521	ATCTTTTGTCTTGGGGCTCACTATTAATTTGGTGTGCTTCTGCTGGGTGCCCCCAGCGCCCATC	2580
Db	2521	ATCTTTTGTCTTGGGGCTCACTATTAATTTGGTGTGCTTCTGCTGGGTGCCCCCAGCGCCCATC	2580
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Db	3301	CCACAGTATGACATCTGGGGGAACACAGTGAATGTCTTAGTCTGATGAGACGACGCGG	3360

Qy	3361	GTCCCCGACCAATTCAGGTGACCGGACCTGTACCAAGTTCTAGCTGCCAAGGGCTAC	3420
Db	3361	GTCCCCGACCAATTCAGGTGACCGGACCTGTACCAAGTTCTAGCTGCCAAGGGCTAC	3420
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Qy	3481	CTCAATGGGGGCCCCAGCAGTGAACAGGGGCCAGGCCACCAAAATTCAGCTGAAGGGACCAAG	3540
Db	3481	CTCAATGGGGGCCCCAGCAGTGAACAGGGGCCAGGCCACCAAAATTCAGCTGAAGGGACCAAG	3540
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Db	3541	GTGGGCACCT	3549
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; Sequence 10, Application US/09750240			
; Patent No. US20020103147A1			
; GENERAL INFORMATION:			
; APPLICANT: Hammon, H. K.			
; APPLICANT: Insel, P. A.			
; APPLICANT: Ping, P.			
; APPLICANT: Post, S. R.			
; APPLICANT: Gao, M.			
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART			
; TITLE OF INVENTION: FAILURE			
; FILE REFERENCE: 220002056723			
; CURRENT APPLICATION NUMBER: US/09/750,240			
; CURRENT FILING DATE: 2001-10-12			
; PRIOR APPLICATION NUMBER: US 09/472,667			
; PRIOR FILING DATE: 1999-12-27			
; PRIOR APPLICATION NUMBER: US 09/008,097			
; PRIOR FILING DATE: 1998-01-16			
; PRIOR APPLICATION NUMBER: US 08/924,757			
; PRIOR FILING DATE: 1997-09-05			
; PRIOR APPLICATION NUMBER: US 60/048,933			
; PRIOR FILING DATE: 1997-06-16			
; PRIOR APPLICATION NUMBER: US 08/708,661			
; PRIOR FILING DATE: 1996-09-05			
; NUMBER OF SEQ ID NOS: 13			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 10			
; LENGTH: 3552			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-09-750-240-10			

Query Match 98.2%; Score 3484.8; DB 10; Length 3552;  
Best Local Similarity 99.0%; Pred. No. 0;  
Matches 3517; Conservative 0; Mismatches 32; Indels 3; Gaps 1;

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QY 2818 CAGGCATACAAACCGGAGGTGCTGCATAAATCTGCCAAAGACGTGGCGGCCACTTC 2877  
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QY 2878 CTGGCCGGGAGGCGCGCAATGATGAACCTACTATCAGTCGTCGAGTGTGGTGTGTT 2937  
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QY 3058 GAGGAGCGGTTCGCGAGCTGGAAAGATCAAGACCATTTGGTAGCACCTACATGGCTGCC 3117  
Db 3061 GAGGAGCGGTTCGCGAGCTGGAAAGATCAAGACCATTTGGTAGCACCTACATGGCTGCC 3120  
QY 3118 TCAGGGCTGAACCCAGCAGCTACGATCAGGTGGCGGCTCCACATCATCACTGCGCTGGCT 3177  
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Db 3541 AAGGTGGGCACT 3552

RESULT 3  
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; Sequence 1, Application US/10201000  
; Publication No. US20020187540A1  
; GENERAL INFORMATION:  
; APPLICANT: Tomlinson, James E.  
; APPLICANT: COR Therapeutics, Inc.  
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL  
; FILE REFERENCE: 44481-5028-01-US  
; CURRENT APPLICATION NUMBER: US/10/201,000  
; CURRENT FILING DATE: 2002-07-24  
; PRIOR APPLICATION NUMBER: US/09/474,076  
; PRIOR FILING DATE: 1999-12-12  
; PRIOR APPLICATION NUMBER: PCT/US98/13694  
; PRIOR FILING DATE: 1998-07-01  
; PRIOR APPLICATION NUMBER: 60/070,904  
; PRIOR FILING DATE: 1997-07-01  
; PRIOR APPLICATION NUMBER: 08/886,550  
; PRIOR FILING DATE: 1997-07-01  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 4942  
; TYPE: DNA  
; ORGANISM: human type VI adenylyl cyclase  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (145)..(3648)  
US-10-201-000-1

Query Match 98.0%; Score 3478.4; DB 9; Length 4942;  
Best Local Similarity 98.9%; Pred. No. 0;  
Matches 3513; Conservative 0; Mismatches 36; Indels 3; Gaps 1;

QY 1 ATCTCATGTTTATGTCCTCTGCTTCCCTAAAGTGGATGAACGGAAACAGCTGGGT 60  
Db 145 ATCTCATGTTTATGTCCTCTGCTTCCCTAAAGTGGATGAACGGAAACAGCTGGGT 204  
QY 61 GAACGCAATGGGAGAGCGTTCCGCGCGCGCTGGGACTCGGCGAGGTGCTTCTGCGACG 120  
Db 205 GAACGCAATGGGAGAGCGTTCCGCGCGCGCTGGGACTCGGCGAGGTGCTTCTGCGACG 264  
QY 121 CCCCCTATATGAGTGTCTCCGCGGATGACAGCCAGCCAGCCAGCCCTGCGGGCCCC 180  
Db 265 CCCCCTATATGAGTGTCTCCGCGGATGACAGCCAGCCAGCCAGCCCTGCGGGCCCC 324  
QY 181 CCTCGTGGCCCTGGCAGGATGACGCTTCCATCCGAGGGGCGGCCAGGAGGCAAG 240  
Db 325 CCTCGTGGCCCTGGCAGGATGACGCTTCCATCCGAGGGGCGGCCAGGAGGCAAG 384  
QY 241 GAGCTGGGGTGGCGGAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACACGACAGCG 300  
Db 385 GAGCTGGGGTGGCGGAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACACGACAGCG 444  
QY 301 GCGGAGACGCTGAGTGGCGCCCGGCGGTCGCCAGGAGTGGCGGATCCTGCTGCGCG 360  
Db 445 GCGGAGACGCTGAGTGGCGCCCGGCGGTCGCCAGGAGTGGCGGATCCTGCTGCGCG 504  
QY 361 CGTTTGTGTCAGTGTTCAGTGAAGCAGTTCCTGCGGCCAGGCTGGAGCGCTGTAC 420  
Db 505 CGTCTGTGTCAGTGTTCAGTGAAGCAGTTCCTGCGGCCAGGCTGGAGCGCTGTAC 564  
QY 421 CAGCGGTACTTTTCCAGATGAACAGAGCAGCTGACGCTGCTGCTGGCGGTGCTGGTG 480  
Db 565 CAGCGGTACTTTTCCAGATGAACAGAGCAGCTGACGCTGCTGCTGGCGGTGCTGGTG 624  
QY 481 CTGCTCACAGCGGTGCTGCTGGCTTTCCAAAGCGGCAGCCCGCCCTCAGCGCTGCTAT 540  
Db 625 CTGCTCACAGCGGTGCTGCTGGCTTTCCAAAGCGGCAGCCCGCCCTCAGCGCTGCTAT 684



Qy	541	GTGGCACTGTTGGCCTGTGCCGCGCCCTGTTCTGTGGGGCTCATGGTGGTGTGAACCGG	600
Db	685		
		GTGGCACTGTTGGCCTGTGCCGCGCCCTGTTCTGTGGGGCTCATGGTGGTGTGAACCGG	744
Qy	601	CATAGCTTCGGCCAGACACTCCATGTGGGTGGTGACTAACTGGTGCCTGGGCATCCTGGCG	660
Db	745		
		CATAGCTTCGGCCAGACACTCCATGTGGGTGGTGACTACGTGGTGTGGGCATCCTGGCG	804
Qy	661	GCAGTGCAGGTTCGGGGCGCTTTCGCAGCAGACCCGCGCAGCCCTCTTCGCGGGCTCTCGG	720
Db	805		
		GCAGTGCAGGTTCGGGGCGCTCTCGCAGCAGACCCGCGCAGCCCTCTTCGCGGGCTCTCGG	864
Qy	721	TGCCCTGTGTTCTTTGTAFACATPCGATACAGCTTCCTCCCATCCCGATCCGATCGCGGCTGCC	780
Db	865		
		TGCCCTGTGTTCTTTGTCTACATCGCCTACACGCTCCTCCCATCCCGATCGCGGCTGCC	924
Qy	781	GTCTTCAGCGCCTGGGCCTCTCCACCTTGCATTTGATCTTTGGCTGGCACTTTAACCGT	840
Db	925		
		GTCTTCAGCGCCTGGGCCTCTCCACCTTGCATTTGATCTTTGGCTGGCACTTTAACCGT	984
Qy	841	GGTGATGCCCTTCCTCTGGAAGCAGCTCGGTGCCAATGTGCTGTCTTCTCTGCACCAAC	900
Db	985		
		GGTGATGCCCTTCCTCTGGAAGCAGCTCGGTGCCAATGTGCTGTCTTCTGCACCAAC	1044
Qy	901	GTCAATTAGCAATTCGCACACACTATCCAGCAGAGTGTCTCAGCGCCAGGCCCTTTCAGGAG	960
Db	1045		
		GTCAATTGGCACTTCGCACACACTATCCAGCAGAGTGTCTCAGCGCCAGGCCCTTTCAGGAG	1104
Qy	961	ACCGCAGTTTACATCCAGCGCCGGCTCCACCTGCAGCATGAGATCGCGCAGCAGAGCGG	1020
Db	1105		
		ACCGCGGTTTACATCCAGCGCCGGCTCCACCTGCAGCATGAGATCGCGCAGCAGAGCGG	1164
Qy	1021	CTGCTGCTGTGCGTATTGCCCCAGCAGCAGTTCGCATGGAGATGAAAGAGACATCAACACA	1080
Db	1165		
		CTGCTGCTGTGCGTATTGCCCCAGCAGCAGTTCGCATGGAGATGAAAGAGACATCAACACA	1224
Qy	1081	AAAAAGAGAC---ATGTTCCACAAGATCTATACATACAGAAGCATGACAATGTCAGCATC	1137
Db	1225		
		AAAAAGAGACATGATGTTCCACAAGATCTATACATACAGAAGCATGACAATGTCAGCATC	1284
Qy	1138	CTGTTTGCAGACATTCAGGGCTTCACAGCCTGGCATCCCACTGCAGTGCAGTGCAGAGAGCTG	1197
Db	1285		
		CTGTTTGCAGACATTCAGGGCTTCACAGCCTGGCATCCCACTGCAGTGCAGAGAGCTG	1344
Qy	1198	GTATGACCTGTAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTGGCGGAGAATCACTGC	1257
Db	1345		
		GTATGACCTGTAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTGGCGGAGAATCACTGC	1404
Qy	1258	CTGAGGATCAAGATCTTGGGGACTGTTACTACTGTGTGTGAGGGCTGCCGGAGGCCCGG	1317
Db	1405		
		CTGAGGATCAAGATCTTGGGGACTGTTACTACTGTGTGTGAGGGCTGCCGGAGGCCCGG	1464
Qy	1318	GCGGACCATGCCACATGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTG	1377
Db	1465		
		GCGGACCATGCCACATGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTG	1524
Qy	1378	GTAGTGAAGTGAACAGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGCGCGCTG	1437
Db	1525		
		GTAGTGAAGTGAACAGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGCGCGCTG	1584
Qy	1438	CAGTGGCGCTCCTTGGCTTCGGAAATGGCAGTTTCGATGTGTGTCCCAATGATGTGACC	1497
Db	1585		
		CAGTGGCGCTCCTTGGCTTCGGAAATGGCAGTTTCGATGTGTGTCCCAATGATGTGACC	1644
Qy	1498	CTGGCCAAACCATGGAAGCAGGACCGGGCTGGCCGCTCCACATCACTTCGGGCAACA	1557
Db	1645		
		CTGGCCAAACCATGGAAGCAGGACCGGGCTGGCCGCTCCACATCACTTCGGGCAACA	1704
Qy	1558	CTCAGTACTGAAOCGGGACTACGAGTGAAGTCAGCGCCGTGTGTGGCAAGCGCAACGCG	1617
Db	1705		
		CTCAGTACTGAAOCGGGACTACGAGTGAAGTCAGCGCCGTGTGTGGCAAGCGCAACGCG	1764

Qy	1618	TAC	TCAAGGAGCAGCACA	T	TGAGACT	T	TTC	TCA	TCTCTGGGGCCAGCCAGCAAA	CGAAA	1617
Db	1765	TAC	TCAAGGAGCAGCACA	T	TGAGACT	T	TTC	TCA	TCTCTGGGGCCAGCCAGCAAA	CGAAA	1824
Qy	1678	GAG	GAGAAAGGCAT	G	TGTGGCCAAAGCT	G	CAGCGACT	CGGGCCAACT	TCCATCGAAGGGCTG	1737	
Db	1825	GAG	GAGAAAGGCAT	G	TGTGGCCAAAGCT	G	CAGCGACT	CGGGCCAACT	TCCATCGAAGGGCTG	1884	
Qy	1738	ATG	CGCGGATGGGT	T	TCTGATCGTGCT	T	TCTCCCGGACCAAGGACT	TCCAAGGCCCTTC	CGCG	1797	
Db	1885	ATG	CGCGGCTGGGT	T	TCTGATCGTGCT	T	TCTCCCGGACCAAGGACT	TCCAAGGCCCTTC	CGCG	1944	
Qy	1798	CAG	ATGGGCAT	T	GATGATTC	CACAGAAACACCGGGCCACCAAGAT	AGATGC	CGCCTGAACCCCT	1857		
Db	1945	CAG	ATGGGCAT	T	GATGATTC	CACAGAAACACCGGGCCACCAAGAT	AGATGC	CGCCTGAACCCCT	2004		
Qy	1858	GAG	ATCAGGTG	GATGAGT	TCTTGACCGCT	GCATCGATGCCCGAGCAT	TGATCAGCTG	1917			
Db	2005	CAG	ATCAGGTG	GATGAGT	TCTTGACCGCT	GCATCGATGCCCGAGCAT	TGATCAGCTG	2064			
Qy	1918	CGA	AGACCACT	GTGCGCGGTT	TTTGCTACCT	TCCAGAGAGAGAT	TTTGGAGAAG	1977			
Db	2065	CGA	AGACCACT	GTGCGCGGTT	TTTGCTACCT	TCCAGAGAGAGAT	TTTGGAGAAG	2124			
Qy	1978	TACT	CCCGGAAGTGGAT	CCCCGCTTCGGAGCCT	ACGTTGCCTGTGC	CGCCTGTGGCTCTC	2037				
Db	2125	TACT	CCCGGAAGTGGAT	CCCCGCTTCGGAGCCT	ACGTTGCCTGTGC	CGCCTGTGGCTCTC	2184				
Qy	2038	TGCT	TCAATCTGCT	TATCAGCTT	CTAATTTTCCACACT	TCACCCCTGATCGTTGGGAT	2097				
Db	2185	TGCT	TCAATCTGCT	TATCAGCTT	CTAATTTTCCACACT	TCACCCCTGATCGTTGGGAT	2244				
Qy	2098	TAT	CCAGCACT	CTCTGCTGCT	GTCTAATCACCGTCTGATCT	GTGCTGCTACTCCCTGT	2157				
Db	2245	TAT	CCAGCACT	CTCTGCTGCT	GTCTAATCACCGTCTGATCT	GTGCTGCTACTCCCTGT	2304				
Qy	2158	GGT	TCTCTGTTCC	CTAAGGCCCTTGCAACGT	CTGTCCCGCAGCAT	TGTCGGCTCACGGGCA	2217				
Db	2305	GGT	TCTCTGTTCC	CTAAGGCCCTTGCAACGT	CTGTCCCGCAGCAT	TGTCGGCTCACGGGCA	2364				
Qy	2218	CAT	AGCACCGCAGT	TGGCACT	TTTCCGCTCTGCTTGTTGTTTACT	CTGCGCATTCGCAAC	2277				
Db	2365	CAT	AGCACCGCAGT	TGGCACT	TTTCCGCTCTGCTTGTTGTTTACT	CTGCGCATTCGCAAC	2424				
Qy	2278	ATG	TTACCTGT	TAAACACACCCCACT	PACGAGCTGTGCAGCCCGGAT	CTCAATTTAA	2337				
Db	2425	ATG	TTACCTGT	TAAACACACCCCACT	PACGAGCTGTGCAGCCCGGAT	CTCAATTTAA	2484				
Qy	2338	CCT	GCTGACAT	CACTGCCTGCC	ACCTGCAGCAGCTCAAT	TACTCTCTGGGCTCGATGCT	2397				
Db	2485	CCT	GCTGACAT	CACTGCCTGCC	ACCTGCAGCAGCTCAAT	TACTCTCTGGGCTCGATGCT	2544				
Qy	2398	CCC	TGTGTGAGG	GCACCAT	TGCCACCTGCAGCTTTCTG	TGAGTGTCCATCGGGAATG	2457				
Db	2545	CCC	TGTGTGAGG	GCACCAT	TGCCACCTGCAGCTTTCTG	TGAGTGTCCATCGGGAATG	2604				
Qy	2458	CTG	CTGAGTCT	TTGGCCAGCT	CTGTCTCTCCGACAT	CAGCAGCATCGGGAAT	2517				
Db	2605	CTG	CTGAGTCT	TTGGCCAGCT	CTGTCTCTCCGACAT	CAGCAGCATCGGGAAT	2664				
Qy	2518	ATG	ATCTTTTCT	CTTTGGGGT	CTACTATTTTGGTGTCT	TCTGCTGGGTCGCCACGCGCC	2577				
Db	2665	ATG	ATCTTTTCT	CTTTGGGGT	CTACTATTTTGGTGTCT	TCTGCTGGGTCGCCACGCGCC	2724				
Qy	2578	ATC	TTTGACAACT	TATGACCT	TACTGTGTGGGTC	CAATAGGCTTGTTC	CAATGAGACC	2637			
Db	2725	ATC	TTTGACAACT	TATGACCT	TACTGTGTGGGTC	CAATAGGCTTGTTC	CAATGAGACC	2784			
Qy	2638	TTT	GATGGGCTG	ACACTGT	CCAGCTCAGGGAGGGT	GGCCCTCAATATATGACCCCTGTG	2697				
Db	2785	TTT	GATGGGCTG	ACACTGT	CCAGCTCAGGGAGGGT	GGCCCTCAATATATGACCCCTGTG	2844				
Qy	2698	ATT	CTGCTGCT	TTTGGCT	TGGCGCTGTATCT	GTGATGTCTCAGCAGGTGGAACTCAGCTGCC	2757				





Db 2899 CTGCCCGGAGGCGCCCAATGATGAACCTACTATCAGTCGCTGAGTGTGGCTGTT 2958  
QY 2938 ATGTTTGGCTCCATGTCACCACTTCTGAGTCTTATGTGAGCTGGAGGCAACAATGAG 2997  
Db 2959 ATGTTTCCCTCCATGTCACCACTTCTGAGTCTTATGTGAGCTGGAGGCAACAATGAG 3018  
QY 2998 GGTGCCAGTGCCTGCGGCTGCACAGAGATCATCGTCTGACTTTGATGAGATTATCAGC 3057  
Db 3019 GGTGTCAGTGCCTGCGGCTGCTCAAGAGATCATCGTCTGACTTTGATGAGATTATCAGC 3078  
QY 3058 GAGAGCGGTTCGGCGAGCTGGAAGATCAAGACGATTGGTAGCAGCTACATGGCTGCC 3117  
Db 3079 GAGAGCGGTTCGGCGAGCTGGAAGATCAAGACGATTGGTAGCAGCTACATGGCTGCC 3138  
QY 3118 TCAGGGCTGAACGCCAGCAGCTAGATCAGTGGCGGCTCCACATCACTGCGCTGGCT 3177  
Db 3139 TCAGGGCTGAACGCCAGCAGCTAGATCAGTGGCGGCTCCACATCACTGCGCTGGCT 3198  
QY 3178 GACTACGCCATGGGCTTCATGGAGCAGATGAAGCACATCAATGAGCACTCTTCAACAAT 3237  
Db 3199 GACTACGCCATGGGCTTCATGGAGCAGATGAAGCACATCAATGAGCACTCTTCAACAAT 3258  
QY 3238 TTCAGATGAAGATTGGGCTGAACATGGGCCAGTGGCCAGTGTGATCGTATGGACGACG 3297  
Db 3259 TTCAGATGAAGATTGGGCTGAACATGGGCCAGTGGCCAGTGTGATCGTATGGACGACG 3318  
QY 3298 AAGCCACAGTATGACATCTGGGGAGACACAGTGAATGTCTAGTCTGATGGACGACG 3357  
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Db 3379 GGGTCCCGACCGAATCCAGGTGACCACGAGCTGTACCAGGTTCTAGCTGCCAAGGC 3438  
QY 3418 TACCAGTGGAGTGTGAGGGGTGGTCAAGGTGAAGGGCAAGGGGAGATGACCACTAC 3477  
Db 3439 TACCAGTGGAGTGTGAGGGGTGGTCAAGGTGAAGGGCAAGGGGAGATGACCACTAC 3498  
QY 3478 TTCTCAATGGGGCCCCAGCAGTTACAGGGCCCCAGCCACAATTCAGCTGAAGGACC 3537  
Db 3499 TTCTCAATGGGGCCCCAGCAGTTACAGGGCCCCAGCCACAATTCAGCTGAAGGACC 3558  
QY 3538 AAGTGGGCCT 3549  
Db 3559 AAGTGGGCCT 3570

RESULT 5  
US-09-750-240-3  
; Sequence 3, Application US/09750240  
; Patent No. US20020103147A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammon, H. K.  
; APPLICANT: Insel, P. A.  
; APPLICANT: Ping, P.  
; APPLICANT: Post, S. R.  
; APPLICANT: Gao, M.  
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART  
; TITLE OF INVENTION: FAILURE  
; FILE REFERENCE: 22002056723  
; CURRENT APPLICATION NUMBER: US/09/750,240  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 09/472,667  
; PRIOR FILING DATE: 1999-12-27  
; PRIOR APPLICATION NUMBER: US 09/008,097  
; PRIOR FILING DATE: 1998-01-16  
; PRIOR APPLICATION NUMBER: US 08/924,757  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: US 60/048,933  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: US 08/708,661  
; PRIOR FILING DATE: 1996-09-05

; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1812  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-750-240-3  
Query Match 51.0%; Score 1808.4; DB 10; Length 1812;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1809; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 636 TAACGTGGTCTGGGATCCTGCGGAGTCAGGTGCGGGCGCTTCGCGAGCAGACCC 695  
Db 3 TAACGTGGTCTGGGATCCTGCGGAGTCAGGTGCGGGCGCTTCGCGAGCAGACCC 62  
QY 696 GCGAGCCCTCTGCGGGCTCTGGTGCCCTGTGTTCTTGTATACATGCGATACAGCT 755  
Db 63 GCGAGCCCTCTGCGGGCTCTGGTGCCCTGTGTTCTTGTATACATGCGATACAGCT 122  
QY 756 CTTCCCATCCGATCGGCTGCCGTCTCAGCGGCTGGGCTCTCCACCTTGCATTT 815  
Db 123 CTTCCCATCCGATCGGCTGCCGTCTCAGCGGCTGGGCTCTCCACCTTGCATTT 182  
QY 816 GATCTTGGCTGGCAACTTAACCGTGTGATGCTTCTCTGGAAGCAGCTCGGTGCCAA 875  
Db 183 GATCTTGGCTGGCAACTTAACCGTGTGATGCTTCTCTGGAAGCAGCTCGGTGCCAA 242  
QY 876 TGTGCTGCTGTTCTCTGCAACAGCTATTAGCATCTGCACACACTATCCAGCAGGT 935  
Db 243 TGTGCTGCTGTTCTCTGCAACAGCTATTAGCATCTGCACACACTATCCAGCAGGT 302  
QY 936 GTCTCAGCGCCAGGCTTTTCCAGGAGCCCGAGTTACATCCAGGCCCGGCTCCACCTGCA 995  
Db 303 GTCTCAGCGCCAGGCTTTTCCAGGAGCCCGAGTTACATCCAGGCCCGGCTCCACCTGCA 362  
QY 996 GCATGAGAATCGGAGGAGGCGCTGCTGCTGCGTATTGCCCCAGCAGCTTGCAT 1055  
Db 363 GCATGAGAATCGGAGGAGGCGGCTGCTGCTGCGTATTGCCCCAGCAGCTTGCAT 422  
QY 1056 GGAGATGAAAGAGACATCAACACAAAAAAGAGACATGTTCCACAAGATCTACATACA 1115  
Db 423 GGAGATGAAAGAGACATCAACACAAAAAAGAGACATGTTCCACAAGATCTACATACA 482  
QY 1116 GAAGCATGACAATGTCAGCATCTGTTTGCAGACATTTAGGGCTTCACCGCTGGCATC 1175  
Db 483 GAAGCATGACAATGTCAGCATCTGTTTGCAGACATTTAGGGCTTCACCGCTGGCATC 542  
QY 1176 CCAGTGCACTGCGCAGGAGCTGGTCAATGAGCTCTTTGCCGGTTTGACAA 1235  
Db 543 CCAGTGCACTGCGCAGGAGCTGGTCAATGAGCTCTTTGCCGGTTTGACAA 602  
QY 1236 GCTGGCTGCGGAGAAATCACTGCTGAGGATCAAGATCTTGGGAGCTTGTACTACTGT 1295  
Db 603 GCTGGCTGCGGAGAAATCACTGCTGAGGATCAAGATCTTGGGAGCTTGTACTACTGT 662  
QY 1296 GTCAGGCTGCCGAGGCGCGGCGGAGCATGCCCATGCTGTGTGAGATGGGGTAGA 1355  
Db 663 GTCAGGCTGCCGAGGCGCGGCGGAGCATGCCCATGCTGTGTGAGATGGGGTAGA 722  
QY 1356 CATGATTGAGGCTCTGCTGCTGAGGTGACAGGTGTGAATGTGAACATGCGCGT 1415  
Db 723 CATGATTGAGGCTCTGCTGCTGAGGTGACAGGTGTGAATGTGAACATGCGCGT 782  
QY 1416 GGGCATCCACAGCGGCGCGCTGCACTGCGGCTCTTGGTGTGCGGAAATGGCAGTTGCA 1475  
Db 783 GGGCATCCACAGCGGCGCGCTGCACTGCGGCTCTTGGTGTGCGGAAATGGCAGTTGCA 842  
QY 1476 TGTGTGTTCAATGATGTGACCTGGCCAAACCATGGAAGAGAGAGCGGCTGCCG 1535  
Db 843 TGTGTGTTCAATGATGTGACCTGGCCAAACCATGGAAGAGAGAGCGGCTGCCG 902  
QY 1536 CATCCACATCACTCGGCAACACTGCACTACCTGAACGGGGACTACGAAGTGGAGCCAGG 1595



QY 934 GTGTCTCAGCGCAGGCTTTTCAGGAGACCCGAGTTACATCCAGGCCCGGCTCCAGCTG 993  
 Db 1342 GTCTCCAGAGACAGGCTTTCCAGGAGACCCGAGAGTGCATCCAGGGCGGCTCCAGCTG 1401  
 QY 994 CAGCATGAGAAATCGGAGCAGGAGCGGCTGCTGCTGTGGTATTTGCCCCAGCAGGTGGC 1053  
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 QY 1054 ATGAGATGAAGAAGACATCAACACAAAAGAGAGAC---ATGTTCCACAGATCTAC 1110  
 Db 1462 ATGAGATGAAGAAGACATCAACGCCAAGCAGGAGATATGATGTCCATAGATTTAC 1521  
 QY 1111 ATACGAAGCATGACAATGTCAGCATCTGTTTTCGAGACATTTGAGGGCTTCACAGCGCTG 1170  
 Db 1522 ATCCAGAARATGACAACTGAGCATCTGTTGCTGACATCAGGGCTTCACAGCGCTG 1581  
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 Db 1582 GCGTCCCACTGCACTGCACAGGAACGGTCAATGACCTCAACGAGCTCTTCGCCCGGCTT 1641  
 QY 1231 GACAAGCTGGCTGGGAGATCACTGCCTGAGGATCAAGATCTTGGGGACTCTTACTAC 1290  
 Db 1642 GACAAGCTGGCCGAGAGATCACTGTTTACGTATTAAAGATCTTGGGGATTTGTTATTAC 1701  
 QY 1291 TGTGTGTAGGGCTGGCGGAGGCGCGGCGGACCATGCCACTGCTGTGTGGAGATGGGG 1350  
 Db 1702 TGCCTCTCGGGCTGCTGAAGCAAGGCTGACCAAGCCCATGCTGTGTGGAGATGGG 1761  
 QY 1351 GTAGACATGATGAGGCGCATCTCGCTGGTACGTGAGGTGACAGGTGTGAATGTGAACATG 1410  
 Db 1762 ATGAGACATGATCAGGCGCATCTCGTTGGTCCGGGAGGTGACAGGGGTGAACGTGAACATG 1821  
 QY 1411 CGCGTGGGATCCACAGCGGCGCTGCACTGCGGCTGCTTGGCTTGGGAAATGCGAG 1470  
 Db 1822 CGTGTGGAAATTCACAGCGGCGAGTACACTGCGGTGCTTGGCTTCAGGAAAGTGGCAG 1881  
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 Db 1882 TTCGAGCTGTGTCTAACGATGTACGCTAGCCAGCAACCATGAGGCTGCGCGCAAGCA 1941  
 QY 1531 GGCGGATCCACATCACTCGGGCAACACGTCAGTACTGTAACGGGAGCTACGAAGTGGAG 1590  
 Db 1942 GAGCGATCCACATCAACCAAGGCTACACTCAACTGCTGAATGGGACTACGAGGTGGAG 2001  
 QY 1591 CCAGGCGGTGGTGGCAAGCGCAACGGTACTCAAGGAGCAGCACATGTAGAGCTTTCCTC 1650  
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 QY 1711 ACTCGGGCCAACTCCATGAGAGGGCTGTATGTCGCGATGGTTCCTGATCGTGCCTTCTCC 1770  
 Db 2122 CAGAGAACCAACTCCATTCGCGGCAACACCCACACACTGCGGGGCTGAGCGCCCTTCTAC 2181  
 QY 1771 -----CGGACCAAGGACTCCAAAGGCTTCGCGCAGATGGGCAATGTGATTC 1818  
 Db 2182 AACCACTGGGTGGCAACCAAGTGTCCAGGAGATGAAGCGATGGGCTTTGAAGACCCC 2241  
 QY 1819 AGCAAGACAAACCGGGGCAACCAAGATGCCCTGAACCCCTGAGGATGAGTGTGATGATTC 1878  
 Db 2242 A-----AGGACAAGAACGCCAGAGAGTGCGAACCCCTGAGGATGAAGTGGATGATTT 2295  
 QY 1879 CTGAGCCGTGCCATCCATGCCCGCAGCATTTGATCAGCTGGGGAAGACCATGTGCGCGG 1938  
 Db 2296 CTGGCGCGTGCATTCACGCCAGGAGATGATGATGAGTTCCTGCTGTGAGCACGTCGCCAAG 2355  
 QY 1939 TTTTCTCACCCTTCCAGAGAGAGGATTTTGAAGAAGTACTCCCGGAGGTGGATCCC 1998  
 Db 2356 TTCTCTGACCTTTCAGGGAGCCTGACTTAGAGAAGAAGTACTCCAAGCAGGTTAGACGAC 2415

QY 1999 CGCTTCGGAGCCTACGTTGCCTGTGTCCTGTGTGTCTCTGCTTCATCTGCTTCATCCAG 2058  
 Db 2416 CGATTTGGTGCCTATGTGGGTGTGCTGCTGCTGCTCTTCTTCATCTGCTTTGTCCAG 2475  
 QY 2059 CTTCTAAATTTCCACACTCCACCCTGATGCTGTTGGGATTTATGCCAGCAGCTTCCTGCTG 2118  
 Db 2476 ATCACCATCTGTGCCCACTCCATATTCATGCTCAGCTTTCACCTGACCTGTTCCTGCTG 2535  
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 Db 2536 CTGACCTTGGTGTGTTGTTGCTGTGATCTACTCTTCGCTAAAGCTTCTCCCTCCCCA 2595  
 QY 2179 CTGCAACGCTGTGCCGAGCATTTGCCGCTCAGCGGCACATAGCAGCGAGTTGGCATC 2238  
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 Db 2656 TTCACCATCACCTGCTGTTCTTGGGGCTTTTGTCAACATGTTACGCTGCAACTCCAGG 2715  
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 Db 2776 CACGTGCGGAGTGGCGGCTCAACTACAGCCTGGGCGATCAGCAGGCTTCTGTGGCAGC 2835  
 QY 2413 ACCATGCCACCTGACAGCTTTTCTGAGGTGTCCATGCGGGAACATGCTGTGAGTCTCTTG 2472  
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 Db 3013 GACCTGCTGTGCTACCGCCCAACGCCATAGACTTCTTCA---ACAACGGGAGCTTCCAGTGC 3069  
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 Db 3070 CCTGAGCATGCACCAAGGTGGCATTTGAAGGTGGTGACGCCCATCATCTCAGTCTTT 3129  
 QY 2713 GCCTGGGCTGTATCTGCACTGCTCAGCAGGTGGAATFCGACTGCCGCTTAAACTTCCCTC 2772  
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 QY 2773 TGGAAACTACAGCAACAGGGGAAAAGAGAGATGGAGGAGCTCAGGCTATCAACCCG 2832  
 Db 3190 TGGAAACTGCAGGCCACAGAGAGAAAGAGAGATGGAGGAGCTGCAAGGCTTCAACCCG 3249  
 QY 2833 AGCTGCTGCTAATCACTTGCCTCAGGAGCTGGCGGCCACTTCTTGGCGCGGAGCGC 2892  
 Db 3250 CGCTGCTGCACAACTCTTGCCTCAGGAGCTGGCGCTCCTTCTTGGCGCGGAGCGG 3309  
 QY 2893 CGCAATGATGAATCTACTATCATCTGCTGAGTGTGTGCTGTTATGTTTGGCTTCCATT 2952  
 Db 3310 CGCAATGATGAGCTACTATCATCTGCTGAGTGTGTGCGGCTCATGTTTGGCTTCCATC 3369  
 QY 2953 GCCAATCTCTGAGTCTATGTTGGAGCTGGAGGCAACAAATGAGGTTGCCGAGTGGCTG 3012  
 Db 3370 GCCAATCTTCCGAGTCTACGTTGAGCTGGAGGCCAACACAGGAGGTGTGAGTGGCTG 3429  
 QY 3013 CGCTGCTCAACAGATCATCTGCTGACTTTGATGAGATTTATCAGCGAGGAGGTTTCCGG 3072  
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 QY 3073 CAGCTGGAAGAAGATCAAGAGGATTTGGTAGCACCTTACATGCTGCTCAGGGGCTGAAGGCC 3132



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QY 3373 ATCCAGGTGACCACGAGCACTGTACCAGGTTCTAGCTGCCAAGGGTACCAGCTGGAGTGT 3432
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QY 3493 CCC 3495
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Db 3910 CCC 3912

RESULT 7
US-09-989-442-23
; Sequence 23, Application US/09989442
; Publication No. US20030013649A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ208
; CURRENT APPLICATION NUMBER: US/09/989,442
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
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; PRIOR FILING DATE: 2000-07-11
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; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/233,065  
; PRIOR FILING DATE: 2000-09-14  
  
Query Match 16.5%; Score 586; DB 9; Length 837;  
Best Local Similarity 85.3%; Pred. No. 1.7e-135;  
Matches 652; Conservative 1; Mismatches 111; Indels 0; Gaps 0;  
  
QY 2732 ATGCTCAGCAGGTGGAATCGACTGCCCGCCTAAACTTCTCTGGAACATACAGGCACAG 2791  
Db 1 ACGCCAGCAGGTGGAGTCCACTGCCCGCCTCGACTTCTCTTGAGACTGCGAGCCACAG 60  
  
QY 2792 GGGAAAAAGAGGAGATGAGGAGCTACAGGCATACAAACCGAGGCTGCTGCATACATTC 2851  
Db 61 AGGAGATAGAGGAGATGAGGAGCTGCAGGCCTACAAACCGCGCTGCTGCACACATCC 120  
  
QY 2852 TGCCCAAGGAGTGGCGGCCACTTCTTGCCCCGGGAGCGCCGAATGATGAATCTACT 2911  
Db 121 TGCCCAAGGAGTGGCGGCCACTTCTTGCCCCGGGAGCGCCGAATGATGAATCTACT 180  
  
QY 2912 ATCAGTCGTGTGAGTGTGCTGTATGTTGCTTCCATTCGCAACTTCTCTCAGTTCT 2971  
Db 181 ATCAGTCTGTGAGTGTGCTGTATGTTGCTTCCATTCGCAACTTCTCTCAGTTCT 240  
  
QY 2972 ATGTGGAGCTGGAGGCAACAAATGAGGCTGCCGAGTGCCTCGCGCTGCTCAACGAGATCA 3031  
Db 241 ACGTTGAGCTGGAGGCCAACAAACGAGGCTGTCGAGTGCCTCGCGCTACTCAATGAGATCA 300  
  
QY 3032 TCGCTGACTTTGATGAGATTATCAGCGAGGAGCGGTTCCCGCAGCTGGAAGAATCAAGA 3091  
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Db 361 CCATCGGCAGCACCTACATGCTGCCCTCAGGCTTCAAGACTCTACCTACGCAAGGTGG 420  
  
QY 3152 GCGCTCCCATCCTGCTGCCCTGGCTGACTACGCCCTCGCGCTCATGGAGCAGATGAAGC 3211  
Db 421 GCAAGACCCACATCAAGGCCTGSCCGACTTTGCCATGAAGCTGAGCCAGATGAAGT 480  
  
QY 3212 ACATCAATGAGCACTCCTTCAACAAATTTCCAGATGAAGATTGGCTGAACATGGGCCAG 3271  
Db 481 ACATCAATGAGCACTCCTTCAACAAATTTCCAGATGAAGATTGGCTGAACATGGGCCAG 540  
  
QY 3272 TCGTGGCAGGTGTCATCGGGCTCGGAAGACACAGATGATGACATCTGGGGGAACACAGTGA 3331  
Db 541 TGGTGGCCGGGTGATAGGGCAGCAAGGCTCAGTACGACATCTGGGGCAATACCGTGA 600  
  
QY 3332 ATGTCTCTAGTCTGATGGACAGCAGCGGGGTGCCCGCAGCAATCCAGGTGAGCCAGGCC 3391  
Db 601 ACGTGGCCAGCCGATGGACAGCAGCGGTGTACCCGACCGCTACAGTCCAGGTCCACACAGA 660  
  
QY 3392 TGTACCAAGGTTCTAGCTGCGCAAGGGCTACCAAGTGGAGTGTGAGGGGTGGTCAAGGTGA 3451  
Db 661 TGTACCAAGGTTCTAGCTGCGCAAGGGCTACCAAGTGGAGTGTGAGGGGTGGTCAAGGTGA 720  
  
QY 3452 AGGCAAGGGGAGATGACCACTTCTCTCAATGGGGCCCC 3495  
Db 721 AGGCAAGGGGAGATGATGACCTTCTCTCAATGGGGCCCC 764

RESULT 8  
US-09-764-868-181  
; Sequence 181, Application US/09764868  
; Patent No. US20020168711A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT232  
; CURRENT APPLICATION NUMBER: US/09/764,868  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - refer to PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 1510  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 181  
; LENGTH: 915  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (815)  
; OTHER INFORMATION: n equals a,t,g, or c  
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; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (878)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (883)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-764-868-181

Query Match 14.9%; Score 529.6; DB 9; Length 915;  
Best Local Similarity 85.2%; Pred. No. 1.6e-121;  
Matches 600; Conservative 2; Mismatches 101; Indels 1; Gaps 1;  
QY 2792 GGGAAAAGAGGAGATGGAGGACATACAGGCATACAAACGGAGGCTGCTGCATAACATTC 2851  
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DB 12 GRAGAAAGAGGAGATGGAGGAGCTGCA-GCCTACAAACCGGGGCTGCTGCACAACATCC 70  
QY 2852 TGCCCAAGACGCGGGCCCACTTCTGCGCGGAGCGCCGATGATGACTTACT 2911  
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DB 71 TGCCCAAGACGCGGGGCTGCTTCTGCGCGGAGCGGCGCAATGATGAGCTTACT 130  
QY 2912 ATCAGTCTGTGAGTGTGGTGTATGTTTGCCTCCATTTGCCAACTTCTCTGAGTTCT 2971  
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DB 131 ATCAGTCTGTGAGTGTGGGCTGATGTTGCTCTCCATCGCCACTTCTCGAGTTCT 190  
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; Sequence 69, Application US/09989442  
; Publication No. US2003001349A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PJ208  
; CURRENT APPLICATION NUMBER: US/09/989,442  
; CURRENT FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: 60/179,065  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: 60/180,628  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: 60/214,886  
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; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 60/236,367  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/237,039  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/237,038  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/236,370  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/236,802  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/237,037  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/237,040  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/240,960  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/239,935  
; PRIOR FILING DATE: 2000-10-13  
; PRIOR APPLICATION NUMBER: 60/239,937  
; PRIOR FILING DATE: 2000-10-13  
; PRIOR APPLICATION NUMBER: 60/241,787  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/246,474  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: 60/246,532  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: 60/249,216  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,210  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/226,681  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/225,759  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/225,213  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/227,182  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/225,214  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/235,836  
; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: 60/230,438  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/215,135  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: 60/225,266  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/249,218  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,208  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,213  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,212  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,207  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,245  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,244  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,217  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,211  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,215  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,264  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,214  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,297  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/232,400  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/231,242  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/232,081  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/232,080  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/231,414  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/231,244  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/233,064  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/233,063  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/232,397  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/232,399  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/232,401  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/241,808  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/241,826  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/241,786  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/241,221  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/246,475  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: 60/231,243  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/233,065  
; PRIOR FILING DATE: 2000-09-14

Query Match 14.9%; Score 529.6; DB 9; Length 915;  
Best Local Similarity 85.2%; Pred. No. 1.6e-121;  
Matches 600; Conservative 2; Mismatches 101; Indels 1; Gaps 1;

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QY 2792 GGGAAAAGAGGAGATGGAGGAGCTACAGGCATCAACCGAGGCTGCTGCATCAATTC 2851
Db 12 GRAGWAAAGAGGAGATGGAGGAGCTGCA-GCCTACAACCGCGGCTGCTGCACATCC 70
QY 2852 TGCCCAAGAGCTGGGGGCCCACTTCCTGGCCGGGAGCGCGCAATGATGAATCTACT 2911
Db 71 TGCCCAAGAGCTGGCGCTCACTTCCTGGCCGGGAGCGCGCAATGATGAGCTCTACT 130
QY 2912 ATCAGTCGTGTGAGTGTGTGTATGTTTGCCTCCATTCGCCACTTCTCTGAGTTCT 2971
Db 131 ATCAGTCCTGTGAGTGTGTGTGTATGTTTGCCTCCATTCGCCACTTCTCTGAGTTCT 190
QY 2972 ATGTGAGCTGGAGGCAAAATAGAGGTGCGAGGTGCGCTGGCGGTGCTCAACAGCATCA 3031
Db 191 ACGTTGAGCTGGAGGCAACACGAGGAGTGTGAGTGTGCGCTGGCGGTGCTCAATGAGATCA 250
QY 3032 TCGCTGACTTTGATGAGATATCAGGAGGAGCGGTTCGCGGAGCTGGAAGATCAAGA 3091
Db 251 TCGCTGACTTTGATGAGATCATCAGCGAGGATCGGTTCCGGAGCTGGAGAAAGATCAAGA 310
QY 3092 CGATTGGTAGCACCTACATGGCTGCTCAGGGCTGAACGCCAGCACCTACGATCAGGTGG 3151
Db 311 CCATCGGCAGCACCTACATGGCTGCTCAGGGCTGAACGCCAGCACCTACGATCAGGTGG 370
QY 3152 GCGCTGCCACATCACTGCGCTGGCTGACTACGCCATGCGGCTCATGGAGCAGATGAAGC 3211
Db 371 GCAAGACCCACATCAAGGCACTGGCGGACTTTGCCATGAAGCTGATGGACCAAGATGAAGT 430
QY 3212 ACATCAATCAGCACCTTCACAAATTCACAGATGAGATGAGGCTGACATGAGGCTGACAT 3271
Db 431 ACATCAATGAGCACCTTCACAACTTCACAGATGAGGCTGACATGAGGCTGACATGAGGCT 490
QY 3272 TCGTGGCAGGTGTCTCGGGGCTCGGAGCCACAGTATGACATCTGGGGAAACACAGTGA 3331
Db 491 TGGTGGCGGGGTGATAGGGGACGAAAGCCCTCAGTACGACATCTGGGGCAATACCGTGA 550
QY 3332 ATGTCTCTAGTGTATGGACAGACGGGGTCCCGACCGAATCAGGTGACACGGAGCC 3391
Db 551 ACGTGGCCAGCGCATGGACAGACCGGTTGTACCGACCGCATCCAGGTTCACACAGACA 610
QY 3392 TGTACAGGTTCTAGCTGCCAAGGCTACACGCTGGAGTGTGAGGGTGGTCAAGGTGA 3451
Db 611 TGTACAGGTTCTAGCTGCCAAGGCTACACGCTGGAGTGTGAGGGTGGTCAAGGTGA 670
QY 3452 AGGCAAGGGGAGATGACCACTACTTCTCTCAATGGGGGCCCC 3495
Db 671 AGGCAAGGGGAGATGATGACCTACTTCTCTCAATGGAGGGCCC 714
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RESULT 10

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US-10-121-911-2
; Sequence 2, Application US/10121911
; Patent No. US20020164632A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: 21529, A NOVEL ADENYLATE CYCLASE
; FILE REFERENCE: 5800-47
; CURRENT APPLICATION NUMBER: US/10/121,911
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US/09/412,210
; PRIOR FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 3518
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: 21529 adenylate cyclase
; NAME/KEY: CDS
; LOCATION: (247)...(3480)
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US-10-121-911-2

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Query Match 14.2%; Score 505.2; DB 9; Length 3518;
Best Local Similarity 50.0%; Pred. No. 3.4e-115;
Matches 1560; Conservative 0; Mismatches 1488; Indels 72; Gaps 9;

QY 435 CCAGATGAACAGAGCAGCCTGACGCTGCTGGTGGCGGTGCTGCTCTCACACGGGT 494
Db 318 CCAGAGTAGTACCGCTGCTGCTGCTGGGATGCTGCTCTGCTGCGCTCGCGCGCT 377
QY 495 GGT----GCTGCTTTCCAAAGCCGACCGCCGCCCTCAG--CCTGCCTATGTGGCACT 548
Db 378 GCTCAGTGGCTGGCGCAGCGGAGGAGTGAACCTCAGACCCGAGCTTCTTGACCAC 437
QY 549 GTTGGCTGTGCGCGCGCTTCTGCTGGGCTCATGGTGTGTGTAAACCGCATAGCTT 608
Db 438 TGTGTGTGCGCGCTGGCGGCTTCTGCTGCTGTGGGCTTCGCTTCCCGGAGCAGCG 497
QY 609 CCGCCAGGACTCCATGTGGTGTGAGTAACGTGGTGTGGCATCTCTGGCGCAGTGCA 668
Db 498 ACTGCAGCGCTGGAGCGCTCCCTGTCCGGCTTGGTATGGGTGCGCTGCTAGCGTAGG 557
QY 669 GGTGCGGGCGCTTTTCGAGCAGACCGCGCAGCCCTCTGCGGCTGCTGTGGCCCTGT 728
Db 558 CCACGCTTCTCTGTTTCAACCGGGGGTGTGAGCGCTGGGACCAAGTGTCTATTTTCT 617
QY 729 GTTCTTTGTATACATCGCATACACGCTCTCTCCCATCGCATCGCGGTGCGCTCCTCAG 788
Db 618 CTTGCTCATCTTCAGCGGTATGCCATGCTGCCCTTGGCATGCGGAGCGCGCTCGC 677
QY 789 CGCGTGGGCTCTCCACCTTGCATTTGATTTGGCTTGGCAA-----CTTAACC 838
Db 678 GGGCTCGCTCTCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 737
QY 839 GTGGTGTAGCTTCTCTCTG--GAAGCAGCTCGGTGCCATGTGCTGCTGCTGCTGCTG 896
Db 738 GGACTCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 797
QY 897 CAACGCTATTAGCATCTGCACACACTATCCAGCAGAGGTGTCTCAGCGCAGCGCTTCA 956
Db 798 GAACGTGGCAGAGTGTACCAAGCGCTGATGAGCGCGCTGCGGGCCACGTTCCG 857
QY 957 GAAGACCGCGATTTACATCCAGCGCGCTCCACCTGAGCATGAGAAATCGCAGCAGGA 1016
Db 858 GGAGGCACTCAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 917
QY 1017 GCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1076
Db 918 ACACCTTCTCTTGTCCATCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 977
QY 1077 CACAA-----AAAAAGAGACATGTTCCACAAGAT 1106
Db 978 GGCAGGCTGCAGGAGGAGGAGGCTCAGGCGCAGAGGAGCTACAAATTTCCAGGCT 1037
QY 1107 CTACATACAGAGCATGACAATGTGAGCATCTGTTTGCAGCATGTGAGGGCTTCAACCA 1166
Db 1038 CTATGTCAAGAGGACACAGGAGTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1097
QY 1167 CTTGCGATCCAGTGCAGTGCAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1226
Db 1098 GCTGGCCAGCGAGTGTTCCTTAAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1157
QY 1227 GTTTCAGAGCTGCTGCGGAGAACTACTGCTGAGGATCAAGATCTTGGGGGACTGTTA 1286
Db 1158 GTTCAGCAGATGCGCAGGAGCATGATGATGCGGATCAAGATCTTGGGGGACTGTTA 1217
QY 1287 CTACTGTGTGAGGGCTGCCGAGGCGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGAG 1346
Db 1218 CTACTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1277
QY 1347 GGGGGTAGACATGATGAGGCGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1406
Db 1278 GGGCGTAGACATGCTGCGCGGCGCATCAGGAAACTGCGGGCAGCGCAGCTGGCGTGAGATCA 1337
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QY	1407	CATGCGCGTGGGCATCCACAGCGGGCGGTGCACTGCGGGCTCCTTGGCTTGGCGAAATG	1466
Db	1338	CATGCGGTGGGGGTGCATCTCAGCAGCGCTACTGTGTGGAGTCACTCGGGCTGCGAAGATG	1397
QY	1467	GCAGTTCCGATGTGTGTCTCAATGATGTGACCTCGCCCAACACATGGAAGCAGGAACCG	1526
Db	1398	GCAGTAGACGTTTGGTCTACATGATGTCACTGCTAACACATGAGCGAGCGGTGT	1457
QY	1527	GGTGGCGGCATCCACATCACTCGGGCAACACTGCAGTACCTGAACCGGGGACTACGAAGT	1586
Db	1458	ACCAGGCGAGTGCATACACAGGGGCTACCTCGGCCCTGCTGGCAGGGCTTATGTGTGT	1517
QY	1587	GGAGCCAGGCGGTGGCAAGCGCAACGCGTACCTCAAGAGAGACACATTTGAGACTTT	1646
Db	1518	GGAGAGCGCAGGCATGGAGCATCGGACCCCTACCTTCGGGAGCTAGGGGAGCCTACTCTA	1577
QY	1647	CCTCATCTGGGCGCCAGCCAGAAACGGAAGAGAGAAAGGCATGCTGGCCAAAGTGC	1706
Db	1578	TCGTGTCATCATCCACGGGCAGAGGAGGATGGAAGGGCACTGCAGAGGCGTTGCT	1637
QY	1707	GCGGACTCGGGCCAACTCCATGGAAGGGCTGATGCCGGATGGGTTCCTGATCGTGCTT	1766
Db	1638	GTCTCTGCTTTGAGGGCTCAAGATGCGTCCATCACTGCTGATGACCCGTTACCTCGGAGTC	1697
QY	1767	CTCCGGNACCAAGGACTCCAAGGCCCTTCGCGCAGATGGGCATTTGATGATTCACCAAGA	1826
Db	1698	CTGGGGGAGCCAAAGCCCTTTTGGCCACCTGAGCCACGAGACAGCCCTGTGTCCACCTC	1757
QY	1827	CAACCGGGGACCCAAAGATGCCCTTG - AACCCCTGAGGATGAGGTGA - TGAAGTTCCTGAG	1883
Db	1758	CACCCCTCTCCCGAGAGAACCTTGGCTCTCTTACAGCACCCAGTGGAGCGCTGGATCGGAG	1817
QY	1884	CCGTGCCATCGATGCCCGCAGCATTTGATCAGTGCAGGAGACCATGTGCGCCGGTTTTT	1943
Db	1818	CCGTACCCCGGGGACTAGATGATGAATGACACTGCACACCGGGGATGCCAAGTTCTTCCAGGT	1877
QY	1944	GCTCACTTCCAGAGAGAGATTTTGAGNAGAAGTACTCCCGGAAGTGGATCCCCGCTT	2003
Db	1878	CATTGAGAGCTCAACTCGCAGAAACAGTGAAGACAGTCGAAGGACTTCAACCCCACTGC	1937
QY	2004	CGGAGCCTAGCTTGCCCTGTGGCTTCTGCTTCTGCTTCATCTGCTTCTATCCACAGCTTCT	2063
Db	1938	ACTGTACTCAGAGAGAAGGATGGAGNAGAAGTACCGACTCTCTGCAATCCCGGCTT	1997
QY	2064	AATTTTCCCACTCCACCCCTGATGCTTGGGATTTATGCCAGCATCTTCCTGCTGCTGCT	2123
Db	1998	CAAACTATGAAAGCTGCACCTTCTGCTTTCTCTCCAACTTCTCATCATCCAGATGCT	2057
QY	2124	AATCAGGTGCTGATGTGCTGTGTACTCCTGTTGGTTCTCTGTTCCCTTAGGCCCTTGC	2183
Db	2058	AGTGACAAACAGCCCCAGCTCTGGCCATCAG - -TATAGATCACTTTTCTCTCTCTT	2114
QY	2184	ACGTCTGTCCCGCAGCATTTGCCGTTCACGGGCACATAGCACCGCAGTTGGCATCTTTTC	2243
Db	2115	CTCTCTATCTTTTGTCTGCTTCTCAGAGACCTGATGAGTGTGTCTCTGAAGGCC	2174
QY	2244	CGTCTGCTGTGTTTACTTCTGCAATGGCCAAATGTTTACCTGTAAACACACCCCAT	2303
Db	2175	CAAGATGCTGCATGTGCTGCTGCATGCTGTGGCTGTGGCCACACGACACGAGCATGTAG	2234
QY	2304	ACGAGCTGTGCACCGCGGATGCTGAATTTAACACCTGCTGACATCACTGCTGCCACCT	2363
Db	2235	ANTAGCCTGGGACCGCCACCATCTGCTGCTTTTGGCATGGCCATTTACGACCTGTT	2294
QY	2364	GCAGCAGCTCAATTACTCTCTGGGCTGGATGCTCCCTGTGTGAGGCGACATCGCCAC	2423
Db	2295	CTTCTTCCCAACATCATCAGATGCCCTTTTCCAAAGCTCCCAATGTGTCTCCATGATTC	2354
QY	2424	CTGAGCTTTCTGAGGTGTCCATCGGAAACATGCTGCTGAGTCTCTTTGGCCAGCTCTGT	2483
Db	2355	CAACCTCTCTGGGAGCTCCCTGGGTCTGTGCTCTCTCATAGTGTGCCATCTCCATGCA	2414

## RESULT.T 11

US-09-925-297-352

03-03-323-297-332  
; sequence 352, Application US/09925297

; Patent No. US20020081659A1

Qy	2484	CTTCTCGCATCAGCAGCATCGGGAAGTTGGCCATGATCTTTGTCTTGGGGCTCATCTA	254
Db	2415	CTGTGCAACGCTGGGGTTCCTCTCCCTGCTCCCTCTTTCTTGCACATGAGCTTCGAGCTGAA	2474
Qy	2544	TTTGGTGTCTTCTGTGTGGGTCCCCAGCCGCATCTTTGACAACTATGACCTACTGCT	2603
Db	2475	GCTGCTGCTGCTCTGCTGTGGCTGGGGCATCTCTCCCTCTTCTTCCATGCCATGCCATGC	2534
Qy	2604	TGGCGTCCATGTGGCTTCTTCCAAATGAGACCTTTGATGAGGCTGGAGCTGTCAGCTGC	2663
Db	2535	CTGGCTGTCGGAATGCTCATCTGTCGCCCTCTATCTGGGCCCTTGGACTCCAGAGCCCGG	2594
Qy	2664	AGGAGGGTGGCCCTCAAAATATATGACCCTGTGATCTGCTGGTGTTTGGCTGGCGCT	2723
Db	2595	AGTCTGAAGAGGCCAACTGATGGGTGCTATCTCTTCTTCACTCTTCTTCCACCGCT	2654
Qy	2724	GTATCTCATGCTCAGCAGGTGGAATCGACTGCCCGCTAAACTTCTCTGTGAAACTACA	2783
Db	2655	CCTTGTCTTGGCTCGCAGAATCAGTACTACTGCCGCTTGACTTCTCTTGGGAAGAA	2714
Qy	2784	GGCAACAGGGGAAAAGAGAGATGGAGAGCTACAGGCATACAACCGGAGGCTGCTGCA	2843
Db	2715	GCTCAGCAGGAGAGGAGGAGACAGAGACGATGGAGAACCTTGACTCGGCTGCTCTTGG	2774
Qy	2844	TAACATTTCTGCCAAGACCTGGCGGCCACCTTCTTGCCCGCGGAGCGCCGAATGTA	2903
Db	2775	GAACTGCTCCCTGCACACTGGCCCCCAGTTTCAATGTGCCAGAACCGGCGCAACGAGA	2834
Qy	2904	ACTTACTATCAGTCGTGTGAGTGTGTGGCTGTATGTTTGTGCTGCATTTGCCACTTCTC	2963
Db	2835	TCTCTACCACCGTCTATGAATGCGTTTGTGTCTCTTTCGCTCAGTCCCAGACTTCAA	2894
Qy	2964	TGAGTTCTATGTGGAGCTGGAGCAACAATAGGGTGCCGAGTGCCTGCGGCTGCTCAA	3023
Db	2895	GGAGTTTCTACTCTGAATCCAACATCAATCATGAGGCCCTAGAGTGTCTGAGCTGCTCAA	2954
Qy	3024	CGAGATCATCGCTGACTTTTATGATGAGATTATCAGCGAGGAGCGGTTCCGCGCAGCTGGA	3083
Db	2955	TGAGATAATTGTGATTTTGTATGAGCTGTCTCTCAAGCCCAAGTTTCACTGTTGGGGTGG	3014
Qy	3084	GATCAAGCAGATTGGTAGCACCCTACATGGCTGTGCTCAGGGCTGAACGCCAGCAC	3133
Db	3015	GATCAAGACCATCGCAGCACCTTACATGGCAGCCACAGGCTTAAATGCCACCTCTGGACA	3074
Qy	3138	-----CTAGATCAGGTGGGCGCTCCACATCATCTGCCCTGGCTGACTAGCGC	3185
Db	3075	GGATGCAACAACAGGATGCTGAACGGAGCTGCAAGCCACTTGGCACTATGGTGGAAATTGC	3134
Qy	3186	CATCGGCTCATGGCAGATGAACACATCAATGAGCACTCTTCAACAATTTCCAGAT	3245
Db	3135	CGTGGCCCTGGGTCTTAAGCTGACGCTCATCAACAGCATTCATTCAACACTTCCGCT	3194
Qy	3246	GAAGATTGGGCTGAACATGGGCCAGTCGTGGCAGGTGTTCATCGGGGCTCGGAAGCCACA	3305
Db	3195	GCGAGTGGGTTGAACCATGGACCCCTAGTAGCTGGAGTTATTGGGGCCCAAGAGCCGCA	3254
Qy	3306	GTATGACATCTGGGGNACACAGTGAATGTCCTAGTCTGATGGACAGCACCGGGGGTCCC	3365
Db	3255	ATATGACATTTGGGGCAACACAGTGAACCTGGCTGGCCAGCCGATGGAGAGTACAGAGTCT	3314
Qy	3366	CGACCGAATCCAGGTGACCAACGACCTGTACCAGGTTCTAGCTGTGCCAAGGGGTACACGT	3425
Db	3315	TGGCAAAATCCAGTGACTGAGGAGACGATGGGCCCTACAGTCCCTGGGCTACACCTG	3374
Qy	3426	GGAGTGTGAGGGGTGTCAAGGTGAAGGGCAAGGGGGAGATGACACACTTCTTCTCAA	3485
Db	3375	CTACAGCCGGGTGCTCATCAAGTGAAGGCAAAAGGGCAGCTCTGCACTTCTTCTGAA	3434

## RESULT.T 11

US-09-925-297-352

03-03-323-297-332  
; sequence 352, Application US/09925297

; Patent No. US20020081659A1

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; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA105
; CURRENT APPLICATION NUMBER: US/09/925,297
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05989
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 928
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 352
; LENGTH: 2601
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2520)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (2572)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-297-352

Query Match          11.2%; Score 395.8; DB 10; Length 2601;
Best Local Similarity 51.1%; Pred. No. 3.8e-88;
Matches 1301; Conservative 1; Mismatches 1143; Indels 100; Gaps 12;

QY  927 AGCAGAGGTGCTCAGCGCCAGCGCTTTCAGAGACCGCGCAGTTCATCCAGGCCGGCT 986
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Db   34 AACAGCGCCNAGCACCGCAGGCGCTTCTTGAGGCCGCCGACGTCGCTGGAGGTGAAGAT 93

QY  987 CCACCTCAGCATGAGAAATCGGCAGCAGGCGGCTGCTGCTGCGGTATTGCCCCAGCA 1046
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   94 GAACCTGGAAGAGCAGAGCCAGCAGCAGGAGAACTCATGCTTTCCATCCTGCCCAAGCA 153

QY  1047 CGTTGCCATGAGATGAAGAAGACATCACACA-----AAAAAGAGACAT 1094
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   154 CGTGGCTGACGAGATGCTGAAGACATGAAGAAAGACGAGAGCAGAAAGCACCAGCACA 213

QY  1095 GTTCCACAAGATCTACATACAGAAAGCATGACAAATGTCAGCATCTCTTTGCAGACATTGA 1154
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   214 GTTCAACACCATGTACATGTACCGTCAAGGACAGCTCAGCATCTCTTTGCGGACATGCT 273

QY  1155 GGGTTTCAACAGCTGGCATCCAGTCGATCGCAGCAGAGAGCTGTCATGACCCCTGAATGA 1214
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   274 GGGCTTTACCCAGCTGTCTTCTGCTGCAGCTGCCCAGGAGCTTGTGAAGCTGCTCAAGGA 333

QY  1215 GCTCTTTGCCCGTTTGACAAGCTGGCTGCGGAGAATCACTGCTGAGGATCAAGATCTT 1274
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   334 GCCTTTTGCCCGCTTTGACAAGCTGGCAGCTTAAATCACCCAGCTGCGGATTAAGATCCT 393

QY  1275 GGGGAGCTGTACTACTGTGTGTCAGGGCTGCCGGAGCGCCGGCCGACCATGCCCCACTG 1334
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   394 GGGCGAGCTACTACTGTCATCTCGCGCTTGCCCGACTACGCGGAGGACACGCGGCTG 453

QY  1335 CTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTGCTGTCAGTGTACAGG 1394
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   454 CTCATCCTCATGGGGCTGGCCATGTTGGTGGAGGCCATCTCGTATGTGCGGGAGAAGACCAA 513

QY  1395 TGTGAATGTGAACATGCGGTGGGCATCCACAGCGGGCGCTGTCACCTGCGGCGTCCCTGG 1454
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   514 GACTGGGGTGGACATGCGTGTGGGGGTGCACACGGGCACCGCTGCTGGGGGGCGTCCCTGG 573

QY  1455 CTTGCGGAAATGGCAGTTTCGATGTGTGGTCCAAATGATCTGACCTTGGCCCAACACCATGGA 1514
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   574 CCAGAAGCGCTGGCAGTACGACGTGTGCTGACATGATGTCTACTGTAGCCACAAGATGGA 633

QY  1515 ACAGGAAGCGGCTGGCCGCATCCAAATCATTCTCGGGCAACATCTGCAGTACCTTGAACGG 1574
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   634 GGGCGGGCGGATCCCTGGGGCGTGTGCATCTCCAGAGCACCATGGACTGCTCTGAAAGG 693

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Db 1758 AAGGATCAACCCCTGGGCTCAATGGCACTGACAGGCTGC--CCCTGGTGCCTTCCAAGTA 1815
QY 2685 TATGACCCCTGATCTGCTGCTGTTGGCTGGCGCTGTATCTGATGCTCAGCAGGT 2744
Db 1816 CTCTATGACGGTGATGGTGTCTCATGATGCTCAGCTTCTACTACTTCTCCGCCACGT 1875
QY 2745 GGAATGACTGCCCGCTAAACTTCTCTGAAACTACAGCAACAGGGGAAAAAGAGGA 2804
Db 1876 AGAAAACTGGCAGGACACTTTCTGTGGAAGATTGAGGTCCACGACACGAGGAACG 1935
QY 2805 GATGGAGGAGCTACAGCATACACCGGAGGCTGCTGCATAACATTTCTGCCCAAGACGT 2864
Db 1936 TGTCTATGAGATCGAGCGCTGGAGACGAGGCTTGGTCACCAACATGTTGCTCAGCAGCT 1995
QY 2865 GCGGGCCCACTTCTGGCGGGGAGCGCCCAATGATGAACCTACTATCAGTCGTGTGA 2924
Db 1996 GGCAGCCCAATTTCTGGGTCGAAGAGAGATGAGGAGCTGTATAGCCAGACGTATGA 2055
QY 2925 GTGTGTGGTGTATGTTTGGCTCCATTTGCCAACTTCTCTGAGTTCTATGTGGAGCTGGA 2984
Db 2056 TGAGATTGGAGTCATGTTGGCTCCCTGCCCACTTGTGACTTCTACACAGAGGAG 2115
QY 2985 GCGAAACAATGAGGTCGCGAGTGCCTGCGGCTGCTCAACGAGATCATCGCTGACTTTGA 3044
Db 2116 CATCAACAATGGTGTATTGAGTGTCTGCGTTTCTCAATGAATCATCTCRGATTTGA 2175
QY 3045 TGAGATTATCAGGAGAGGCGGTTCCGCGAGCTGGAAAGATCAACACGATTTGGTAGCAC 3104
Db 2176 CTCTCTCCCTGGACAATCCCAAGTTCCGGGTGATCACCAAGATCAAAACCATTTGGCAGCAC 2235
QY 3105 CTACATGGTGCCTCAGGGCTGAACGCC----- 3132
Db 2236 GTATATGGCGGCTCAGGAGTACCCCCGATGTCACACCAATGGCTTTGCCAGCTCCAA 2295
QY 3133 -----AGCACTACGATAGTGGCGCGCTCCACATCACTGCTGCTGCTGACTACGC 3185
Db 2296 CAAGGAAGACAACTCGCGAGAGAGCGCTGGCAGCACCTGGCTGACTGCGCCGACTTCGC 2355
QY 3186 CATCGGCTCATGAGCAGATGAAGCAGACATGAATGAGCAGCTCCTTCAACAATTTCCAGAT 3245
Db 2356 GCTGGCCATGAAGATACGCTACCAACATCAACACCACTGCTTCAATAACTTCATGCT 2415
QY 3246 GAAGATTGGCTGAACATGGGCCAGTCGCTGGCAGGTGTATCGGGGCTCGGAAGCCACA 3305
Db 2416 GCGCATAGGATCAACAAAGCGGGGTCTGCTGGGTCATCGGAGCCGGAACACACA 2475
QY 3306 GTATGACATCTGGGGGAACACAGTGAATGCTCTAGTCGTATGG-ACAGCACGGGGTCC 3364
Db 2476 CTACGACATCTGGGGCAATACAGTCAATGTAGCCAGCAGGATGGNAGTCCACGGGGTCA 2535
QY 3365 CCGACCGAATCCAGGTGACCCACGA 3389
Db 2536 TGGGCAACATTACAGTGGAGAGGA 2560
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RESULT 12
US-09-750-240-1
; Sequence 1, Application US/09750240
; Patent No. US2002010317A1
; GENERAL INFORMATION:
; APPLICANT: Hammond, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; FILE REFERENCE: 220002056723
; CURRENT APPLICATION NUMBER: US/09/750,240
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
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; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 314
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)...(314)
; OTHER INFORMATION: n = A,T,C or G
US-09-750-240-1

Query Match 8.3%; Score 295.2; DB 10; Length 314;
Best Local Similarity 97.1%; Pred. No. 1.2e-63;
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ATGTCTATGTTTGTAGTGGCTCTCTGCTTAAAGTGGATGAACGGAACAGCTGGGGT 60
Db 1 ATGTCTATGTTTGTAGTGGCTCTCTGCTTAAAGTGGATGAACGGAACAGCTGGGGT 60
QY 61 GAACGCAATGGGAGAGGCTTCGCGGCGCGCTGGGCACTCGGCGAGGTGGCTTTCGACG 120
Db 61 GAACGCAATGGGAGAGGCTTCGCGGCGCGCTGGGCACTCGGCGAGGTGGCTTTCGACG 120
QY 121 CCCCCTATATGAGTGCCTCCCGGATGACAGCCACCCAGCCACCCCTGCGGGCCCC 180
Db 121 CCCCCTATATGAGTGCCTCCCGGATGACAGCCACCCAGCCACCCCTGCGGGCCCC 180
QY 181 CTTCTGGTGCCTTCGGGAGGATGACGCTTCATCCGAGGGGCGGCGCCAGCAAGGCAAG 240
Db 181 CTTCTGGTGCCTTCGGGAGGATGACGCTTCATCCGAGGGGCGGCGCCAGCAAGGCAAG 240
QY 241 GAGCTGGGGCTGGGGGAGTGGCCCTGGGCTTCGAGATACCGAGGTGACAGCAGCG 300
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QY 301 GCGGGGACG 309
Db 301 GCGGGGACG 309
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RESULT 13
US-09-915-582-11
; Sequence 11, Application US/09915582
; Patent No. US20020120103A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 17 Human Secreted Proteins
; FILE REFERENCE: PS723P1
; CURRENT APPLICATION NUMBER: US/09/915,582
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/US01/01431
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/231,968
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 1180
; TYPE: DNA
; ORGANISM: Homo sapiens
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; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1163)
; OTHER INFORMATION: n equals a,t,g, or c
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; NAME/KEY: SITE
; LOCATION: (1164)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-915-583-11

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Query Match 8.0%; Score 284.4; DB 10; Length 1180;  
Best Local Similarity 59.8%; Pred. No. 1e-60;  
Matches 505; Conservative 0; Mismatches 321; Indels 18; Gaps 1;

2660	QY	CTGCAGGAGGTGGCCCTCAAAATATATACCCCTGATCTCTGCTGGTGTTCGGCTGG	2711	Db	189	CGGAGTCTGAAGGAGCCCAAACTGATGGGTGTATCTCTCTTCATCTTCTTCATCA	248
2720	QY	CGTGATCTGCATGCTCAGCAGGTGGAATCGACTGCCGGCTAAACTTCCTCTCTGGAAC	2779	Db	249	CCCTCCTTCTGCTCGCCAGAATGAGTACTACTGCCCTGGACTTCTCTGTGGAAGA	308
2780	QY	TACAGGCACAGGGGAAAAGAGAGAGATGGAGGAGCTACAGGCATACAAACCGGAGGCTGC	2839	Db	309	AGAACTGTAGGAGGAGGAGGAGAGACAGACAGCATGGAGAACTGACTCGCGTGTCTCT	368
2840	QY	TGCATAAATTTCTGCCAAGGACGTGGCGGCCACTTCTTGCCCGGGAGGCGCGCAATG	2899	Db	369	TGGAGAACGTGCTCCCTGCACACGTGGCCCCCAGTTCATTTGGCCAGAACCGCGCCAAAG	428
2900	QY	ATGAACCTACATATCAGTCGTGTGAGTGTGTGGCTGTATGTTTGCCTCCATATCCAACT	2959	Db	429	AGGATCTCTACCAACCACTCCTATGAATCGGTTGTGTCTCTTGCCTCAGTCCACAGAT	488
2960	QY	TCCTCAGTTCATGTGGAGCTGGAGGCAAACAATGAGGGTGGCCGAGTGCCTGCGGCTGC	3019	Db	489	TCAAGGAGTCTACTTGAATCCACATCAATCATATGAGGGCTTAGAGTGTCTGAGGCTGC	548
3020	QY	TCAACGAGATCATCGCTGACTTTGTATGAGATTATCAGCGAGGAGCGGTTCCGGCAGCTGG	3079	Db	549	TCAATGAGATAATTGCTGATTTTATGATGAGTCTCTCAAGCCCAAGTTCAGTGGGGTGG	608
3080	QY	AAAGATCAAGACGATTTGGTAGACCTACATGGCTGCCTCAGGGCTGAACGCCAGCACCT	3139	Db	609	AGAAGATCAAGACCATCGGCAGCACTACATGGCAGCCACAGGCTTAAATGCCACCTCTG	668
3140	QY	-----ACGATCAGTGGGCGCTCCACATCACTGCCTGCGCTCACT	3181	Db	669	GACAGGATCCACACAGGATGCTGAACGGAGCTGCAGGCCCTTGGGCATATGTTGGGAAT	728
3182	QY	ACGCCATCGGGCTATGGAGCAGATGAAGCACATCAATGAGCACTCTCTCAACAATTTCC	3241	Db	729	TTGCCGTGGCCCTGAAGCTGGAGCTCATCAACAGCATTCATTCAACAACATTCCT	788
3242	QY	AGATGAAGATTGGGCTGAACATGGGCCCAGCTCTGGCAGGTGTATCGGGGCTCGGAAGC	3301	Db	789	GCTCGGAGTGGGGTTGAACCATGACCCGTAGTCTAGTGTGAGTTATTGGGGCCACAGAAGC	848
3302	QY	CACAGTATGACATCTGGGGGAAACAGTGAATGTCTCTAGTCGTATGGACAGCAGCGGGG	3361	Db	849	CGCAATATGACATTTGGGACACAGTGAACGTGGCCAGCCGATGGAGNGTACAGGAG	908
3362	QY	TCCCGACCGAATCCAGGTGACCGGACCTGTGTACCAGTTCTAGTGTCCAAAGGGCTTACC	3421	Db	909	TCTTTGGCAAAAATCCAAGTGACTGAGGAGACAGCATGGGCCCTACAGTCCCTGGGCTACA	968
3422	QY	AGCTGGAGTGTGCGAGGGTGGTCAAGGTGAAGGGCAAGGGGGAGATGACCACCTACTTCC	3481	Db	969	CTGTGTACAGCGGGGTGTATCAAGTGAAGGCAAGGGCAGCTCTGCACCTACTTCTCC	1028
3482	QY	TCAA	3485	Db	1029	TGAA	1032

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RESULT 14
US-09-925-297-56
; Sequence 56, Application US/09925297
; Patent No. US20020081659A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PAL05
; CURRENT APPLICATION NUMBER: US/09/925,297
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05989
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 1140
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (563)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (1115)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (1119)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (1135)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-297-56

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Query Match	7.5%;	Score 265.6;	DB 10;	Length 1140;
Best Local Similarity	59.8%;	Pred. No. 4.6e-56;		
Matches 491;	Conservative 0;	Mismatches 310;	Indels 20;	Gaps 2;

  

QY	2669	GGGTGGCCCTCAATATATGACCCCTGTGATCTGCTGGTCTTTGCGCTGGCGGTGATC	2728
DB			
QY	216	GGAAGACCTTGAAGACCATGGGCTGTGTCTCTCTATATCTTCATCACATGCTTG	275
DB			
QY	2729	TGCATGCTCAGCAGCTGGAAATCGACTGCCGCCCTAAACTTCCTCTGGAACCTACAGGCA	2788
DB			
QY	276	TTCTGGGTAGACAAATGATATTACTGTAGTTAGACTTCTATTGGGAACAATTC	335
DB			
QY	2789	CAGGGGAAAAAGAGGAGATGGAGGCTACAGGCTACAACCGGAGGCTGTCATACA	2848
DB			
QY	336	AAAAAGAGCGGAGGAGATAGAGACCATGGAGACCTGAACCGCTGCTGGAGAAGC	395
DB			
QY	2849	TTCTGCCAAGGAGTGGGGCCACTCTCTGGCCGGGAGCGCGCAATGATGACHT	2908
DB			
QY	396	TGCTTCGCCGCGAGCTGGCTGAGCACTCTCTGGCAGGAGCTGAAGAATGAGGAGCT	455
DB			
QY	2909	ACATACAGTCGTGTGAGTGTGCTGTATTGTTTGCTCCATTCGCCAATTCCTCTGAGT	2968
DB			
QY	456	ACCAAGTCTTATGACTTGGCTGTGCGTCACTGTTTGCTCCATTCGGGATTTCAAGAA	515
DB			
QY	2969	TCTATGTGGAGCTGGAGGCAAAACAAATGAGGTGCGGAGTGCTGCGGTGCTCAACG	3028
DB			
QY	516	TTTATACAGAAATCCGACGTGAACAAGGAGGCTTGGAAATGCTTCGGNTCTGAACG	575
DB			
QY	3029	TCATCGCTGACTTTGATGAGATTTATCAGCGAGGAGCGGTTCCGGAGCTGGAAGAAT	3088
DB			
QY	576	TCATCGCTGACTTTGATGATCTTTCTTCCAAAGCCAAAATTCACTGAGTGTGAAAGA	635
DB			
QY	3089	AGAGATTTGTAGCACCTACATGCTGCCCTCAGGCTCAAGCCGACACCTACCATCAGG	3148
DB			
QY	636	AGACCAATGCGAGCACATACATGCGACCAACGCTGTAGCGCTGTGCCACGACGAGG	695
DB			
QY	3149	TGGSCCG-----CTCCACATCATCTGCCCTGGCTGACTACGCGCATGC	3190

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Db 696 ACTCCAGGAGCCGCGGAGTACATGACATTTGGCACCATTGGTGGAGTTTCCTTTG 755
QY 3191 GGCTCATGGAGCAGATGAACGACATCAATGAGCACTCTTCAACAATTTCCAGATGAAGA 3250
Db 756 CCCTGGTAGGGAAGCTGGATGCCATCAACAGCACTCTTCAACGACTTCAAAATTTGGAG 815
QY 3251 TTGGGCTGAACATGGGCCCGGAGTCTGGCAGGTGTCATCGGGGCTCGGAAGCCACAGTATG 3310
Db 816 TGGTATTACCATGGACCTGTGTAGTCTGGTGTGATTTGGAGCTCAGAAGCCACAATATG 875
QY 3311 ACATCTGGGGAAACACAGTGAATGTCTTAGTCTGATGGACAGCAGGGGTCCTCCGACC 3370
Db 876 ATATCTGGGCAACACTGTCAATGTGGCCAGTAGGATGGACAGCACCGGAGTCTCGACA 935
QY 3371 GAATCCAGGTGACCACGACCTGTACCAGGTCTTAGCTGCAAGGGCTACCAGTGGAGT 3430
Db 936 AATACAGGTTACCGGAGACGAGCCTCTCTCTGACAGCCCTCGGATACACGTGCACCT 995
QY 3431 GTCAGGGGTGGTC--AAGGTGAAGGGCAAGGGGAGATGA 3469
Db 996 GTCGAGGAATAATCCACGTGAAGGGAAGGGGACCTGA 1036

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RESULT 15

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US-09-764-864-792/c
; Sequence 792, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 792
; LENGTH: 7053
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (154)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-864-792

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Query Match 7.0%; Score 248.2; DB 10; Length 7053;
Best Local Similarity 58.0%; Pred. No. 2.2e-51;
Matches 497; Conservative 4; Mismatches 337; Indels 19; Gaps 3;

QY 2669 GGGTGGCCCTCAATATATACCCCTGTGATTCTGTGGTGGTTGGCGCTGGCGTGTATC 2728
Db 6732 GGAAGGACCTGAAGACCATACCAATTTCTACCTGGTCTTCTATACATCACCTGTCTTA 6673
QY 2729 TGCATGCTCAGCAGGTGGAATCGACTCCCGCCCTAAACTTCTCTGGAACCTACAGCAA 2788
Db 6672 CACTCTCCACACAGATTGACTATTACTGCGCTTGGACTGCCTATGGAAGAAGATTCA 6613
QY 2789 CAGGGGAAAAGAGGAGATGGAGAGCTACAGGCATACACCGGAGGCTGCTGCATACA 2848
Db 6612 AGAAGGAGCAGGAGGAGTTTGGAGACCATGGAGAAGTGAACCGCTTCTCTGGAGACG 6553
QY 2849 TTCTGCCAAGGAGGCGGCGCCACTTCTGGCCCGGAGCGCGCAATGATGAATCT 2908
Db 6552 TCCTGCCAGCCACGTGGCTGCCACTTTAT---CGGTGACAGTTAAAGGAGGACTGGT 6496
QY 2909 ACTATCAGTCGTGTGAGTGTGGCTGTATGTTGCTCCATTCGCACTTCTCTAGT 2968
Db 6495 ACCATAGTCTTATGACTGTGTGTCATGTTTGGCTCCGCTCGCGGACTTCAAAGTGT 6436
QY 2969 TCTATGTGGAGCTGGAGGCAACAATGAGGTTGCCAGTGCCTGCGGCTGCTCAACGAGA 3028

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Db 6435 TCTACACAGAGTGGATGTCAACAAAGAGGGCTGGAGTGCTACGCTGCTCAATGAGA 6376
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QY 3134 GCACCTACGATCAGTGGGCGCTCCACATCATCTGCCCTGGTGTAGTACGCCATGGGGC 3193
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QY 3194 TCATGGAGCAGATCAAGCACATCAATGAGCACTCTTCAACAATTTCCAGATGAAGATTG 3253
Db 6195 TGATGATAAGCTGGAGCGGATCAACAGGCACTCTTCAACTCTTCCGCTCGCGCTTC 6136
QY 3254 GGC-TGAACATGGGCCAGTCTGGCAGGTGTCATCGGGGCTCGGAAGCCACATATGAC 3312
Db 6135 GGCATAAACCATGGCCCTGTGATTGCTGGAGTGGGCCCCGAAAACCTCAGTATGAC 6076
QY 3313 ATCTGGGGAAACACAGTGAATGTCTTAGTGTATGACAGCAGCGGGGTCCCCGACCGA 3372
Db 6075 ATCTGGGGAAACACTGTCAATGTGCCAGCGCAATGGAAGCACTGGAGAATTTGGGAAA 6016
QY 3373 ATCCAGGTGACCAGGACCTGTACCAGGTTTCTAGCTGCCAAGGGCTACCAGCTGAGTGT 3432
Db 6015 ATCCAGGTTACCGAGGAGACCTGCACCATCTCCAGGGGCTTCGGGTACTCTPKGTGAATGC 5956
QY 3433 CGAGGGGTGTTCAAGGTGAAGGCAAGGGGAGATGACCACTACTTCTCAATGGGGGC 3492
Db 5955 CSTGSCCTGATCAGTCAAGGCAAGGCAAGGCGAGCTGAGGACTTACTTTGCTGTACGGAC 5896
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Db 5895 ACTGCCAAGTTTCAGGG 5879

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GenCore version 5.1.3  
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Maximum Match 100%  
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- 2: em\_esthum.\*
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- 6: em\_estpl.\*
- 7: em\_estro.\*
- 8: em\_hic.\*
- 9: gb\_est1.\*
- 10: gb\_est2.\*
- 11: gb\_hic.\*
- 12: gb\_est3.\*
- 13: gb\_est4.\*
- 14: gb\_est5.\*
- 15: em\_estfun.\*
- 16: em\_estom.\*
- 17: gb\_gss.\*
- 18: em\_gss\_hum.\*
- 19: em\_gss\_inv.\*
- 20: em\_gss\_pln.\*
- 21: em\_gss\_vrt.\*
- 22: em\_gss\_fun.\*
- 23: em\_gss\_mam.\*
- 24: em\_gss\_mus.\*
- 25: em\_gss\_other.\*
- 26: em\_gss\_pro.\*
- 27: em\_gss\_rod.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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6	565.8	15.9	1043	12	BG297229

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15	463.4	13.1	565	12	BG872335
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44	311	8.8	567	13	BI739363
45	305.8	8.6	824	13	BI257519

ALIGNMENTS

RESULT 1  
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LOCUS BM811640 1039 bp mRNA linear EST 05-MAR-2002  
DEFINITION AGENCOURT\_6489534 NIH\_MGC\_125 Homo sapiens cDNA clone IMAGE:5724057  
5', mRNA sequence.  
ACCESSION BM811640  
VERSION BM811640.1 GI:19128463  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1039)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-r@mail.nih.gov  
Tissue procurement: Invitrogen  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:  
http://image.lnl.gov  
Plate: LLAM12712 row: 1 column: 10  
High quality sequence stop: 644.

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/clone_lib="NIH_MGC_125"					
/lab_host="DH10B"					
/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6; Site_1: EcoRV (destroyed); Site_2: NotI; RNA source pool of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036."					
BASE COUNT	204 a	302 c	262 g	269 t	2 others
ORIGIN					
Query Match	22.88; Score 808.8; DB 14; Length 1039;				
Best Local Similarity	97.28; Pred. No. 2e-173;				
Matches	833; Conservative 0; Mismatches 23; Indels 1; Gaps 1;				
Qy	2109	CTTCCTGCTGCTGAATACACGGTGCTGATCTGTGCTGTGTACTCCTGTTGGTGTCTCTCGTT	2168		
Db	1	CTTCCTGCTGCTAATCACCGTGCTGTAAGTCTGTGCTGTACTCCTGTTGGTGTCTCTCGTT	60		
Qy	2169	CCCTAAGGCCCTCAACAGTCTGTCCCGCAGCATTTCCGCTCAGCGGCACATACACCGC	2228		
Db	61	CCCTAAGGCCCTCAACAGTCTGTCCCGCAGCATTTCCGCTCAGCGGCACATACACCGC	120		
Qy	2229	AGTTGGCATCTTTCCGTCCTGCTGTGTTTACTCTTCGCCATTGCCAACATGTTCACTG	2288		
Db	121	AGTTGGCATCTTTCCGTCCTGCTGTGTTTACTCTTCGCCATTGCCAACATGTTCACTG	180		
Qy	2289	TAAACCACCCCCATACGGAGCTGTGCAGCCCAGTCTGTAATTTAAACCTGCTGACAT	2348		
Db	181	TAAACCACCCCCATACGGAGCTGTGCAGCCCAGTCTGTAATTTAAACCTGCTGACAT	240		
Qy	2349	CAC TGCCCTGCCACTGCAGCAGCTCAATTA CTCTCTGGGCTGGATGCTCCCTGTGTGA	2408		
Db	241	CAC TGCCCTGCCACTGCAGCAGCTCAATTA CTCTCTGGGCTGGATGCTCCCTGTGTGA	300		
Qy	2409	GGGCACCATGCCACCTGCAGCTTCTCTGAGTCTCCATCGGGAACATGCTGCTGACTCT	2468		
Db	301	GGGCACCATGCCACCTGCAGCTTCTCTGAGTCTCCATCGGGAACATGCTGCTGACTCT	360		
Qy	2469	CTTGCCAGCTCTGCTCTTCCTGCACATCAGCAGCATCGGGAAGTTGGCCATGATCTTTGT	2528		
Db	361	CTTGCCAGCTCTGCTCTTCCTGCACATCAGCAGCATCGGGAAGTTGGCCATGATCTTTGT	420		
Qy	2529	CTTTGGGCTCATCTATT TTGGTGCTCTCTGCTGGGTCCCGCAGCCGCATCTTTGACA	2588		
Db	421	CTTTGGGCTCATCTATT TTGGTGCTCTCTGCTGGGTCCCGCAGCCGCATCTTTGACA	480		
Qy	2589	CTATGACCTACTGCTTGCGGTCCTAGCTTGCTTGCTTCTTCCAATCAGACCTTTGATGGCT	2648		
Db	481	CTATGACCTACTGCTTGCGGTCCTAGCTTGCTTGCTTCTTCCAATGAGACCTTTGATGGCT	540		
Qy	2649	GGACTGTCAGCTGCAGGGAGGGTGGCCCTCAAATATATGACCCCTGTGATCTTCGTGGT	2708		
Db	541	GGACTGTCAGCTGCAGGGAGGGTGGCCCTCAAATATATGACCCCTGTGATCTTCGTGGT	600		
Qy	2709	GTTTTGCCTGGCGCTGTATCTGCATGCTCAGCAGGTGGAATCGACTGCCGCCCTAACTT	2768		
Db	601	GTTTTGCCTGGCGCTGTATCTGCATGCTCAGCANGTGGAGTCGACTGCCGCCCTAGACTT	660		
Qy	2769	CCTCTGAAACTACAGCAACAGGCGAAAAAGAGAGATGGAGAGCTACAGGCATACAA	2828		
Db	661	CCTCTGAAACTACAGCAACAGGCGAAAAAGAGAGATGGAGAGCTACAGGCATACAA	720		
Qy	2829	CCGAGGCTGCTGCATAACATCTTGCCCAAGAGCGTGGCGGCCACTTCCTGGCCCCGGA	2888		
Db	721	CCGAGGCTGCTGCATAACATCTTGCCCAAGAGCGTGGCGGCCACTTCCTGGCCCCGGA	780		

QY	2889	GGCGCGCAATGATGAACCTCTACTATFACGTGCTGTGAGTGTGTG-GCTGTTATGTTTGCCCT	2947
Db	781	GGCGCGCGATGATGAACCTCTACTATFACGTGCTGTGAGTGTGTGAGTGTGCTGTTATGTTTGCCCT	840
QY	2948	CCATTGCCAACTTCTCT	2964
Db	841	CCATTGGCCAACTTCCT	857
RESULT 2			
BQ881496			
LOCUS			
DEFINITION	BQ881496	1016 bp	linear
ACCESSION	AGENCOURT_8229097	Lupski_dorsal_root_ganglion	Homo sapiens
VERSION	BQ881496	clone IMAGE:6182035	5', mRNA sequence.
KEYWORDS	BQ881496.1	GI:22273504	
SOURCE	EST.		
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
JOURNAL	1 (bases 1 to 1016)		
COMMENT	NH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> . National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Dr. James R. Lupski cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LLAM13567 row: f column: 20 High quality sequence start: 31 High quality sequence stop: 645.		
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source	Location/Qualifiers		
	1..1016		
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	/clone="IMAGE:6182035"		
	/clone_lib="Lupski_dorsal_root_ganglion"		
	/sex="male"		
	/tissue_type="dorsal root ganglia"		
	/dev_stage="adult, 36 yr"		
	/lab_host="DH10B"		
	/note="vector: pCMV-SPORT6 (Life Technologies); Site_1: NotI; Site_2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCCACGCGCCG-3' and 5'-GACTAGTCTAGATCGGACGCGCCCT(15)-3'. Size selected > 1 kb for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life Technologies."		
BASE COUNT	186 a	297 c	268 g
ORIGIN	265 t		
Query Match	21.8%	Score 772;	DB 14; Length 1016;
Best Local Similarity	94.1%	Pred. No. 4.8e-165;	
Matches	890;	Conservative	0; Mismatches 45; Indels 11; Gaps
QY	2066	TTTTCCACACTCCACCCCTGATGCTTGGATTTATGCCAGCATCTTCCTGCTGCTAA	2125
Db	42	TCTTCCACACTCCACCCCTGATGCTTGGATTTATGCCAGCATCTTCCTGCTGCTAA	101
QY	2126	TACCGTGCTGATCTGCTGTACCTCCTGTGCTCTCTCTCCCTAAGCCCTGAAC	2185
Db	102	TACCGTGCTGATCTGCTGTGACCTCCTGTGCTCTCTCTCCCTAAGCCCTGAAC	161
QY	2186	GTCTGTCCCGCAGCATTTCTCCGCTCACGGGGCACATAGCACCGCATCTTTTCCG	2245

Db	162	GTCTGTCGCCGACATTTGTCGCTACGGGCACATAGCACCGCAGTTGGCATCTTTTCCG	221
QY	2246	TCCTGCTGTGTTTACTTCTGCTGATGTCGCAATGTCGCAATGTTTCACCTGTACCCACACACCCCATAC	2305
Db	222	TCTGCTGTGTTTACTTCTGCTGATGTCGCAATGTCGCAATGTTTCACCTGTACCCACACACCCCATAC	281
QY	2306	GGAGCTGTGAGCCGCGATGCTGAAATTAACACCTGCTGACATCACTGCTGTCACCTGC	2365
Db	282	GGAGCTGTGAGCCGCGATGCTGAAATTAACACCTGCTGACATCACTGCTGTCACCTGC	341
QY	2366	AGCAGCTCAATTAATCTCTGTGGGCTGGATGCTCCCTGTGTGAGGACACCATGCCACCT	2425
Db	342	AGCAGCTCAATTAATCTCTGTGGGCTGGATGCTCCCTGTGTGAGGACACCATGCCACCT	401
QY	2426	GCAGCTTCTCTGAGTGTCCATCGGAACATGCTGCTGAGTCTCTTGGCCAGCTGTCT	2485
Db	402	GCAGCTTCTCTGAGTGTCCATCGGAACATGCTGCTGAGTCTCTTGGCCAGCTGTCT	461
QY	2486	TCTGCACATCAGCAGCATCGGGAAGTTGGCCATGATCTTTGCTTGGGCTCATCTATT	2545
Db	462	TCTGCACATCAGCAGCATCGGGAAGTTGGCCATGATCTTTGCTTGGGCTCATCTATT	521
QY	2546	TGCTGCTGCTTCTGCTGGTTCCTCCAGCCGCTTGTGACACTATGACCTACTGCTTG	2605
Db	522	TGCTGCTGCTTCTGCTGGTTCCTCCAGCCGCTTGTGACACTATGACCTACTGCTTG	581
QY	2606	GCCTCATGCTTGGCTTCTTCAATGAGACCTTTGATGGCTGGAGCTGCCAGCTGCAG	2665
Db	582	GCCTCATGCTTGGCTTCTTCAATGAGACCTTTGATGGCTGGAGCTGCCAGCTGCAG	640
QY	2666	GGAGGCT-GGCCCTCAAAATATATGACCCCTGTGATCTGCTGTTGGCTGGGCTG	2724
Db	641	GGAGGCTGGGCCCTCAAAATATATGACCCCTGTGATCTGCTGTTGGCTGGGCTG	700
QY	2725	TATCTGATGCTCAGCAGTGGATGACCTG-CCGCGCTAAACTTCTCTGGAATACATA	2783
Db	701	TATCTGATGCTCAGCAGTGGAGTGGAGCTGCCCGCTAGACTTCTCTGGAATACATA	760
QY	2784	GGCAACAGGGGAAAGAGAGATGG-AGGAGCTACAGGCATACACCGGAGGCTGCTGC	2842
Db	761	GGCAACAGGGGAAAGAGAGATGGAGGAGCTACAGGCATACACCGGAGGCTGCTGC	820
QY	2843	ATAACATCTGCCAAGGAGCTGGCGCCCTTCTCTGG-CCGCGGAGCGCGCAATGA	2900
Db	821	ATAACATCTGCCAAGGAGCTGGCGCCCTTCTCTGGCGCGGAGCGCGCAATGA	880
QY	2901	TGAATCTACTATCAGTC---GTGTGAGTGTGGCTGTTATGTTTGGCTTCCATT-GCCA	2956
Db	881	TGGACTCTACTATCAATCTCTTGTGAATGGTGGGCTGTTATGTTTGGCTTCCATTGGCCA	940
QY	2957	ACTTCTGAGTCTAT-GTGGAGCTGGAGGCAACAATGAGGTTG	3001
Db	941	CTTCTGAGTTCATGAGGGAGCTGGGAGGAAACAATGAAGGGG	986
RESULT 3			
BF792125			
LOCUS	BF792125	775 bp	mRNA linear EST 12-JAN-2001
DEFINITION	602252571F1 NTH_MGC_84 Homo sapiens cDNA clone IMAGE:4345144 5', mRNA sequence.		
ACCESSION	BF792125		
VERSION	BF792125.1		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 775)		
TITLE	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D.		

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LAM964 row: m column: 17

High quality sequence stop: 711.

Location/Qualifiers

1..775

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:4345144"

/clone\_lib="NIH\_MGC\_84"

/tissue\_type="adrenal cortex carcinoma, cell line"

/lab\_host="DH10B (phage-resistant)"

/note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally; oligo-dt primed. Average insert size 1.229 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH\_MGC Library."

BASE COUNT 184 a 199 c 239 g 153 t

ORIGIN

Query Match 20.3%; Score 718.8; DB 12; Length 775;

Best Local Similarity 98.1%; Pred. No. 5.9e-153;

Matches 738; Conservative 0; Mismatches 12; Indels 2; Gaps 1;

QY 2743 GTGGAATCGACTCCGCGCTAAACTTCTCTGGAAACTACAGGCACACAGGGGAAAAAGAG 2802

Db 11 GTGAGTTCGACTCCGCGCTAGACTTCTCTGGAAACTACAGGCACACAGGGGAAAGAG 70

QY 2803 GACATGGAGGAGCTACAGGCATACACCGGAGGCTGCTGATACATCTTGCCCAAGGAC 2862

Db 71 GAGATGGAGGAGCTACAGGCATACACCGGAGGCTGCTGATACATCTTGCCCAAGGAC 130

QY 2863 GTGCGGCCCCACATCTCTGGCCGGAGCGCGCAATGATCAACTCTACTATCAGTCTGT 2922

Db 131 GTGCGGCCCCACATCTCTGGCCGGAGCGCGCAATGATCAACTCTACTATCAGTCTGT 190

QY 2923 GAGTGTGTGCTTATGTTTGCTCCATTGCCAACTTCTCTGAGTTCTATGTGGAGCTG 2982

Db 191 GAGTGTGTGCTTATGTTTGCTCCATTGCCAACTTCTCTGAGTTCTATGTGGAGCTG 250

QY 2983 GAGGCAACAATCAGGTCGCGAGTGGCTGCGGTGCTCAACGAGATCATCGTGACTTT 3042

Db 251 GAGGCAACAATCAGGTCGCGAGTGGCTGCGGTGCTCAACGAGATCATCGTGACTTT 310

QY 3043 GATGAGATTATCAGCGAGGAGCGGTTCCCGCAGCTGGAAGATCAAGACGATTGGTAGC 3102

Db 311 GATGAGATTATCAGCGAGGAGCGGTTCCCGCAGCTGGAAGATCAAGACGATTGGTAGC 370

QY 3103 ACCTACATGGCTGCCCTCAGGGCTGAACGCCAGCACCTTACGATCAGGTGGCGCGCTCCAC 3162

Db 371 ACCTACATGGCTGCCCTCAGGGCTGAACGCCAGCACCTTACGATCAGGTGGCGCGCTCCAC 430

QY 3163 ATCAGTCCCTGGCTGACTACGCCATGCGGCTCATGAGCAGATGAAGACATCAATGAG 3222

Db 431 ATCAGTCCCTGGCTGACTACGCCATGCGGCTCATGAGCAGATGAAGACATCAATGAG 490

QY 3223 CACCTCTCAACAATTTCCAGATGAAGATTGGGCTGAACATGGGCCAGTCGTTGGCAGGT 3282

Db 491 CACCTCTCAACAATTTCCAGATGAAGATTGGGCTGAACATGGGCCAGTCGTTGGCAGGT 550

QY 3283 GTGATCGGGCTCGGAAGCCACAGTATGACATCTGGGGGAAACACAGTGAATGTCTTAGT 3342

Db 551 GTGATCGGGCTCGGAAGCCACAGTATGACATCTGGGGGAAACACAGTGAATGTCTTAGT 610

QY 3343 CGTATGACACGACGGGGTCCCGGACCGGAATCCAGTGCACCGACCGACCTGTACCGAGTT 3402

Db 611 CGTATGACACGACGGGGTCCCGGACCGGAATCCAGTGCACCGACCGACCTGTACCGAGTT 670

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QY 3403 CTAGTGGCAAGGCTACAGCTGAGTGTCTGAGGGTGGTCAAGGTGAAGGCAAGGGG 3462
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Db 671 CTAGTGGCAAGGCTACAGCTGAGTGTCTGAGGGTGGTCCAGCTGAAGGCAAGGGG 730
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QY 3463 GAGATGACACCTACTTCTCAATGGGGCCC 3494
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Db 731 GAGATGACACCTAA--TTCTCAATGGGGCCC 760
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RESULT 4
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LOCUS QVO-FN0181-100800-335-Q08 FN0181 Homo sapiens cDNA, mRNA sequence.
DEFINITION BE840188
ACCESSION BE840188
VERSION BE840188.1 GI:10272566
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 676)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.P.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-QV0-FN0181-100
800-335-d08&t3=2000-08-10&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 5
High quality sequence stop: 625.
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Location/Qualifiers
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/clone_lib="FN0181"
/dev_stage="Adult"
/note="Organ: prostate_normal; Vector: puc18; Site_1: SmaI
; Site_2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the puc 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
BASE COUNT 125 a 203 c 193 g 155 t
ORIGIN
Query Match 16.7%; Score 593.4; DB 12; Length 676;
Best Local Similarity 95.9%; Pred. No. 2.1e-124;
Matches 609; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY 1582 GAAGTGGAGCCAGGCCGTGGGCAAGCGCAACGCGTACCTCAAGAGCAGCACATTGAG 1641
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Db 2 GACCAGCAGCGGGTGGTGGCGAGCTGCAAGCGTACCTCAAGAGCAGCACATTGAG 61
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QY 1642 ACTTTTCCTCATCTGGCGCCAGCCAGAACGGAAGGAGGAGGAGGATGCTGCCCAAG 1701
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```

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Db 62 ACTTTTCCTCATCTGGCGCCAGCCAGAAAGAGAGAGAGGCCATGCTGCCCAAG 121
QY 1702 CTGACGCGGACTCGGCGCAACTCCATGAAGGGCTGATGCGCGGATGGTTCTCTGATGCT 1761
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Db 122 CTGACGCGGACTCGGCGCAACTCCATGAAGGGCTGATGCGCGGATGGTTCTCTGATGCT 181
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QY 1762 GCCTTCTCCCGGACCAAGGACTCCAAGGCCTTCCGCCAGATGGGCAATTGATTCACAGC 1821
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QY 1822 AAAGACAACCGGGGACCCAGATGCCCTGAACCCCTGAGGATGAGGTGATGAGTTCCTG 1881
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QY 1882 AGCCGTGCAATCGATGCGCGGAGCATTTGATCAGCTGCGGAAGGACCATCTGCGCGGTTT 1941
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Db 422 TTCGAGCGCTAGTGGCCCTGTGCGCTGTGGTCTTCTGCTTCATCTGCTTCATCCAGCTT 481
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QY 2062 CTAATTTTCCACACTCCACCTGTGCTGAGGATTTATGCCAGCATCTTCCCTGCTGCTG 2121
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Db 482 CTAATTTTCCACACTCCACCTGTGCTGAGGATTTATGCCAGCATCTTCCCTGCTGCTG 541
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QY 2122 CTAATCACCGTCTGATCTGTGCTGTACTCTCTGTGTTCTCTTCCCTAAGGCCCTG 2181
|||||
Db 542 CTAATCACCGTCTGATCTGTGCTGTACTCTCTGTGTTCTCTTCCCTAAGGCCCTG 601
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QY 2182 CAACGCTGTCTCCGAGCATTTGCCGCTCACGGGC 2216
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Db 602 CAACGCTGTCTCCGAGCATTTGCCGCTCCGGGGC 636
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RESULT 5
BI691747 1225 bp mRNA linear EST 18-SEP-2001
LOCUS 603307455F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5343565 5',
DEFINITION mRNA sequence.
ACCESSION BI691747
VERSION BI691747.1 GI:15654376
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1225)
NIH-MGC http://mgc.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11872 row: n column: 14
High quality sequence start: 2
High quality sequence stop: 693.
FEATURES
Location/Qualifiers
1..1225
/organism="Mus musculus"
/db_xref="FVB/N"
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source
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RESULT 6	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	source	BASE COUNT	ORIGIN
602394937F1	NH_MGC_94	Mus musculus cDNA clone IMAGE:4506705 5', mRNA sequence.	CG297229	CG297229	CG297229	CG297229	house mouse	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1043)	NIH-MGC	http://mgc.nci.nih.gov/	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)	Contact: Robert Strausberg, Ph.D. Email: cgabbs@mail.nih.gov Tissue procurement: The Cepko Laboratory cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LAM10382 row: i column: 10 High quality sequence stop: 647.	1..1043 /organism="Mus musculus" /db_xref="taxon:10090" /clone="IMAGE:4506705" /clone.lib="NIH_MGC_94" /tissue.type="retina" /lab_host="DH10B (phage-resistant)" /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dr primed. Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."	278 a 295 c 312 g 158 t	Query Match 15.9%; Score 565.8; DB 12; Length 1043; Best Local Similarity 87.1%; Pred. No. 4.7e-118; Matches 644; Conservative 0; Mismatches 92; Indels 3; Gaps 2; QY 2771 TCTGSAACATACAGGCAACAGGGGAAAGAGGAGATGAGGAGCTACAGGCATACAAACC 2830 Db 10 TGTGGTGGCCACAGGCAACAGGGGAGAGGAGATGAGGAGCTACAGGCATACAAACC 69 QY 2831 GAGGCTGCTGCATACATCTTCCCAAGGAGCTGGCGGCCACATCTCTGGCGGGAGC 2890 Db 70 GGAGGTGCTGGCATAACATCTTCCCAAGGAGCTGGCGGCCACATCTCTGGCGGGAGC 129 QY 2891 GCAGCAATGATGAACCTCTACTATCATCTGCTGAGTGTGTGGCTGTATGTTGGCTCCA 2950 Db 130 GCAGCAACGATGAGCTGATACCATCTGCTGATGATGATGCTGCTGCTGCTGCTGCTGCT 189 QY 2951 TTGCCAATCTCTCTGAGTTCTATGTGGAGCTGGAGGCAACAAATGAGGCTGCCGAGTGCC 3010 Db 190 TCGCCAATTTCTCGGAGTTCTACGTGGAGCTCGAGGCAACAAACAGGCGCGTGGAGTGCC 249 QY 3011 TGGCGCTGCTCAGGAGATCATCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3070 Db 250 TGGCGCTGCTCAATGAGATCATCGCAGACTTTTGACGAGATCATCATGAGGAGAGATGCC 309 QY 3071 GCAGCTGGAAGAGATCAAGAGCATTTGGTAGCACCTACATGCTGCCTCAGGCGTGAACG 3130 Db 310 GGCAGTTCGAGAGATCAAGACCATCGGTAGCACCTACATGCTGCCTCAGGCGTGAACG 369 QY 3131 CCAGCACCTACGATAGGTGGCGCGCTCCACATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3190	

Db 370 CCAGCACCTATGACAGGTGGCGCTCACACATCATCGCGCTGGCTGACTATGCCATGC 429

QY 3191 GGCTCATGGAGCAGATGAACACATCAATGAGCAGCTCTTCAACAATTTCCAGATGAAGA 3250

Db 430 GGCTCATGGAGCAGATGAACACATCAATGAGCAGCTCTTCAACAATTTCCAGATGAAGA 489

QY 3251 TTGGGTGAACATGGGCCCCAGTGGTGGCAGGTGTCATCGGGGTCGGAAGCCACAGATG 3310

Db 490 TCGGGTTGAACATGGGTCGGTTGTAGCAGGCGTCATCGGGGCCGAAAGCCACAGATG 549

QY 3311 ACATCTGGGGGAACACAGTGAATGTCTCTAGTGTATGACACACAGGGGGTCCCCGACC 3370

Db 550 ACATCTGGGGGAATACCGTGAATGTCTCCAGTGTATGACACAGCTGGAGTTCTCGACC 609

QY 3371 GAATCAGGTGACACAGGAGCTTACACAGGTCTAGCTGCAAGGCTACACAGCTGGAGT 3430

Db 610 GAATCAGGTGACTACGGAGCTATACCGAGTTCTAGCTGCCAAGGCTACACAGCTGGAG 669

QY 3431 G-TCGAGGGTGTCTAAGGTGAAGGCAAGGGGAGATGACACCTACTTCTCAATGGG 3489

Db 670 GCCCGAGGGTGTCTAAGGTGAAGGCAAGGGGAGATGAC--ACATACATCTCAAGGGG 727

QY 3490 GGGCCAGCAGTTAACAGG 3508

Db 728 GGCACCGACAGGTAGCAAG 746

RESULT 7

BI685206

LOCUS 743 bp mRNA linear EST 18-SEP-2001

DEFINITION 603310213F1 NCI\_CGAP\_Mam6 Mus musculus cDNA clone IMAGE:5346147 5', mRNA sequence.

ACCESSION BI685206

VERSION BI685206.1 GI:15647834

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 743)

AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Jeffrey Green M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLAM1879 row: j column: 04  
High quality sequence stop: 741.

FEATURES

source Location/Qualifiers

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/dev\_stage="5 months"

/lab\_host="DH10B"

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BASE COUNT 149 a 208 c 213 g 173 t

ORIGIN

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Best Local Similarity 87.7%; Pred. No. 9.8e-117;

Matches 634; Conservative 0; Mismatches 87; Indels 2; Gaps 2;

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QY 2484 CTTCCTGCACATCAGCAGCATCGGGAAGTTGGCCATGATCTTTGTCTTGGGGCTCATCTA 2543

Db 83 CTTCCTACACATCAGCAGCATCGGCAAGCTGGCCATGACCTTCATCTTGGGGTTCACCTA 142

QY 2544 TTTGGTGTGCTTCTGCTGGGTCCCCAGCCGCTTCTTTGACAACTATGACCTACTGCT 2603

Db 143 CTTCGTGCTGCTTCTGCTGGTCCCCGCCGCATCTTTGACAACTATGATCTACTGCT 202

QY 2604 TGGCTGCCATGGCTTGGCTTCTTCCATGAGACCTTTGATGGGCTGGACTGTCCAGCTGC 2663

Db 203 TGGCTGCCATGGCTTGGCTTCTTCCATGAGACCTTTGATGGGCTGGACTGTCCAGCTGT 262

QY 2664 AGGGAGGGTGGCCCTCAAAATATATGACCCCTGTGATCTTCTGCTGCTTTCGCGTGGCGCT 2723

Db 263 GGGAGGGTAGCGCTCAAAATATATGACCCCGTGATCTGCTGCTTTCGCGCTGGCACT 322

QY 2724 GTATCTGCATGCTCAGCAGGTGGAATCGACTGCCCGCTTAACTTCTCTTGGAACTACA 2783

Db 323 GTATCTGCATGTCACAAACAGGTGGAATCGACTGCCCGCTTAACTTCTCTTGGAACTACA 382

QY 2784 GGCAACAGGGGAAAAAGAGAGATGGAGAGCTACAGGATACAAACCGGAGGCTGCTGCA 2843

Db 383 GGCAACAGGGGAGAGAGAGATGGAGAGCTACAGGATACAAACCGGAGGTTGCTGCA 442

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Db 443 TAACATCTCTCCCAAGAGCTGGCGGCCACCTTCTTGGCCGGGAGCGCGCAACGATGA 502

QY 2904 ACTCTACTATCATGCTGCTGAGTGTGCTGCTGTTATGTTTGGCTTCCATTCGCAACTCTC 2963

Db 503 GCTGTACTACCATGCTGTGTAATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 562

QY 2964 TGAGTCTTATGTGAGCTGGAGCAACAAATGAGGTGGCGAGTGGCTGCTGCTGCTGCTCA 3023

Db 563 GGAGTCTTACGTGGAGCTCGAGCAACACAGAGGGGCTGGAGTGGCTGCTGCTGCTCA 622

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Db 623 TGAGATCATGCGCAGACTTTGACGAGATCATGCTGAGGAGAGATTCGCGCAG-TGGAGAA 681

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QY 3144 TCA 3146

Db 741 CCA 743

RESULT 8

LOCUS BG287169

DEFINITION BG287169 796 bp mRNA linear EST 21-FEB-2001

ACCESSION BG287169

VERSION BG287169.1 GI:13040741

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 796)

AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: c9apbs-r@mail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
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Matches 613; Conservative 0; Mismatches 14; Indels 5; Gaps 5;  
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QY 3040 TTGTGATGATATTCAGCGAGGAGCGGTTCGGCAGCTGGAAGATCAAGACGATTTGGT 3099  
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Db 120 -TTGATGAGATATTCAGCGAGGAGCGGTTCGGCAGCTGGAAGATCAAGACGAT-TGGT 177  
QY 3100 AGCACCTACATGGTGGCTCAGGGCTGAACGCCAGCACCTACGATCAGTGGGCGCGTCC 3159  
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Db 178 AGCACCTACATGGTGGCTCAGGGCTGAACGCCAGCACCTACGATCAGTGGGCGCGTCC 237  
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Db 238 CACATCACTCCCTGGTGTACTACGCCATCGGGCTCATGAGCAGATGAAGCACATCAAT 297  
QY 3220 GAGCAGTCCCTTCAACATTTCCAGATGAAGATTTGGGCTGACATGGGCCAGTGGTGGCA 3279  
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QY 3280 GGTGTATCGGGGCTCGGAAGCCACAGATGACATCTGGGGGACACAGTGAATGTCTCT 3339  
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Db 358 GGTGTATCGGGGCTCGGAAGCCACAGATGACATCTGGGGGACACAGTGAATGTCTCT 417  
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Db 418 AGTCGTATGACAGCAGCGGGGTCCCGGACCGAATCCAGGTGACCCAGCACCTGTACCCAG 477  
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ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
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1 (bases 1 to 581)  
AUTHORS  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.  
TITLE  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
JOURNAL  
MEDLINE  
COMMENT  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR3&td=MR3-HR0999-070201-003-h04&t3=2001-02-07&t4=1>)  
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No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."  
BASE COUNT 118 a 157 c 199 g 106 t 1 others  
ORIGIN  
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Db 136 TGGTACGTGAGGTACACAGGTGTGAATGTGAACATGCCGCTGGGCATCCACAGCGGCGCG 195  
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mRNA sequence.
ACCESSION B1255147
VERSION B1255147.1 GI:14808265
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 790)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/;
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Arrayed by: Life Technologies, Inc.
cDNA Library Sequenced by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11298 row: d column: 03
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Average insert size 1.4 kb. Library prepared by Life
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ORIGIN
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QY 3250 ATTGGGCTGAACA-TGGGCCCCAGTCGTGGCAGGTGTCTATCGGGGCTCGGAAGCCACAGTA 3308
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ACCESSION BQ231940
VERSION BQ231940.1 GI:20413340
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 905)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/;
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
```

COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: c9apbs@email.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLNL3345 row: p column: 01  
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FEATURES

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Average insert size 2.5 kb. Library enriched for  
full-length clones and constructed by Life Technologies.  
Note: this is a NIH\_MGC Library."  
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Db 481 CACAAATTCAGCTGAAGGGACCAAGTGGGCAT 514

RESULT 12

BM943080/c  
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DEFINITION  
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607 bp mRNA linear EST 29-APR-2002  
UI-M-CGOp-beo-d-02-0-UI 5', mRNA sequence.

ACCESSION

BM943080.1 GI:19402943

VERSION

KEYWORDS

SOURCE

ORGANISM

house mouse.  
Mus musculus

REFERENCE

AUTHORS

TITLE

1 (bases 1 to 607)  
Bonaldo,M.F., Lennon,G. and Soares,M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)

JOURNAL

MEDLINE

COMMENT

Contact: Chin, H  
National Institute of Mental Health  
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD  
20892-9643, USA  
Tel: 301 443 1706  
Fax: 301 443 9890  
Email: mestr@mail.nih.gov

Tissue Procurement: Dr. Xin-Yuan Fu, Yale University School of  
Medicine  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.resgen.com).

Seq primer: M13 REVERSE.  
Location/Qualifiers  
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ultimately derived from mouse retina tissue libraries at  
various stages of development. For a detailed description  
of the library from which this clone was derived, please  
visit our web site at brainest.eng.uiowa.edu. The tissue  
for this library was contributed by Dr. Xin-Yuan Fu, Yale  
University School of Medicine"

FEATURES

source

BASE COUNT 136 a 180 c 162 g 126 t 3 others  
ORIGIN  
Query Match 13.9%; Score 494.8; DB 14; Length 607;  
Best Local Similarity 88.9%; Pred. No. 5.9e-102;  
Matches 547; Conservative 0; Mismatches 60; Indels 8; Gaps 1;  
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Db 427 CTGTATCTGATGCTCAGCAGGTGAATCAGCTGCCCGCTAACTTCCTCTCGTGAAGCTA 368  
QY 2782 CAGGCACAGGGGAAAAGAGGAGATGAGGAGCTACAGCATACACCGGAGCTGCTG 2841  
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RESULT 13
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AUTHORS
TITLE
JOURNAL
COMMENT
MIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No si sequence available.
This clone (DKFZp761N2323) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
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RESULT 14
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DEFINITION
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KEYWORDS
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ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
WashU-HHMI Mouse EST Project
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LiNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:407635
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High quality sequence stop: 417.
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FEATURES
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QY	1544	TCACTCGGGCAACACTGCAGTACCTGAAACGGGGACTACGA-AGTGGAGCCAGGCCGCTGGT	1602
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Job time : 3447.62 secs